



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 12:38 PM GMT

PDB ID : 3RK3
Title : Truncated SNARE complex with complexin
Authors : Kuemmel, D.; Reinisch, K.M.
Deposited on : 2011-04-17
Resolution : 3.50 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 ⓘ 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

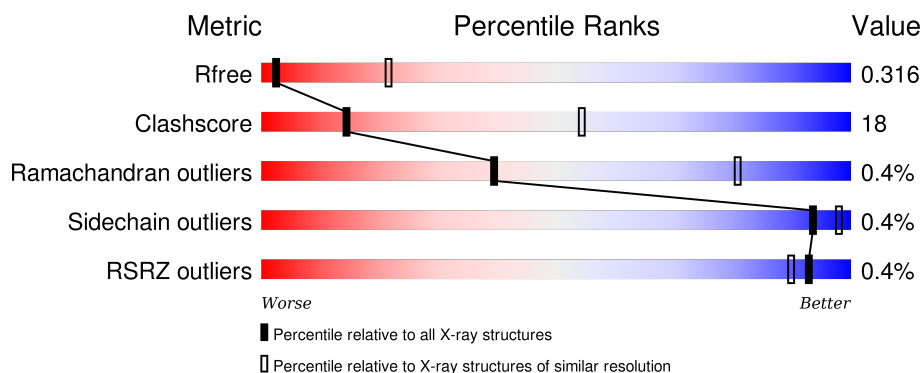
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.50 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	1051 (3.60-3.40)
Clashscore	102246	1157 (3.60-3.40)
Ramachandran outliers	100387	1120 (3.60-3.40)
Sidechain outliers	100360	1121 (3.60-3.40)
RSRZ outliers	91569	1058 (3.60-3.40)

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 $\leq 5\%$. 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	37	
2	B	65	
3	C	81	
4	D	65	
5	E	63	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 2215 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 Vamp2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	34	Total	C	N	O	S	0	0	0
			278	166	55	56	1			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	24	GLY	-	EXPRESSION TAG	UNP P63027
A	25	PRO	-	EXPRESSION TAG	UNP P63027
A	26	LEU	-	EXPRESSION TAG	UNP P63027
A	27	GLY	-	EXPRESSION TAG	UNP P63027

- Molecule 2 is a protein called Syntaxin 1a.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	62	Total	C	N	O	S	0	0	0
			499	306	84	104	5			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	189	GLY	-	EXPRESSION TAG	UNP P32851
B	190	SER	-	EXPRESSION TAG	UNP P32851

- Molecule 3 is a protein called SNAP25.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	65	Total	C	N	O	S	6	0	0
			525	311	95	114	5			

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	3	GLY	-	EXPRESSION TAG	UNP P60880
C	4	SER	-	EXPRESSION TAG	UNP P60880
C	5	HIS	-	EXPRESSION TAG	UNP P60880
C	6	MET	-	EXPRESSION TAG	UNP P60880
C	83	TRP	-	EXPRESSION TAG	UNP P60880

- Molecule 4 is a protein called SNAP25.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	65	Total	C	N	O	S	4	0	0
			510	298	98	109	5			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	139	GLY	-	EXPRESSION TAG	UNP P60880
D	140	SER	-	EXPRESSION TAG	UNP P60880

- Molecule 5 is a protein called Complexin-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	50	Total	C	N	O	S	7	0	0
			403	248	76	78	1			

There are 8 discrepancies between the modelled and reference sequences:

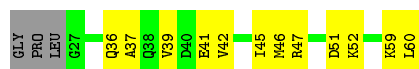
Chain	Residue	Modelled	Actual	Comment	Reference
E	21	GLY	-	EXPRESSION TAG	UNP O14810
E	22	PRO	-	EXPRESSION TAG	UNP O14810
E	23	LEU	-	EXPRESSION TAG	UNP O14810
E	24	GLY	-	EXPRESSION TAG	UNP O14810
E	25	SER	-	EXPRESSION TAG	UNP O14810
E	27	LEU	ASP	ENGINEERED MUTATION	UNP O14810
E	34	PHE	GLU	ENGINEERED MUTATION	UNP O14810
E	37	ALA	ARG	ENGINEERED MUTATION	UNP O14810

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.

