



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 7MW0 / pdb_00007mw0
Title : Crystal structure of Homo sapiens NUP93 solenoid (residues 174-819)
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Deposited on : 2021-05-15
Resolution : 2.00 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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

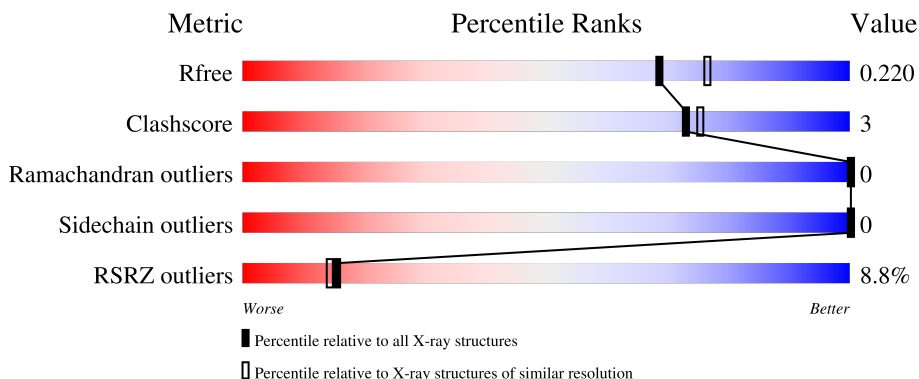
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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}	180053	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	672	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 10316 atoms, of which 5058 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 Nuclear pore complex protein Nup93.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	624	Total	C	H	N	O	S	0	0	0
			10114	3214	5052	878	944	26			

There are 26 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	148	SER	-	expression tag	UNP Q8N1F7
A	149	SER	-	expression tag	UNP Q8N1F7
A	150	GLY	-	expression tag	UNP Q8N1F7
A	151	LEU	-	expression tag	UNP Q8N1F7
A	152	ASN	-	expression tag	UNP Q8N1F7
A	153	ASP	-	expression tag	UNP Q8N1F7
A	154	ILE	-	expression tag	UNP Q8N1F7
A	155	PHE	-	expression tag	UNP Q8N1F7
A	156	GLU	-	expression tag	UNP Q8N1F7
A	157	ALA	-	expression tag	UNP Q8N1F7
A	158	GLN	-	expression tag	UNP Q8N1F7
A	159	LYS	-	expression tag	UNP Q8N1F7
A	160	ILE	-	expression tag	UNP Q8N1F7
A	161	GLU	-	expression tag	UNP Q8N1F7
A	162	TRP	-	expression tag	UNP Q8N1F7
A	163	HIS	-	expression tag	UNP Q8N1F7
A	164	GLU	-	expression tag	UNP Q8N1F7
A	165	GLY	-	expression tag	UNP Q8N1F7
A	166	SER	-	expression tag	UNP Q8N1F7
A	167	ALA	-	expression tag	UNP Q8N1F7
A	168	GLY	-	expression tag	UNP Q8N1F7
A	169	GLY	-	expression tag	UNP Q8N1F7
A	170	SER	-	expression tag	UNP Q8N1F7
A	171	GLY	-	expression tag	UNP Q8N1F7
A	172	GLY	-	expression tag	UNP Q8N1F7
A	173	SER	-	expression tag	UNP Q8N1F7

- Molecule 2 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	H	O	0	0
			10	2	6	2		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	192	Total	O	0	0
			192	192		

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	74.87Å 66.07Å 79.18Å 90.00° 116.28° 90.00°	Depositor
Resolution (Å)	40.00 – 2.00 40.00 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.0 (40.00-2.00) 99.1 (40.00-2.00)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.31 (at 2.00Å)	Xtriage
Refinement program	PHENIX 1.19.1_4122	Depositor
R, R_{free}	0.225 , 0.254 (Not available) , 0.220	Depositor DCC
R_{free} test set	2005 reflections (4.25%)	wwPDB-VP
Wilson B-factor (Å ²)	41.9	Xtriage
Anisotropy	0.238	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 37.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.017 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	10316	wwPDB-VP
Average B, all atoms (Å ²)	63.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.89% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: EDO

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	0.12	0/5156	0.27	0/6963

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	A	5062	5052	5051	32	0
2	A	4	6	6	0	0
3	A	192	0	0	2	0
All	All	5258	5058	5057	32	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 3.

