Full wwPDB X-ray Structure Validation Report (i)

Jan 31, 2016 – 07:55 PM GMT

PDB ID	:	1HVV
Title	:	SELF-ASSOCIATION OF THE H3 REGION OF SYNTAXIN 1A: IMPLICATIONS FOR SNARE COMPLEX ASSEMBLY
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Deposited on	:	2001-01-08
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:

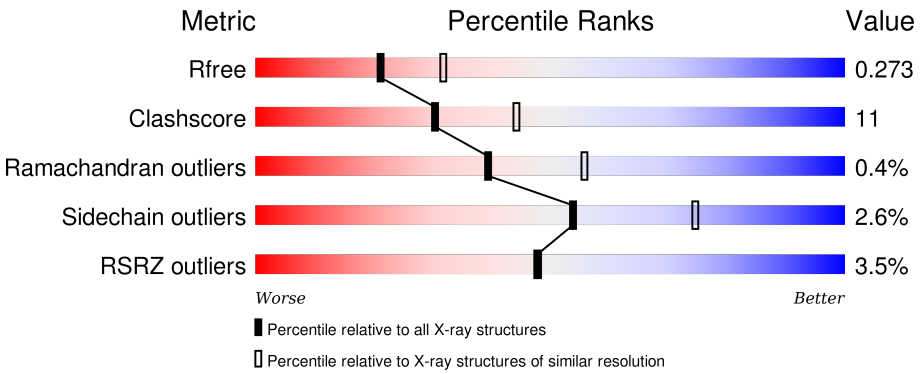
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	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	75	3%, 71%, 19%, 11%
1	B	75	4%, 64%, 19%, 17%
1	C	75	%, 60%, 25%, •, 12%
1	D	75	4%, 60%, 17%, •, 19%

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
2	TAR	C	1352	-	-	X	X

2 Entry composition (i)

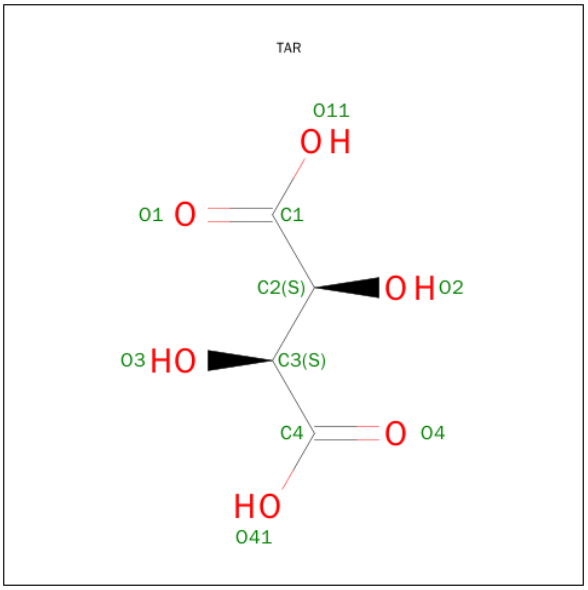
There are 3 unique types of molecules in this entry. The entry contains 2141 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 1A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	67	540	333	92	110	5	0	0	0
1	B	62	506	311	86	104	5	0	0	0
1	C	66	535	330	91	109	5	0	0	0
1	D	61	497	305	84	103	5	0	0	0

- Molecule 2 is D(-)-TARTARIC ACID (three-letter code: TAR) (formula: $C_4H_6O_6$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
2	C	1	10	4	6	0	0

- Molecule 3 is water.

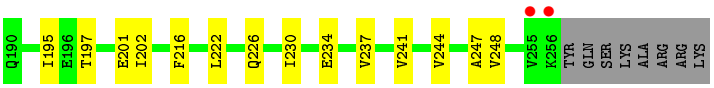
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	19	19	19	0	0
			Total	O		
3	B	6	6	6	0	0
			Total	O		
3	C	15	15	15	0	0
			Total	O		
3	D	13	13	13	0	0

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: SYNTAXIN 1A

Chain A:



