



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 08:16 AM GMT

PDB ID : 3DYU
Title : Crystal structure of Snx9PX-BAR (230-595), H32
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Deposited on : 2008-07-28
Resolution : 4.10 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
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) 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

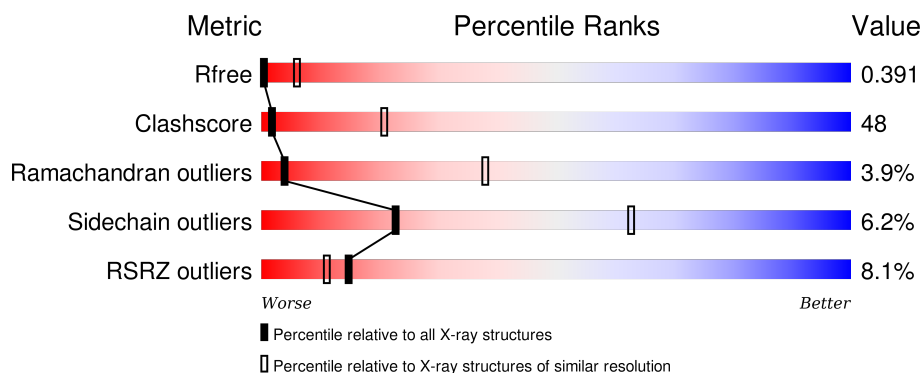
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.10 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	1018 (4.60-3.60)
Clashscore	102246	1117 (4.60-3.60)
Ramachandran outliers	100387	1063 (4.60-3.60)
Sidechain outliers	100360	1049 (4.60-3.60)
RSRZ outliers	91569	1022 (4.60-3.60)

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 $\leq 5\%$. 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	366	<div> <div>5%</div> <div>50%</div> <div>45%</div> <div>• •</div> </div>
1	B	366	<div> <div>6%</div> <div>53%</div> <div>42%</div> <div>5% •</div> </div>
1	C	366	<div> <div>13%</div> <div>49%</div> <div>42%</div> <div>5% •</div> </div>

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 8931 atoms, of which 0 are hydrogens and 0 are deuteriums.

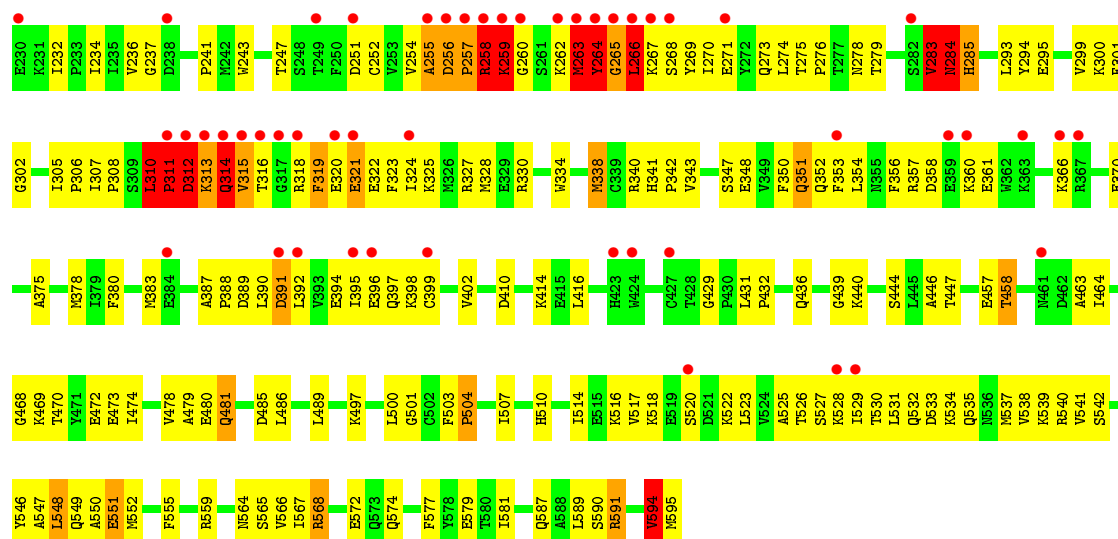
In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Sorting nexin-9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	366	Total	C	N	O	S	0	0	0
			2977	1898	503	556	20			
1	B	366	Total	C	N	O	S	0	0	0
			2977	1898	503	556	20			
1	C	366	Total	C	N	O	S	0	0	0
			2977	1898	503	556	20			



