

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

#### Aug 12, 2024 – 08:50 PM EDT

PDB ID : 8TTT

Title: Structure of SNX27 FERM complexed with Fam21A repeat 15 (1124-1140)

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Deposited on : 2023-08-15

Resolution : 2.35 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

Mogul: 1.8.5 (274361), CSD as541be (2020)

Xtriage (Phenix) : 1.13

EDS : 2.37.1

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

 $Refmac \quad : \quad 5.8.0158$ 

CCP4 : 7.0.044 (Gargrove)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

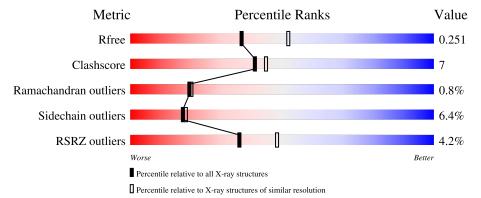
Validation Pipeline (wwPDB-VP) : 2.37.1

### 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 2.35 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 $(\# \mathrm{Entries})$	$\begin{array}{c} {\rm Similar\ resolution} \\ (\#{\rm Entries,\ resolution\ range(\AA)}) \end{array}$
$R_{free}$	130704	1164 (2.36-2.36)
Clashscore	141614	1232 (2.36-2.36)
Ramachandran outliers	138981	1211 (2.36-2.36)
Sidechain outliers	138945	1212 (2.36-2.36)
RSRZ outliers	127900	1150 (2.36-2.36)

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				
1	A	261	4%	77%	20%		
2	В	17	35%	65%			

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:



Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	PEG	A	604	_	-	X	-



## 2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 2258 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-27.

N	/Iol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace			
	1	A	256	Total 2143	As 2	C 1375	N 357	O 394	S 15	2	1	0

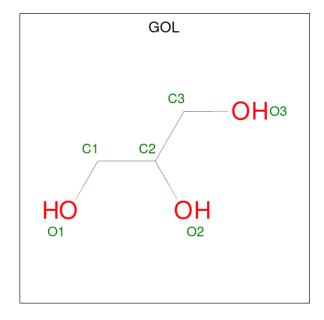
There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	268	SER	-	expression tag	UNP Q96L92
A	269	ASN	-	expression tag	UNP Q96L92
A	270	ALA	-	expression tag	UNP Q96L92

• Molecule 2 is a protein called Fam21A repeat 15 peptide.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace		
2	В	6	Total 44	C 28	N 6	O 10	0	0	0

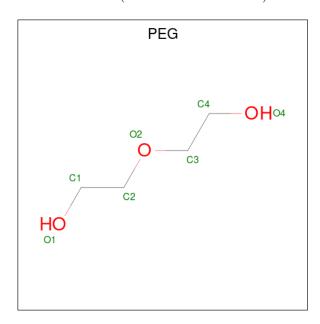
• Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 6 3 3	0	0
3	A	1	Total C O 6 3 3	0	0

 $\bullet \ \, \text{Molecule 4 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$)}. \\$ 



$\mathbf{Mol}$	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 7 4 3	0	0
4	A	1	Total C O 7 4 3	0	0

• Molecule 5 is water.

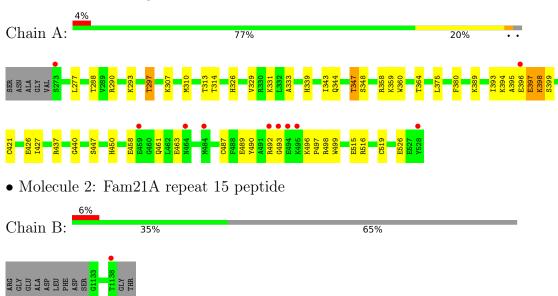
$\mathbf{Mol}$	Chain	Residues	${f Atoms}$	ZeroOcc	AltConf
5	A	45	Total O 45 45	0	0



## 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: Sorting nexin-27





## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	37.57Å 74.37Å 105.23Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	42.95 - 2.35	Depositor
recontion (11)	42.95 - 2.35	EDS
% Data completeness	98.8 (42.95-2.35)	Depositor
(in resolution range)	98.8 (42.95-2.35)	EDS
$R_{merge}$	0.20	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	$1.00 \; (at \; 2.34 \text{Å})$	Xtriage
Refinement program	PHENIX (1.19.2_4158: ???)	Depositor
$R, R_{free}$	0.191 , 0.251	Depositor
it, it free	0.191 , $0.251$	DCC
$R_{free}$ test set	1271  reflections  (9.99%)	wwPDB-VP
Wilson B-factor $(A^2)$	39.1	Xtriage
Anisotropy	0.173	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	$0.35 \; ,  36.5$	EDS
L-test for twinning <sup>2</sup>	$ < L > = 0.50, < L^2> = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	2258	wwPDB-VP
Average B, all atoms $(Å^2)$	44.0	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.

