Full wwPDB X-ray Structure Validation Report (i)

Nov 22, 2023 – 07:15 PM JST

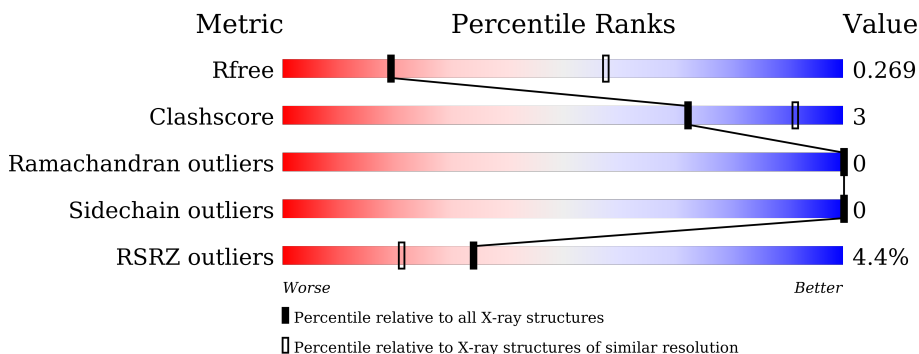|		
PDB ID	:	7XSJ
Title	:	The structure of the Mint1/Munc18-1/syntaxin-1 complex
Authors	:	Feng, W.; Li, W.
Deposited on	:	2022-05-14
Resolution	:	3.20 Å(reported)

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 3.20 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	Percentile Ranks	Value
Rfree		0.269
Clashscore		3
Ramachandran outliers		0
Sidechain outliers		0
RSRZ outliers		4.4%

Worse ... *Better*

▌Percentile relative to all X-ray structures

❘Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1133 (3.20-3.20)
Clashscore	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)
RSRZ outliers	127900	1095 (3.20-3.20)

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	600	3% / 84% / 10% / 6%
2	B	249	6% / 82% / 6% / 12%
3	C	83	5% / 18% / • / 78%

2 Entry composition ⓘ

There are 3 unique types of molecules in this entry. The entry contains 6400 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 Syntaxin-binding protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	561	Total 4485	C 2843	N 757	O 860	S 25	0	0	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	GLY	-	expression tag	UNP P61765
A	-4	PRO	-	expression tag	UNP P61765
A	-3	GLY	-	expression tag	UNP P61765
A	-2	SER	-	expression tag	UNP P61765
A	-1	GLU	-	expression tag	UNP P61765
A	0	PHE	-	expression tag	UNP P61765

- Molecule 2 is a protein called Syntaxin-1A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	219	Total 1772	C 1088	N 309	O 364	S 11	0	0	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	19	GLY	-	expression tag	UNP P32851
B	20	PRO	-	expression tag	UNP P32851
B	21	GLY	-	expression tag	UNP P32851
B	22	SER	-	expression tag	UNP P32851
B	23	GLU	-	expression tag	UNP P32851
B	24	PHE	-	expression tag	UNP P32851

- Molecule 3 is a protein called Amyloid-beta A4 precursor protein-binding family A member 1.

| Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	C	18	143	85	22	35	1	0	0	0

There are 6 discrepancies between the modelled and reference sequences:

| Chain	Residue	Modelled	Actual	Comment	Reference
C	221	GLY	-	expression tag	UNP O35430
C	222	PRO	-	expression tag	UNP O35430
C	223	GLY	-	expression tag	UNP O35430
C	224	SER	-	expression tag	UNP O35430
C	225	GLU	-	expression tag	UNP O35430
C	226	PHE	-	expression tag	UNP O35430