- Molecule 1: SYNTAXIN 1A

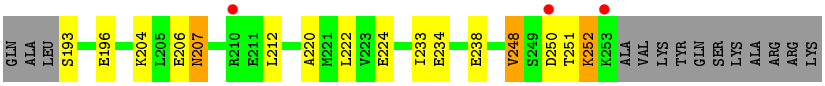
Chain B:

- Molecule 1: SYNTAXIN 1A

Chain C:

- Molecule 1: SYNTAXIN 1A

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α, β, γ	88.32Å 88.32Å 115.62Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	30.00 – 2.40 46.12 – 2.40	Depositor EDS
% Data completeness (in resolution range)	96.3 (30.00-2.40) 96.2 (46.12-2.40)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	5.61 (at 2.39Å)	Xtriage
Refinement program	CNS 0.5	Depositor
R, R_{free}	0.238 , 0.273 0.237 , 0.273	Depositor DCC
R_{free} test set	1563 reflections (7.77%)	DCC
Wilson B-factor (Å^2)	35.6	Xtriage
Anisotropy	0.019	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 40.0	EDS
Estimated twinning fraction	0.033 for -h,-k,l	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Outliers	1 of 20870 reflections (0.005%)	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	2141	wwPDB-VP
Average B, all atoms (Å^2)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 27.70 % of the origin peak, indicating pseudo translational symmetry.The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 2.0994e-03.The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[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 (i)

5.1 Standard geometry (i)

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

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	0.37	0/545	0.51	0/731
1	B	0.33	0/511	0.46	0/684
1	C	0.37	0/540	0.51	0/724
1	D	0.35	0/502	0.51	0/673
All	All	0.35	0/2098	0.50	0/2812

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	540	0	524	12	0
1	B	506	0	489	11	0
1	C	535	0	522	20	0
1	D	497	0	473	16	0
2	C	10	0	4	4	0
3	A	19	0	0	0	0
3	B	6	0	0	0	0
3	C	15	0	0	2	0
3	D	13	0	0	0	0
All	All	2141	0	2012	45	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 11.

All (45) 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:C:213:HIS:HA	2:C:1352:TAR:H3	1.52	0.91
1:B:248:VAL:HG22	1:C:195:ILE:HD11	1.57	0.85
1:A:195:ILE:HG13	1:D:248:VAL:HG22	1.71	0.73
1:C:197:THR:O	1:C:201:GLU:HG3	1.91	0.70
1:C:212:LEU:HD21	1:D:212:LEU:HD23	1.75	0.69
1:A:197:THR:O	1:A:201:GLU:HG3	1.94	0.67
1:A:234:GLU:HG3	3:C:1357:HOH:O	1.95	0.66
1:D:204:LYS:HA	1:D:207:ASN:HD22	1.60	0.65
1:C:213:HIS:CA	2:C:1352:TAR:H3	2.27	0.64
1:B:241:VAL:O	1:B:245:GLU:HG3	2.01	0.61
1:D:250:ASP:OD2	1:D:251:THR:N	2.37	0.58
1:A:241:VAL:HG22	1:C:202:ILE:HG23	1.84	0.58
1:D:251:THR:O	1:D:251:THR:HG22	2.03	0.57
1:A:195:ILE:HG12	1:C:248:VAL:HG22	1.86	0.57
1:D:252:LYS:NZ	1:D:252:LYS:HB2	2.21	0.55
1:C:246:ARG:HH11	1:C:246:ARG:HG3	1.71	0.54
1:C:249:SER:O	1:C:253:LYS:HG2	2.07	0.53
1:C:204:LYS:HE3	3:C:1358:HOH:O	2.07	0.53
1:D:204:LYS:HA	1:D:207:ASN:ND2	2.24	0.52
1:C:217:MET:O	1:C:221:MET:HG3	2.08	0.52
1:B:208:SER:O	1:D:233:ILE:HD11	2.10	0.51
1:D:220:ALA:O	1:D:224:GLU:HG3	2.10	0.51
1:A:237:VAL:HG12	1:C:206:GLU:HB2	1.93	0.50
1:B:244:VAL:HG23	1:C:198:ARG:HB3	1.94	0.49
1:A:216:PHE:HE1	1:C:226:GLN:HE21	1.61	0.49
1:B:210:ARG:HH11	1:B:210:ARG:HG3	1.77	0.49
1:A:202:ILE:HG23	1:C:241:VAL:HG22	1.94	0.48
1:A:247:ALA:CB	1:B:248:VAL:HG13	2.45	0.47
1:D:193:SER:N	1:D:196:GLU:OE1	2.48	0.46
1:C:199:HIS:O	1:C:202:ILE:HG22	2.16	0.45
1:B:224:GLU:O	1:B:228:GLU:HG3	2.16	0.45
1:A:230:ILE:HG21	2:C:1352:TAR:O3	2.17	0.45
1:B:210:ARG:NH1	1:B:210:ARG:HG3	2.32	0.44
1:B:211:GLU:O	1:B:215:MET:HG3	2.16	0.44
1:D:251:THR:O	1:D:252:LYS:O	2.35	0.44
1:C:204:LYS:HZ3	1:D:206:GLU:HG2	1.82	0.44
1:B:219:MET:HA	1:D:222:LEU:HD21	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:204:LYS:NZ	1:D:206:GLU:HG2	2.34	0.43
1:A:222:LEU:O	1:A:226:GLN:HG3	2.19	0.43
1:A:244:VAL:O	1:A:248:VAL:HG23	2.19	0.43
1:D:234:GLU:O	1:D:238:GLU:HG2	2.18	0.43
1:B:202:ILE:O	1:B:206:GLU:HG3	2.19	0.42
1:D:250:ASP:C	1:D:252:LYS:H	2.22	0.42
1:C:213:HIS:HA	2:C:1352:TAR:C3	2.38	0.42
1:C:205:LEU:O	1:C:209:ILE:HG12	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	65/75 (87%)	64 (98%)	1 (2%)	0	100	100
1	B	60/75 (80%)	60 (100%)	0	0	100	100
1	C	64/75 (85%)	63 (98%)	1 (2%)	0	100	100
1	D	59/75 (79%)	57 (97%)	1 (2%)	1 (2%)	11	14
All	All	248/300 (83%)	244 (98%)	3 (1%)	1 (0%)	39	56

