



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 15, 2023 – 12:49 PM JST

PDB ID : 6J0W
Title : Crystal Structure of Yeast Rtt107 and Nse6
Authors : Wan, B.; Wu, J.; Lei, M.
Deposited on : 2018-12-27
Resolution : 2.40 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 ⓘ 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
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

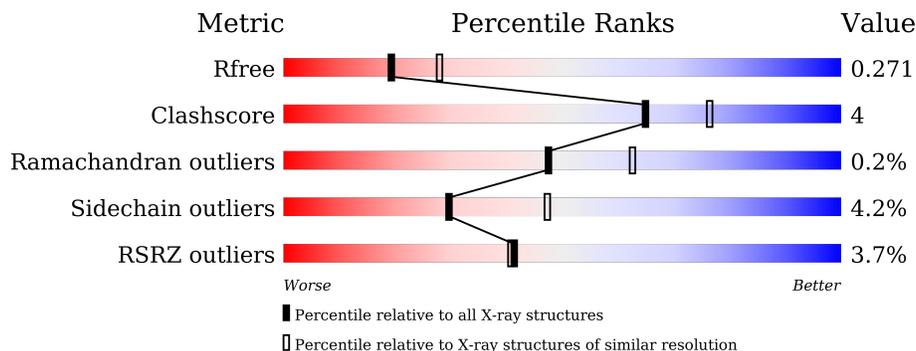
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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	513	 82% 7% • 10%
1	B	513	 77% 11% • 11%
2	C	29	 52% 21% • 24%
2	D	29	 62% 34% •

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 7963 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 Regulator of Ty1 transposition protein 107.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	460	3772	2458	617	679	18	0	0	0
1	B	457	3750	2446	614	672	18	0	0	0

- Molecule 2 is a protein called Peptide from DNA repair protein KRE29.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	C	22	169	105	26	38	0	0	0
2	D	29	222	137	33	52	0	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	26	Total 26	O 26	0	0
3	B	18	Total 18	O 18	0	0
3	C	2	Total 2	O 2	0	0
3	D	4	Total 4	O 4	0	0

Chain D: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	71.78Å 101.42Å 86.56Å 90.00° 108.57° 90.00°	Depositor
Resolution (Å)	45.71 – 2.40 82.05 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.6 (45.71-2.40) 99.6 (82.05-2.40)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.09 (at 2.40Å)	Xtrriage
Refinement program	PHENIX 1.13_2998	Depositor
R, R_{free}	0.218 , 0.271 0.219 , 0.271	Depositor DCC
R_{free} test set	2263 reflections (4.91%)	wwPDB-VP
Wilson B-factor (Å ²)	42.0	Xtrriage
Anisotropy	0.293	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 51.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	7963	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.45% 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	0.48	0/3878	0.61	0/5262
1	B	0.46	0/3856	0.60	1/5232 (0.0%)
2	C	0.53	0/172	0.78	0/234
2	D	0.52	0/227	0.67	0/310
All	All	0.47	0/8133	0.61	1/11038 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	380	LEU	CA-CB-CG	5.07	126.96	115.30

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	A	3772	0	3745	19	0
1	B	3750	0	3727	41	0
2	C	169	0	153	4	0
2	D	222	0	194	12	0
3	A	26	0	0	0	0
3	B	18	0	0	0	0
3	C	2	0	0	0	0
3	D	4	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	7963	0	7819	64	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 4.

