Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 10:51 AM GMT

PDB ID	:	3ND2
Title	:	Structure of Yeast Importin-beta (Kap95p)
Authors	:	Forwood, J.K.; Kobe, B.
Deposited on	:	2010-06-06
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
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

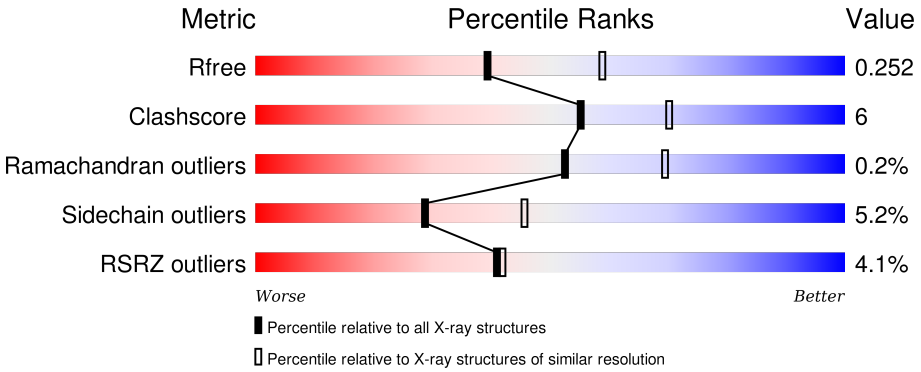
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

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}	91344	2919 (2.40-2.40)
Clashscore	102246	3407 (2.40-2.40)
Ramachandran outliers	100387	3351 (2.40-2.40)
Sidechain outliers	100360	3352 (2.40-2.40)
RSRZ outliers	91569	2928 (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 on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. 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	861	4% 84% 14%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 6759 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 Importin subunit beta-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	861	Total	C	N	O	S	0	0	0
			6653	4206	1100	1311	36			

- Molecule 2 is water.

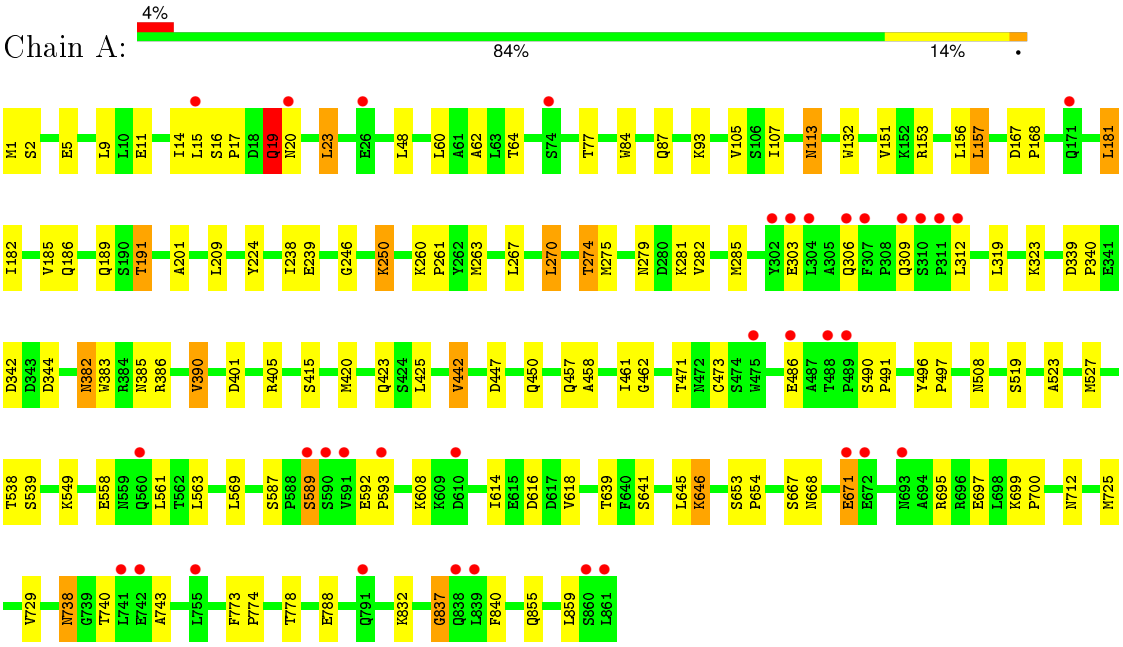
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	106	Total	O	0	0
			106	106		

3 Residue-property plots (i)

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.