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	252	LYS

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	60/68 (88%)	60 (100%)	0	100	100
1	B	57/68 (84%)	56 (98%)	1 (2%)	66	84
1	C	60/68 (88%)	57 (95%)	3 (5%)	30	48
1	D	56/68 (82%)	54 (96%)	2 (4%)	42	63
All	All	233/272 (86%)	227 (97%)	6 (3%)	54	74

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	198	ARG
1	C	190	GLN
1	C	204	LYS
1	C	217	MET
1	D	207	ASN
1	D	248	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	226	GLN
1	A	236	ASN
1	B	226	GLN
1	C	190	GLN
1	C	226	GLN
1	D	207	ASN
1	D	226	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)

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	TAR	C	1352	-	3,9,9	0.96	0	6,12,12	1.06	1 (16%)

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	TAR	C	1352	-	-	0/4/12/12	0/0/0/0

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	C	1352	TAR	O3-C3-C2	2.18	114.75	108.61

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	1352	TAR	4	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, 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	67/75 (89%)	0.11	2 (2%)	54	53	24, 34, 66, 83	0
1	B	62/75 (82%)	0.16	3 (4%)	34	35	26, 40, 78, 90	0
1	C	66/75 (88%)	0.13	1 (1%)	76	75	25, 36, 63, 79	0
1	D	61/75 (81%)	0.17	3 (4%)	33	34	28, 38, 74, 80	0
All	All	256/300 (85%)	0.14	9 (3%)	48	48	24, 37, 76, 90	0

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	195	ILE	4.6
1	D	250	ASP	4.1
1	A	255	VAL	3.9
1	C	255	VAL	3.2
1	D	210	ARG	2.9
1	B	254	ALA	2.5
1	B	196	GLU	2.1
1	A	256	LYS	2.1
1	D	253	LYS	2.1

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)

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å^2)	Q<0.9
2	TAR	C	1352	10/10	0.73	0.54	13.51	77,78,80,81	0

6.5 Other polymers (i)

There are no such residues in this entry.