All (64) 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:385:THR:OG1	1:B:426:LYS:HD2	1.41	1.18
1:B:160:ARG:HH12	2:D:22:GLY:HA3	1.38	0.87
1:B:385:THR:OG1	1:B:426:LYS:CD	2.23	0.85
1:A:256:GLN:HB3	1:A:259:LEU:HD22	1.67	0.76
1:B:109:LEU:HD23	2:D:20:ILE:HA	1.71	0.71
1:B:385:THR:HG1	1:B:426:LYS:HD2	1.54	0.70
1:B:144:ASP:OD2	1:B:346:SER:OG	2.05	0.68
2:D:16:PRO:HB3	2:D:23:PHE:HD1	1.59	0.68
1:B:107:ARG:NH1	2:D:21:SER:HA	2.14	0.62
1:B:392:ARG:HH12	2:D:19:GLN:HG3	1.63	0.62
1:B:160:ARG:NH1	2:D:22:GLY:HA3	2.14	0.60
1:B:166:VAL:O	1:B:206:PRO:HD3	2.01	0.60
1:B:160:ARG:HH12	2:D:22:GLY:CA	2.12	0.59
1:B:392:ARG:NH1	2:D:19:GLN:HG3	2.17	0.58
2:C:29:PRO:HG2	2:C:32:VAL:HG23	1.86	0.57
1:A:131:LYS:NZ	1:A:400:GLU:OE2	2.35	0.56
1:B:145:LEU:HD21	1:B:349:PHE:CD1	2.40	0.56
2:D:17:ASP:OD2	2:D:19:GLN:HG2	2.06	0.55
1:A:447:MET:CE	1:A:482:ILE:HD11	2.38	0.54
1:A:392:ARG:NH1	2:C:19:GLN:OE1	2.40	0.54
1:A:275:PRO:HD3	1:A:301:LEU:HB2	1.90	0.53
1:A:211:TYR:CD2	1:A:219:LEU:HG	2.44	0.53
1:A:387:TYR:O	1:A:392:ARG:HD2	2.07	0.53
1:A:391:GLN:O	1:A:395:ILE:HG12	2.10	0.52
1:B:321:ILE:HD11	1:B:348:LEU:HD21	1.91	0.52
1:B:316:ASP:N	1:B:316:ASP:OD1	2.43	0.52
1:B:14:ILE:HB	1:B:42:ILE:HD13	1.92	0.52
1:B:113:MET:HA	1:B:123:ARG:HG3	1.94	0.50
1:B:270:HIS:HB3	1:B:317:ILE:HA	1.94	0.49
1:B:109:LEU:CD2	2:D:20:ILE:HA	2.40	0.49
1:A:85:VAL:HG13	1:A:91:ILE:HB	1.95	0.49
1:B:385:THR:CB	1:B:426:LYS:CD	2.92	0.48
1:B:436:ASP:HB3	1:B:439:ASN:HB2	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:244:GLU:O	1:A:248:GLY:HA3	2.15	0.47
1:B:211:TYR:CD2	1:B:219:LEU:HG	2.50	0.47
1:A:447:MET:HE2	1:A:482:ILE:HD11	1.97	0.47
1:B:277:LEU:HD23	1:B:323:HIS:HB2	1.96	0.46
1:B:120:HIS:O	1:B:123:ARG:HB3	2.17	0.45
1:B:385:THR:CB	1:B:426:LYS:HD3	2.47	0.45
1:B:277:LEU:CD2	1:B:323:HIS:HB2	2.47	0.44
1:A:426:LYS:HG3	2:C:15:VAL:HG11	1.97	0.44
1:A:392:ARG:NH2	2:C:17:ASP:OD2	2.49	0.44
1:A:254:SER:OG	1:A:255:SER:N	2.49	0.44
1:A:325:ALA:HB2	1:A:369:PRO:O	2.18	0.44
1:B:210:LEU:HG	1:B:286:PHE:CZ	2.53	0.44
2:D:16:PRO:HB3	2:D:23:PHE:CD1	2.46	0.43
1:B:166:VAL:CG1	1:B:173:ILE:HD11	2.48	0.43
1:A:395:ILE:HG21	1:A:395:ILE:HD12	1.81	0.43
1:B:385:THR:HB	1:B:426:LYS:HD3	2.00	0.43
1:B:382:VAL:HG23	1:B:383:ALA:O	2.19	0.43
1:B:72:VAL:O	1:B:93:VAL:HA	2.19	0.43
1:A:68:THR:HA	1:A:475:MET:HE2	2.01	0.42
1:B:110:ARG:HB3	2:D:20:ILE:HD11	2.01	0.42
1:B:166:VAL:HG11	1:B:174:ILE:HD11	2.01	0.42
1:B:69:VAL:H	1:B:475:MET:HE1	1.84	0.42
1:B:232:GLN:O	1:B:234:THR:N	2.52	0.42
1:B:454:MET:HE1	1:B:482:ILE:HG22	2.02	0.41
1:B:261:PRO:O	1:B:263:LYS:HG3	2.20	0.41
1:A:447:MET:HE3	1:A:482:ILE:HD11	2.02	0.41
1:A:447:MET:H	1:A:447:MET:HG3	1.71	0.41
1:B:4:SER:HB3	1:B:35:ASN:OD1	2.21	0.40
1:B:145:LEU:HD21	1:B:349:PHE:CE1	2.56	0.40
1:B:69:VAL:H	1:B:475:MET:CE	2.34	0.40
1:B:451:GLN:HB3	1:B:459:LEU:HD12	2.02	0.40