- Molecule 1: Importin subunit beta-1

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	58.84Å 128.27Å 69.05Å 90.00° 102.68° 90.00°	Depositor
Resolution (Å)	29.83 – 2.40 29.82 – 2.40	Depositor EDS
% Data completeness (in resolution range)	97.1 (29.83-2.40) 97.1 (29.82-2.40)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.47 (at 2.39Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.213 , 0.267 0.201 , 0.252	Depositor DCC
R_{free} test set	1901 reflections (5.28%)	DCC
Wilson B-factor (Å^2)	45.5	Xtriage
Anisotropy	0.759	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 32.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.34$	Xtriage
Outliers	0 of 37892 reflections	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	6759	wwPDB-VP
Average B, all atoms (Å^2)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.88% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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	0.54	4/6767 (0.1%)	0.60	3/9200 (0.0%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	19	GLN	CG-CD	16.87	1.89	1.51
1	A	19	GLN	CD-NE2	12.94	1.65	1.32
1	A	23	LEU	CG-CD2	7.82	1.80	1.51
1	A	20	ASN	CG-OD1	5.41	1.35	1.24

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	19	GLN	CG-CD-OE1	12.75	147.10	121.60
1	A	19	GLN	CG-CD-NE2	-9.78	93.23	116.70
1	A	157	LEU	CA-CB-CG	5.51	127.96	115.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-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 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	6653	0	6607	84	0
2	A	106	0	0	1	0
All	All	6759	0	6607	84	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.