<sup>&</sup>lt;sup>2</sup>Theoretical values of <|L|>,  $<L^2>$  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)

Bond lengths and bond angles in the following residue types are not validated in this section: PEG, GOL, CAF

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	0.47	0/2179	0.64	0/2943	
2	В	0.44	0/44	0.49	0/58	
All	All	0.47	0/2223	0.64	0/3001	

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)	$\mathbf{H}(\mathbf{added})$	Clashes	Symm-Clashes
1	A	2143	0	2071	31	0
2	В	44	0	38	0	0
3	A	12	0	16	1	0
4	A	14	0	20	5	0
5	A	45	0	0	1	0
All	All	2258	0	2145	31	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 7.

All (31) 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:515:GLU:HB3	4:A:604:PEG:H32	1.65	0.78
1:A:519:CAF:HB3	4:A:604:PEG:H41	1.67	0.75
1:A:496:LYS:HG2	1:A:497:PRO:HD2	1.68	0.73
1:A:297:THR:HG21	1:A:333:ALA:O	1.88	0.73
1:A:427:ILE:HG23	3:A:602:GOL:H11	1.74	0.68
1:A:516:ARG:HD3	4:A:604:PEG:H11	1.76	0.66
1:A:492:ARG:HH11	1:A:493:GLY:H	1.46	0.62
1:A:395:ALA:O	1:A:397:GLU:N	2.33	0.61
1:A:331:LYS:HE3	1:A:360:TRP:CE2	2.41	0.56
1:A:288:THR:O	1:A:307:LYS:NZ	2.31	0.54
1:A:516:ARG:HA	4:A:604:PEG:H11	1.90	0.53
1:A:394:LYS:HE3	1:A:394:LYS:HA	1.90	0.51
1:A:426:GLU:HG3	1:A:447:SER:HB3	1.96	0.47
1:A:359:LYS:HG3	1:A:380:PHE:CE1	2.50	0.46
1:A:277:LEU:HD11	1:A:339:HIS:HA	1.97	0.46
1:A:490:TYR:O	1:A:497:PRO:HA	2.17	0.45
1:A:389:LYS:NZ	4:A:603:PEG:H22	2.33	0.44
1:A:277:LEU:HD12	1:A:277:LEU:HA	1.65	0.44
1:A:329:VAL:HG21	1:A:358:ARG:HD3	1.99	0.43
1:A:293:LYS:HA	1:A:293:LYS:HD2	1.90	0.42
1:A:398:LYS:HE2	1:A:421:CYS:SG	2.59	0.42
1:A:440:GLY:HA2	1:A:458:GLU:HG3	2.00	0.42
1:A:310:MET:HG2	1:A:314:THR:HG22	2.01	0.42
1:A:359:LYS:HG3	1:A:380:PHE:HE1	1.83	0.42
1:A:347:THR:OG1	1:A:348:SER:N	2.53	0.41
1:A:498:ARG:HG3	5:A:727:HOH:O	2.21	0.40
1:A:526:GLU:HA	1:A:526:GLU:OE2	2.21	0.40
1:A:489:GLU:HB2	1:A:499:TRP:CD2	2.56	0.40
1:A:492:ARG:HA	1:A:492:ARG:HD2	1.86	0.40
1:A:343:ILE:HD13	1:A:343:ILE:HA	1.88	0.40
1:A:277:LEU:O	1:A:288:THR:HA	2.22	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	253/261 (97%)	244 (96%)	7 (3%)	2 (1%)	19 20
2	В	4/17~(24%)	2 (50%)	2 (50%)	0	100 100
All	All	257/278 (92%)	246 (96%)	9 (4%)	2 (1%)	19 20

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	396	GLU
1	A	463	GLU

#### 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	Rotameric Outliers		Percentiles		
1	A	$230/232 \ (99\%)$	214 (93%)	16 (7%)	15	15		
2	В	5/13 (38%)	5 (100%)	0	100	100		
All	All	235/245 (96%)	219 (93%)	16 (7%)	17	16		