• Molecule 1: Sorting nexin-9



4 Data and refinement statistics

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, α , β , γ	131.76 Å 131.76 Å 569.07 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	32.94 – 4.10 47.42 – 4.10	Depositor EDS
% Data completeness (in resolution range)	89.2 (32.94-4.10) 89.0 (47.42-4.10)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	0.11	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.24 (at 4.14 Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.388 , 0.403 0.391 , 0.391	Depositor DCC
R_{free} test set	682 reflections (4.95%)	DCC
Wilson B-factor (Å ²)	129.3	Xtriage
Anisotropy	0.469	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 71.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	1 of 15467 reflections (0.006%)	Xtriage
F_o, F_c correlation	0.81	EDS
Total number of atoms	8931	wwPDB-VP
Average B, all atoms (Å ²)	153.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.37% 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, 0.375 respectively for untwinned datasets, and 0.333, 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	0.42	0/3044	0.71	6/4100 (0.1%)
1	B	0.43	0/3044	0.65	2/4100 (0.0%)
1	C	0.44	1/3044 (0.0%)	0.67	3/4100 (0.1%)
All	All	0.43	1/9132 (0.0%)	0.68	11/12300 (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	3	6
1	B	0	3
1	C	5	16
All	All	8	25

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	548	LEU	C-N	5.73	1.47	1.34

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	390	LEU	O-C-N	-12.41	102.84	122.70
1	C	548	LEU	O-C-N	10.65	139.75	122.70
1	A	390	LEU	C-N-CA	8.87	143.88	121.70
1	A	390	LEU	CA-C-N	8.63	136.18	117.20
1	C	548	LEU	CA-C-N	-7.93	99.75	117.20

5 of 8 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	503	PHE	CA
1	A	592	PHE	CA
1	A	594	VAL	CA
1	C	266	LEU	CA
1	C	284	ASN	CA

5 of 25 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	503	PHE	Peptide
1	A	504	PRO	Peptide
1	A	508	GLY	Peptide
1	A	591	ARG	Peptide
1	A	592	PHE	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	2977	0	2958	358	0
1	B	2977	0	2958	279	0
1	C	2977	0	2958	369	2
All	All	8931	0	8874	855	2

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 48.

The worst 5 of 855 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:523:LEU:CD2	1:A:529:ILE:HG12	1.50	1.41
1:A:523:LEU:HD22	1:A:529:ILE:CG1	1.53	1.37
1:C:312:ASP:HB2	1:C:313:LYS:CG	1.56	1.33
1:C:255:ALA:CB	1:C:273:GLN:HE21	1.40	1.32
1:C:283:VAL:HG22	1:C:284:ASN:CG	1.51	1.29

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the sym-

metry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:579:GLU:OE2	1:C:579:GLU:OE2[10_455]	1.88	0.32
1:C:457:GLU:OE2	1:C:559:ARG:NH2[10_455]	2.07	0.13

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	364/366 (100%)	313 (86%)	35 (10%)	16 (4%)	3	35
1	B	364/366 (100%)	319 (88%)	34 (9%)	11 (3%)	5	45
1	C	364/366 (100%)	314 (86%)	34 (9%)	16 (4%)	3	35
All	All	1092/1098 (100%)	946 (87%)	103 (9%)	43 (4%)	4	38

5 of 43 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	263	MET
1	A	314	GLN
1	A	315	VAL
1	A	503	PHE
1	A	504	PRO

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	326/326 (100%)	308 (94%)	18 (6%)	27	67
1	B	326/326 (100%)	308 (94%)	18 (6%)	27	67
1	C	326/326 (100%)	301 (92%)	25 (8%)	16	55
All	All	978/978 (100%)	917 (94%)	61 (6%)	23	63

5 of 61 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	416	LEU
1	B	587	GLN
1	C	551	GLU
1	B	434	GLU
1	B	481	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 29 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	443	GLN
1	B	535	GLN
1	C	535	GLN
1	B	481	GLN
1	B	549	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 carbohydrates 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, 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	366/366 (100%)	0.45	19 (5%) 31 23	153, 153, 153, 153	0
1	B	366/366 (100%)	0.44	21 (5%) 27 20	153, 153, 153, 153	0
1	C	366/366 (100%)	0.69	49 (13%) 4 5	153, 153, 153, 153	0
All	All	1098/1098 (100%)	0.53	89 (8%) 15 11	153, 153, 153, 153	0

The worst 5 of 89 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	392	LEU	6.4
1	C	316	THR	6.3
1	C	315	VAL	5.7
1	B	317	GLY	5.5
1	B	318	ARG	5.5

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.