All (32) 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:794:THR:HG22	1:A:798:MET:HE3	1.71	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:794:THR:HG22	1:A:798:MET:CE	2.29	0.62
1:A:436:THR:HG23	1:A:439:GLN:H	1.65	0.61
1:A:544:PRO:CG	1:A:582:MET:HE1	2.31	0.60
1:A:417:LYS:O	1:A:421:VAL:HG13	2.02	0.59
1:A:544:PRO:HG2	1:A:582:MET:HE1	1.84	0.59
1:A:530:ARG:NH1	3:A:1003:HOH:O	2.28	0.57
1:A:286:VAL:N	1:A:287:PRO:CD	2.71	0.53
1:A:780:ASP:N	3:A:1013:HOH:O	2.43	0.52
1:A:757:PHE:HA	1:A:818:MET:HE2	1.92	0.51
1:A:593:ARG:CZ	1:A:605:THR:HG21	2.41	0.50
1:A:757:PHE:CA	1:A:818:MET:HE2	2.44	0.48
1:A:371:LEU:C	1:A:371:LEU:HD23	2.39	0.48
1:A:526:LEU:HD21	1:A:531:LEU:HD13	1.96	0.46
1:A:286:VAL:N	1:A:287:PRO:HD2	2.30	0.46
1:A:178:LEU:HD21	1:A:539:PHE:CG	2.51	0.45
1:A:440:PHE:CZ	1:A:444:LEU:HD11	2.52	0.45
1:A:201:LEU:HD12	1:A:201:LEU:O	2.17	0.45
1:A:731:VAL:HG13	1:A:799:ILE:HD11	1.99	0.44
1:A:235:LEU:HD11	1:A:501:LEU:HD21	1.98	0.44
1:A:308:LEU:HD13	1:A:317:PRO:CB	2.47	0.44
1:A:314:GLU:OE1	1:A:340:ARG:NH1	2.50	0.44
1:A:555:ARG:O	1:A:564:ASN:ND2	2.51	0.43
1:A:655:ALA:O	1:A:658:SER:OG	2.30	0.43
1:A:454:THR:HG22	1:A:454:THR:O	2.18	0.43
1:A:479:LEU:HB3	1:A:489:ALA:HB2	2.02	0.42
1:A:422:CYS:O	1:A:436:THR:HA	2.19	0.42
1:A:220:ILE:N	1:A:220:ILE:HD12	2.34	0.42
1:A:354:GLU:OE1	1:A:367:THR:HG21	2.20	0.41
1:A:319:TRP:CZ2	1:A:345:LEU:HD22	2.55	0.41
1:A:305:LEU:HB3	1:A:306:PRO:HD2	2.02	0.41
1:A:453:PHE:O	1:A:454:THR:C	2.64	0.41

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	616/672 (92%)	606 (98%)	10 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	559/594 (94%)	559 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	280	GLN
1	A	309	GLN
1	A	706	HIS
1	A	819	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	EDO	A	901	-	3,3,3	0.43	0	2,2,2	0.38	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	EDO	A	901	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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(Å ²)	Q<0.9
1	A	624/672 (92%)	0.79	55 (8%) 15 14	33, 60, 98, 125	0

All (55) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	201	LEU	5.4
1	A	453	PHE	5.0
1	A	763	LEU	4.3
1	A	281	ALA	4.0
1	A	454	THR	3.7
1	A	455	VAL	3.7
1	A	286	VAL	3.6
1	A	305	LEU	3.4
1	A	215	LEU	3.4
1	A	734	PHE	3.3
1	A	522	CYS	3.2
1	A	456	ASN	3.2
1	A	379	LEU	3.2
1	A	385	PRO	3.2
1	A	448	TYR	3.1
1	A	343	HIS	3.1
1	A	422	CYS	2.9
1	A	307	GLY	2.9
1	A	760	PHE	2.9
1	A	423	PHE	2.8
1	A	282	GLN	2.7
1	A	449	GLY	2.7
1	A	298	ASN	2.6
1	A	290	TYR	2.6
1	A	790	ARG	2.6
1	A	816	VAL	2.5
1	A	320	ALA	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	276	GLY	2.5
1	A	301	LEU	2.4
1	A	346	GLY	2.4
1	A	313	VAL	2.4
1	A	386	TYR	2.4
1	A	341	ALA	2.4
1	A	603	SER	2.4
1	A	302	PRO	2.3
1	A	306	PRO	2.3
1	A	218	LYS	2.3
1	A	299	ILE	2.3
1	A	785	LEU	2.3
1	A	351	TRP	2.2
1	A	436	THR	2.2
1	A	338	VAL	2.2
1	A	213	ALA	2.2
1	A	279	HIS	2.2
1	A	445	LEU	2.2
1	A	280	GLN	2.1
1	A	316	HIS	2.1
1	A	375	TYR	2.1
1	A	378	ALA	2.1
1	A	196	ILE	2.1
1	A	783	SER	2.1
1	A	817	LEU	2.0
1	A	383	THR	2.0
1	A	605	THR	2.0
1	A	799	ILE	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	EDO	A	901	4/4	0.91	0.12	46,56,59,61	0

6.5 Other polymers [i](#)

There are no such residues in this entry.