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	454/513 (88%)	442 (97%)	12 (3%)	0	100	100
1	B	451/513 (88%)	417 (92%)	33 (7%)	1 (0%)	47	62
2	C	18/29 (62%)	16 (89%)	2 (11%)	0	100	100
2	D	27/29 (93%)	23 (85%)	3 (11%)	1 (4%)	3	2
All	All	950/1084 (88%)	898 (94%)	50 (5%)	2 (0%)	47	62

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	19	GLN
1	B	233	ASP

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	428/480 (89%)	410 (96%)	18 (4%)	30	47
1	B	425/480 (88%)	412 (97%)	13 (3%)	40	60
2	C	21/27 (78%)	18 (86%)	3 (14%)	3	4
2	D	27/27 (100%)	23 (85%)	4 (15%)	3	3
All	All	901/1014 (89%)	863 (96%)	38 (4%)	30	47

All (38) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	9	GLN
1	A	67	GLN
1	A	68	THR
1	A	113	MET
1	A	124	ASP
1	A	160	ARG

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Mol	Chain	Res	Type
1	A	201	TRP
1	A	219	LEU
1	A	228	GLU
1	A	239	LEU
1	A	257	LEU
1	A	259	LEU
1	A	265	LEU
1	A	374	LEU
1	A	377	SER
1	A	380	LEU
1	A	395	ILE
1	A	465	ARG
1	B	108	HIS
1	B	123	ARG
1	B	130	SER
1	B	143	SER
1	B	159	ASN
1	B	207	ILE
1	B	265	LEU
1	B	281	THR
1	B	324	SER
1	B	374	LEU
1	B	380	LEU
1	B	382	VAL
1	B	451	GLN
2	C	15	VAL
2	C	27	LEU
2	C	37	ARG
2	D	14	THR
2	D	15	VAL
2	D	25	SER
2	D	37	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	112	ASN
1	A	362	GLN
1	A	439	ASN
1	B	67	GLN
1	B	159	ASN
1	B	268	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 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

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	460/513 (89%)	0.01	4 (0%) 84 82	16, 37, 72, 114	0
1	B	457/513 (89%)	0.39	18 (3%) 39 38	23, 51, 90, 111	0
2	C	22/29 (75%)	1.32	6 (27%) 0 0	49, 78, 103, 107	0
2	D	29/29 (100%)	1.55	8 (27%) 0 0	53, 83, 95, 99	0
All	All	968/1084 (89%)	0.26	36 (3%) 41 41	16, 45, 90, 114	0

All (36) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	20	ILE	5.9
2	D	23	PHE	5.3
2	D	41	ASP	5.2
2	C	28	ILE	4.2
2	D	21	SER	4.2
2	D	22	GLY	3.9
1	B	339	GLU	3.9
2	D	19	GLN	3.8
1	B	314	PHE	3.7
1	A	439	ASN	3.5
2	C	26	PRO	3.3
1	A	201	TRP	3.2
2	C	32	VAL	3.0
1	B	64	PHE	3.0
1	B	60	PHE	2.8
1	B	65	GLY	2.7
1	B	59	TRP	2.6
1	B	2	SER	2.5
1	B	68	THR	2.4
2	C	35	TYR	2.4
1	B	440	ALA	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	30	LYS	2.2
1	B	70	HIS	2.2
1	A	438	GLN	2.2
2	C	30	THR	2.2
1	B	307	LEU	2.2
2	C	27	LEU	2.2
1	B	475	MET	2.2
1	A	175	ALA	2.2
1	B	439	ASN	2.2
2	D	30	THR	2.1
1	B	312	GLN	2.1
1	B	54	LYS	2.1
2	D	25	SER	2.0
1	B	31	LEU	2.0
1	B	437	PRO	2.0

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.