3 Residue-property plots ⓘ

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.
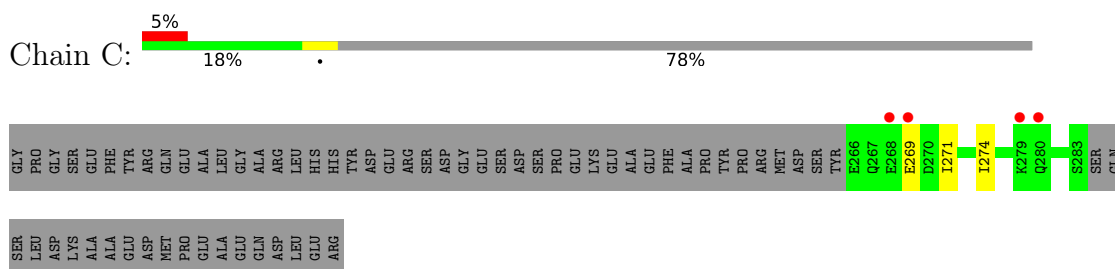
• Molecule 1: Syntaxin-binding protein 1
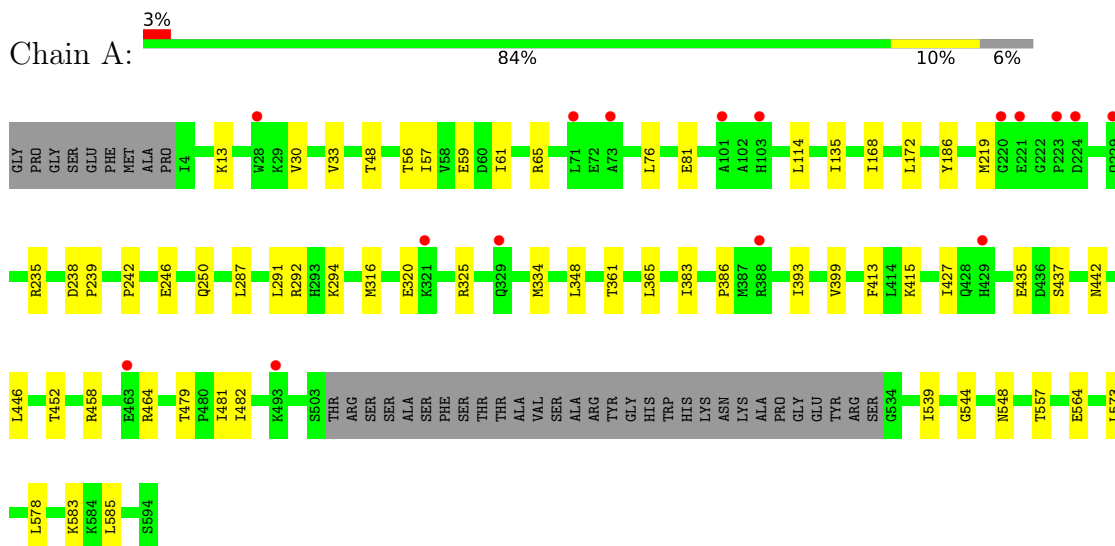
• Molecule 2: Syntaxin-1A
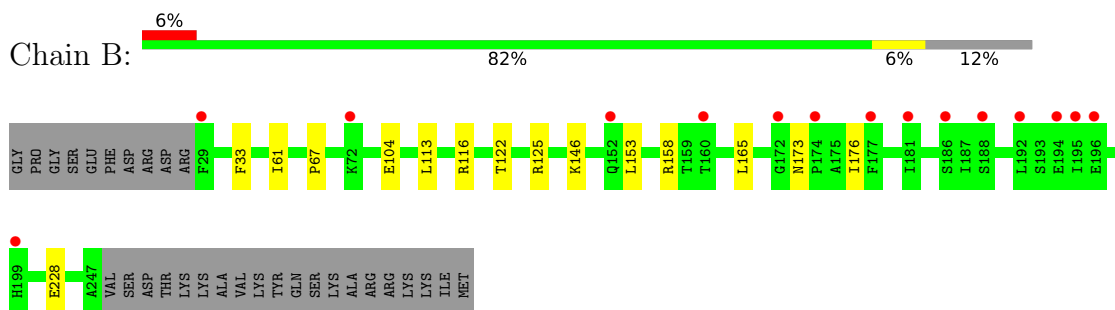
• Molecule 3: Amyloid-beta A4 precursor protein-binding family A member 1

4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	P 4 21 2	Depositor
Cell constants a, b, c, α, β, γ	156.24Å 156.24Å 78.86Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	41.87 – 3.20 41.87 – 3.20	Depositor EDS
% Data completeness (in resolution range)	99.8 (41.87-3.20) 99.8 (41.87-3.20)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	5.99 (at 3.19Å)	Xtriage
Refinement program	PHENIX 1.18.2_3874	Depositor
R, R_{free}	0.235 , 0.270 0.235 , 0.269	Depositor DCC
R_{free} test set	824 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å^2)	91.3	Xtriage
Anisotropy	0.720	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 38.6	EDS
L-test for twinning[2]	$< |L| > = 0.51, < L^2 > = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	6400	wwPDB-VP
Average B, all atoms (Å^2)	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.79% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.

[2]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.

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	0.23	0/4564	0.41	0/6163
2	B	0.23	0/1790	0.36	0/2394
3	C	0.22	0/142	0.33	0/189
All	All	0.23	0/6496	0.39	0/8746