All (84) 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:23:LEU:CG	1:A:23:LEU:CD2	1.80	1.55
1:A:19:GLN:CD	1:A:19:GLN:CG	1.89	1.40
1:A:738:ASN:HD21	1:A:740:THR:HG22	1.18	1.09
1:A:738:ASN:ND2	1:A:740:THR:HG22	1.79	0.96
1:A:725:MET:O	1:A:729:VAL:HG23	1.83	0.78
1:A:729:VAL:HG22	1:A:778:THR:HG21	1.71	0.72
1:A:23:LEU:CD2	1:A:23:LEU:CB	2.68	0.68
1:A:60:LEU:O	1:A:64:THR:HG23	1.95	0.67
1:A:19:GLN:NE2	1:A:19:GLN:CG	2.58	0.66
1:A:382:ASN:HB3	1:A:385:ASN:HD22	1.61	0.65
1:A:740:THR:HG23	1:A:743:ALA:H	1.62	0.65
1:A:14:ILE:HD11	1:A:60:LEU:HD11	1.78	0.64
1:A:1:MET:HG2	1:A:5:GLU:HG3	1.81	0.62
1:A:654:PRO:HD3	1:A:695:ARG:HH21	1.64	0.60
1:A:558:GLU:OE1	1:A:608:LYS:HE3	2.02	0.60
1:A:279:ASN:HD22	1:A:282:VAL:HG23	1.68	0.59
1:A:699:LYS:HB3	1:A:700:PRO:HD3	1.84	0.58
1:A:87:GLN:HG3	2:A:962:HOH:O	2.03	0.58
1:A:738:ASN:HD21	1:A:740:THR:CG2	2.07	0.57
1:A:19:GLN:CD	1:A:19:GLN:CB	2.73	0.56
1:A:668:ASN:ND2	1:A:712:ASN:HD21	2.02	0.56
1:A:646:LYS:O	1:A:646:LYS:HE3	2.05	0.56
1:A:592:GLU:CD	1:A:592:GLU:H	2.11	0.54
1:A:209:LEU:HD12	1:A:250:LYS:HB3	1.90	0.54
1:A:185:VAL:HG11	1:A:224:TYR:HE2	1.74	0.53
1:A:84:TRP:O	1:A:93:LYS:HE3	2.09	0.53
1:A:420:MET:HG3	1:A:458:ALA:HB1	1.92	0.52
1:A:382:ASN:HD22	1:A:383:TRP:N	2.08	0.52
1:A:182:ILE:O	1:A:186:GLN:HG3	2.11	0.51
1:A:303:GLU:HB3	1:A:312:LEU:HD11	1.92	0.51
1:A:339:ASP:HB3	1:A:342:ASP:HB2	1.93	0.51
1:A:641:SER:O	1:A:645:LEU:HG	2.09	0.51
1:A:587:SER:C	1:A:589:SER:H	2.14	0.51
1:A:263:MET:CE	1:A:267:LEU:CB	2.89	0.50
1:A:167:ASP:OD2	1:A:738:ASN:HB2	2.11	0.50
1:A:561:LEU:HD11	1:A:569:LEU:HD22	1.93	0.50
1:A:457:GLN:O	1:A:461:ILE:HG12	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:340:PRO:HB2	1:A:425:LEU:HD23	1.94	0.49
1:A:209:LEU:CD1	1:A:250:LYS:HB3	2.42	0.49
1:A:837:GLY:HA3	1:A:840:PHE:CD2	2.48	0.49
1:A:497:PRO:HG3	1:A:538:THR:HG21	1.93	0.49
1:A:263:MET:HE2	1:A:267:LEU:HB2	1.95	0.49
1:A:671:GLU:HB2	1:A:712:ASN:OD1	2.13	0.48
1:A:263:MET:CE	1:A:267:LEU:HB3	2.43	0.48
1:A:2:SER:OG	1:A:5:GLU:HG2	2.14	0.48
1:A:48:LEU:HD13	1:A:62:ALA:HB2	1.96	0.48
1:A:471:THR:HG23	1:A:519:SER:OG	2.13	0.48
1:A:654:PRO:HD3	1:A:695:ARG:NH2	2.29	0.47
1:A:386:ARG:O	1:A:390:VAL:HG23	2.14	0.47
1:A:11:GLU:O	1:A:15:LEU:HB2	2.14	0.47
1:A:263:MET:HE3	1:A:267:LEU:HB3	1.96	0.47
1:A:263:MET:HA	1:A:263:MET:HE2	1.97	0.47
1:A:773:PHE:HB3	1:A:774:PRO:HD3	1.97	0.46
1:A:667:SER:O	1:A:671:GLU:HA	2.15	0.46
1:A:23:LEU:CD2	1:A:23:LEU:HG	2.21	0.46
1:A:405:ARG:HH11	1:A:442:VAL:HG22	1.81	0.45
1:A:671:GLU:CB	1:A:712:ASN:OD1	2.65	0.45
1:A:263:MET:HA	1:A:267:LEU:HB2	1.99	0.45
1:A:270:LEU:O	1:A:274:THR:HG23	2.16	0.45
1:A:263:MET:CE	1:A:267:LEU:HB2	2.47	0.44
1:A:508:ASN:OD1	1:A:549:LYS:HE2	2.17	0.44
1:A:447:ASP:HB3	1:A:450:GLN:HB3	2.00	0.43
1:A:490:SER:HA	1:A:491:PRO:HD3	1.91	0.43
1:A:113:ASN:ND2	1:A:157:LEU:HD11	2.34	0.43
1:A:105:VAL:HG12	1:A:151:VAL:HG22	2.01	0.43
1:A:189:GLN:HG3	1:A:191:THR:HG22	2.01	0.43
1:A:281:LYS:HD2	1:A:281:LYS:HA	1.86	0.43
1:A:855:GLN:NE2	1:A:859:LEU:HD11	2.34	0.42
1:A:260:LYS:HB3	1:A:261:PRO:HD3	1.99	0.42
1:A:738:ASN:HD22	1:A:740:THR:H	1.67	0.42
1:A:246:GLY:HA2	1:A:285:MET:CE	2.50	0.42
1:A:270:LEU:O	1:A:274:THR:CG2	2.68	0.42
1:A:16:SER:HA	1:A:17:PRO:HD3	1.87	0.42
1:A:156:LEU:HD13	1:A:201:ALA:HB2	2.01	0.42
1:A:209:LEU:HD12	1:A:250:LYS:HD2	2.02	0.42
1:A:167:ASP:HA	1:A:168:PRO:HD3	1.93	0.41
1:A:592:GLU:N	1:A:593:PRO:HD2	2.35	0.41
1:A:263:MET:HE3	1:A:267:LEU:CB	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:523:ALA:O	1:A:527:MET:HG2	2.20	0.41
1:A:462:GLY:HA3	1:A:473:CYS:SG	2.61	0.41
1:A:614:ILE:O	1:A:618:VAL:HG23	2.21	0.40
1:A:342:ASP:O	1:A:344:ASP:N	2.48	0.40
1:A:263:MET:HE2	1:A:267:LEU:CB	2.51	0.40
1:A:181:LEU:HD23	1:A:181:LEU:HA	1.93	0.40