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	290	ARG
1	A	297	THR
1	A	313	THR
1	A	326	HIS
1	A	344	GLN
1	A	347	THR
1	A	364	THR
1	A	375	LEU
1	A	393	ILE
1	A	397	GLU
1	A	398	LYS

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Mol	Chain	Res	Type
1	A	399	SER
1	A	437	ARG
1	A	450[A]	HIS
1	A	450[B]	HIS
1	A	461	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	344	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)

2 non-standard protein/DNA/RNA residues are 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	True	Chain	Dag	Link	В	Bond lengths			Bond angles		
MIOI	Type	Chain	Res	Lilik	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z  > 2	
1	CAF	A	519	1	3,9,10	1.19	0	1,12,14	1.59	0	
1	CAF	A	487	1	3,9,10	0.82	0	1,12,14	2.06	1 (100%)	

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
1	CAF	A	519	1	-	0/0/8/10	-
1	CAF	A	487	1	-	0/0/8/10	-



There are no bond length outliers.

All (1) bond angle outliers are listed below:

$\mathbf{Mol}$	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\mathbf{Observed}(^{o})$	$\operatorname{Ideal}({}^{o})$
1	A	487	CAF	CA-CB-SG	2.06	117.03	112.76

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	519	CAF	1	0

#### 5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

### 5.6 Ligand geometry (i)

4 ligands are 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	Tuno	Chain	Dog	Link	Bond lengths			Bond angles		
MIOI	Type	Chain	nes	LIIIK	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	PEG	A	604	-	6,6,6	0.49	0	5,5,5	0.47	0
3	GOL	A	601	-	5,5,5	0.70	0	5,5,5	0.90	0
4	PEG	A	603	-	6,6,6	0.25	0	5,5,5	0.12	0
3	GOL	A	602	-	5,5,5	1.26	0	5,5,5	0.89	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
4	PEG	A	604	-	-	3/4/4/4	-
3	GOL	A	601	-	-	2/4/4/4	-
4	PEG	A	603	-	-	4/4/4/4	-
3	GOL	A	602	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	601	GOL	O1-C1-C2-C3
4	A	604	PEG	O2-C3-C4-O4
4	A	604	PEG	O1-C1-C2-O2
3	A	602	GOL	C1-C2-C3-O3
3	A	602	GOL	O2-C2-C3-O3
3	A	601	GOL	O1-C1-C2-O2
4	A	603	PEG	C4-C3-O2-C2
4	A	603	PEG	O2-C3-C4-O4
4	A	604	PEG	C4-C3-O2-C2
4	A	603	PEG	O1-C1-C2-O2
4	A	603	PEG	C1-C2-O2-C3

There are no ring outliers.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	604	PEG	4	0
4	A	603	PEG	1	0
3	A	602	GOL	1	0

### 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 $>$	$\# \mathrm{RSRZ}{>}2$	$OWAB(A^2)$	Q<0.9
1	A	254/261 (97%)	0.11	10 (3%) 39 52	28, 40, 71, 120	2 (0%)
2	В	6/17 (35%)	1.85	1 (16%) 1 2	57, 63, 76, 81	0
All	All	$260/278 \ (93\%)$	0.15	11 (4%) 36 48	28, 41, 74, 120	2 (0%)

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	493	GLY	12.2
2	В	1138	THR	5.6
1	A	494	GLU	4.9
1	A	464	ASN	4.4
1	A	492	ARG	3.8
1	A	528	TYR	3.7
1	A	396	GLU	2.8
1	A	459	GLU	2.6
1	A	484	MET	2.6
1	A	495	LYS	2.6
1	A	273	SER	2.2

### 6.2 Non-standard residues in protein, DNA, RNA chains (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,  $95^{th}$  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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q < 0.9
1	CAF	A	487	10/11	0.90	0.22	35,39,76,108	0
1	CAF	A	519	10/11	0.91	0.15	32,40,71,81	0



#### 6.3 Carbohydrates (i)

There are no monosaccharides 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,  $95^{th}$  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	$\operatorname{Res}$	Atoms	RSCC	RSR	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
4	PEG	A	603	7/7	0.83	0.19	47,54,58,61	0
4	PEG	A	604	7/7	0.86	0.32	33,42,48,51	0
3	GOL	A	601	6/6	0.90	0.10	54,56,58,60	0
3	GOL	A	602	6/6	0.90	0.13	34,41,42,42	0

#### 6.5 Other polymers (i)

There are no such residues in this entry.