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 ⓘ

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	4485	0	4571	34	0
2	B	1772	0	1749	8	0
3	C	143	0	132	2	0
All	All	6400	0	6452	43	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 (43) 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:427:ILE:HD13	1:A:437:SER:HB2	1.74	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:13:LYS:HD3	1:A:135:ILE:HD11	1.79	0.65
1:A:325:ARG:HD3	1:A:348:LEU:HB3	1.82	0.62
2:B:173:ASN:HB3	2:B:176:ILE:HB	1.84	0.60
1:A:291:LEU:HD23	1:A:294:LYS:HD2	1.85	0.58
1:A:464:ARG:NH1	1:A:479:THR:O	2.36	0.58
3:C:269:GLU:HB2	3:C:274:ILE:HD11	1.87	0.56
1:A:246:GLU:HG3	1:A:548:ASN:HB3	1.89	0.54
2:B:104:GLU:HG2	2:B:113:LEU:HD21	1.91	0.53
1:A:30:VAL:HG13	1:A:57:ILE:HG23	1.91	0.53
1:A:33:VAL:HG12	1:A:76:LEU:HB3	1.90	0.52
1:A:81:GLU:HG2	1:A:114:LEU:HD21	1.92	0.51
1:A:56:THR:HG23	1:A:57:ILE:HG22	1.91	0.50
1:A:415:LYS:O	1:A:458:ARG:NH2	2.45	0.50
1:A:361:THR:HG21	1:A:399:VAL:HG22	1.94	0.49
1:A:435:GLU:HG2	1:A:583:LYS:HD2	1.94	0.49
1:A:316:MET:HE3	1:A:334:MET:HB2	1.96	0.47
1:A:287:LEU:O	1:A:291:LEU:HB2	2.15	0.46
1:A:452:THR:OG1	1:A:458:ARG:NH1	2.49	0.46
2:B:153:LEU:HD22	2:B:158:ARG:HD3	1.98	0.46
1:A:544:GLY:HA3	1:A:573:LEU:HG	1.98	0.46
1:A:186:TYR:HB2	1:A:219:MET:HG2	1.97	0.45
1:A:48:THR:HG23	2:B:122:THR:HG23	1.99	0.45
1:A:464:ARG:HE	1:A:481:ILE:HG12	1.81	0.44
2:B:61:ILE:HG23	2:B:67:PRO:HG3	1.99	0.44
1:A:557:THR:HG23	1:A:564:GLU:HA	1.99	0.44
1:A:61:ILE:HA	1:A:65:ARG:HE	1.81	0.44
1:A:168:ILE:O	1:A:172:LEU:HG	2.17	0.44
1:A:482:ILE:HD11	1:A:539:ILE:HG21	1.99	0.44
2:B:146:LYS:HG3	2:B:165:LEU:HD22	1.99	0.44
1:A:59:GLU:HB3	1:A:65:ARG:HD3	2.01	0.42
1:A:442:ASN:HB3	1:A:585:LEU:HD12	2.01	0.42
1:A:365:LEU:HD23	1:A:393:ILE:HD13	2.01	0.42
1:A:239:PRO:HB2	1:A:413:PHE:CZ	2.54	0.42
2:B:125:ARG:HH22	2:B:228:GLU:HA	1.85	0.42
2:B:33:PHE:CZ	2:B:116:ARG:HA	2.55	0.42
3:C:271:ILE:H	3:C:271:ILE:HD12	1.84	0.41
1:A:235:ARG:HH21	1:A:238:ASP:HB3	1.84	0.41
1:A:242:PRO:HB2	1:A:578:LEU:HD22	2.02	0.41
1:A:320:GLU:H	1:A:320:GLU:HG2	1.67	0.41
1:A:235:ARG:HB3	1:A:446:LEU:HD23	2.02	0.41
1:A:250:GLN:HB2	1:A:292:ARG:HB2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:383:ILE:HG21	1:A:386:PRO:HG3	2.02	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	557/600 (93%)	527 (95%)	30 (5%)	0	100	100
2	B	217/249 (87%)	212 (98%)	5 (2%)	0	100	100
3	C	16/83 (19%)	16 (100%)	0	0	100	100
All	All	790/932 (85%)	755 (96%)	35 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	507/537 (94%)	507 (100%)	0	100	100
2	B	200/226 (88%)	200 (100%)	0	100	100
3	C	17/71 (24%)	17 (100%)	0	100	100
All	All	724/834 (87%)	724 (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. There are no such sidechains identified.

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 monosaccharides 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, 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	561/600 (93%)	0.37	16 (2%)	51	36	20, 55, 114, 170	0
2	B	219/249 (87%)	0.56	15 (6%)	17	10	24, 63, 113, 151	0
3	C	18/83 (21%)	1.47	4 (22%)	0	0	98, 120, 151, 163	0
All	All	798/932 (85%)	0.45	35 (4%)	34	21	20, 57, 121, 170	0

All (35) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	229	GLN	3.7
1	A	223	PRO	3.4
2	B	177	PHE	3.4
2	B	181	ILE	3.3
2	B	72	LYS	3.2
3	C	268	GLU	3.1
2	B	195	ILE	3.1
1	A	388	ARG	3.0
3	C	280	GLN	3.0
1	A	220	GLY	2.9
3	C	279	LYS	2.8
2	B	174	PRO	2.7
1	A	321	LYS	2.6
3	C	269	GLU	2.6
2	B	29	PHE	2.6
2	B	194	GLU	2.6
1	A	103	HIS	2.5
1	A	28	TRP	2.5
1	A	71	LEU	2.4
2	B	186	SER	2.4
1	A	221	GLU	2.4
2	B	199	HIS	2.4
2	B	172	GLY	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	101	ALA	2.2
2	B	188	SER	2.2
1	A	429	HIS	2.2
1	A	493	LYS	2.2
1	A	463	GLU	2.1
1	A	329	GLN	2.1
2	B	196	GLU	2.1
2	B	192	LEU	2.1
1	A	73	ALA	2.1
2	B	160	THR	2.1
1	A	224	ASP	2.1
2	B	152	GLN	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no monosaccharides in this entry.

6.4 Ligands ⓘ

There are no ligands in this entry.

6.5 Other polymers ⓘ

There are no such residues in this entry.