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	859/861 (100%)	836 (97%)	21 (2%)	2 (0%)	52 69

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	671	GLU
1	A	837	GLY

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	726/726 (100%)	688 (95%)	38 (5%)	29 45

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

Mol	Chain	Res	Type
1	A	9	LEU
1	A	19	GLN
1	A	77	THR
1	A	107	ILE
1	A	113	ASN
1	A	132	TRP
1	A	153	ARG
1	A	181	LEU
1	A	191	THR
1	A	238	ILE
1	A	239	GLU
1	A	250	LYS
1	A	270	LEU
1	A	274	THR
1	A	275	MET
1	A	306	GLN
1	A	309	GLN
1	A	319	LEU
1	A	323	LYS
1	A	382	ASN
1	A	390	VAL
1	A	401	ASP
1	A	415	SER
1	A	423	GLN
1	A	442	VAL
1	A	486	GLU
1	A	496	TYR
1	A	539	SER
1	A	563	LEU
1	A	589	SER
1	A	616	ASP
1	A	639	THR
1	A	646	LYS
1	A	653	SER
1	A	697	GLU
1	A	738	ASN
1	A	788	GLU
1	A	832	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	113	ASN
1	A	215	ASN
1	A	279	ASN
1	A	382	ASN
1	A	385	ASN
1	A	515	ASN
1	A	650	GLN
1	A	668	ASN
1	A	722	ASN
1	A	738	ASN
1	A	781	GLN

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 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

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	A	861/861 (100%)	0.04	35 (4%) 41 42	32, 51, 86, 119	0

All (35) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	312	LEU	5.5
1	A	839	LEU	5.0
1	A	307	PHE	4.9
1	A	311	PRO	4.6
1	A	306	GLN	4.3
1	A	302	TYR	4.1
1	A	310	SER	4.1
1	A	20	ASN	3.8
1	A	671	GLU	3.8
1	A	741	LEU	3.7
1	A	489	PRO	3.7
1	A	860	SER	3.7
1	A	590	SER	3.5
1	A	861	LEU	3.5
1	A	486	GLU	3.2
1	A	591	VAL	3.2
1	A	488	THR	3.1
1	A	838	GLN	2.9
1	A	755	LEU	2.8
1	A	15	LEU	2.8
1	A	742	GLU	2.6
1	A	672	GLU	2.6
1	A	309	GLN	2.6
1	A	304	LEU	2.5
1	A	589	SER	2.5
1	A	74	SER	2.4
1	A	593	PRO	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	475	TRP	2.3
1	A	693	ASN	2.2
1	A	610	ASP	2.2
1	A	26	GLU	2.1
1	A	303	GLU	2.1
1	A	560	GLN	2.1
1	A	171	GLN	2.1
1	A	791	GLN	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 carbohydrates 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.