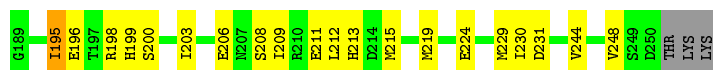
• Molecule 1: Vamp2

Chain A: 



• Molecule 2: Syntaxin 1a

Chain B: 



• Molecule 3: SNAP25

Chain C: 



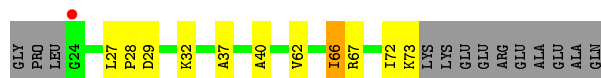
• Molecule 4: SNAP25

Chain D: 



• Molecule 5: Complexin-1

Chain E: 



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	75.86 Å 52.73 Å 128.71 Å 90.00° 95.21° 90.00°	Depositor
Resolution (Å)	32.05 – 3.50 32.05 – 3.09	Depositor EDS
% Data completeness (in resolution range)	99.1 (32.05-3.50) 96.6 (32.05-3.09)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.38 (at 3.12 Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.270 , 0.316 0.224 , 0.316	Depositor DCC
R_{free} test set	314 reflections (5.08%)	DCC
Wilson B-factor (Å ²)	82.1	Xtriage
Anisotropy	0.603	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 80.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 9168 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	2215	wwPDB-VP
Average B, all atoms (Å ²)	99.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 11.41% 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 ⓘ

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	0.63	0/277	0.80	0/369
2	B	0.58	0/504	0.63	0/676
3	C	0.54	0/525	0.67	0/699
4	D	0.70	1/510 (0.2%)	0.72	0/679
5	E	0.79	1/406 (0.2%)	0.89	4/535 (0.7%)
All	All	0.65	2/2222 (0.1%)	0.74	4/2958 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	E	73	LYS	CB-CG	-11.43	1.21	1.52
4	D	151	GLU	CB-CG	5.76	1.63	1.52

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	E	72	ILE	CA-CB-CG1	-11.35	89.43	111.00
5	E	72	ILE	CG1-CB-CG2	8.44	129.98	111.40
5	E	72	ILE	CA-CB-CG2	-5.62	99.66	110.90
5	E	72	ILE	CB-CG1-CD1	-5.29	99.08	113.90

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	278	0	284	19	0
2	B	499	0	475	25	0
3	C	525	0	506	23	0
4	D	510	0	489	32	0
5	E	403	0	409	10	0
All	All	2215	0	2163	78	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 18.

All (78) 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)
5:E:66:ILE:HD12	5:E:66:ILE:C	1.84	0.97
1:A:47:ARG:N	2:B:215:MET:HE1	1.86	0.91
2:B:209:ILE:HG22	3:C:35:LEU:HD13	1.61	0.82
1:A:46:MET:HB3	2:B:215:MET:HE2	1.61	0.82
5:E:66:ILE:HD12	5:E:67:ARG:N	1.93	0.82
3:C:26:LEU:O	3:C:29:THR:OG1	1.99	0.80
3:C:60:VAL:HG12	4:D:181:ILE:HD13	1.63	0.79
1:A:42:VAL:HG12	2:B:212:LEU:HD11	1.66	0.78
2:B:199:HIS:O	2:B:203:ILE:HD12	1.89	0.73
3:C:60:VAL:CG1	4:D:181:ILE:HD13	2.23	0.68
3:C:36:VAL:HG12	4:D:156:ILE:HG21	1.76	0.68
3:C:60:VAL:HG12	4:D:181:ILE:CD1	2.28	0.63
4:D:161:ARG:HG2	4:D:165:LEU:HD11	1.83	0.61
5:E:37:ALA:O	5:E:40:ALA:HB3	2.02	0.60
4:D:161:ARG:O	4:D:165:LEU:HD12	2.01	0.59
3:C:47:LEU:HD11	4:D:163:MET:HG2	1.84	0.57
5:E:66:ILE:CD1	5:E:66:ILE:C	2.62	0.57
4:D:161:ARG:HG2	4:D:165:LEU:CD1	2.35	0.56
2:B:206:GLU:N	3:C:32:MET:HE2	2.19	0.56
1:A:46:MET:CB	2:B:215:MET:HE2	2.33	0.56
1:A:41:GLU:O	1:A:45:ILE:HD12	2.06	0.55
3:C:71:MET:HE1	4:D:192:ILE:HA	1.87	0.55
1:A:39:VAL:O	1:A:42:VAL:N	2.41	0.53
3:C:36:VAL:HG11	4:D:156:ILE:HB	1.91	0.53
3:C:67:ILE:HG21	4:D:188:ASN:ND2	2.24	0.53
1:A:42:VAL:CG1	2:B:212:LEU:HD11	2.37	0.53
2:B:213:HIS:CG	3:C:35:LEU:HD22	2.45	0.52
3:C:20:GLN:O	3:C:24:GLU:HG3	2.09	0.52
4:D:157:ILE:HA	4:D:160:LEU:HD12	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:29:ASP:O	5:E:32:LYS:N	2.43	0.50
3:C:64:MET:HE1	4:D:185:ALA:HA	1.93	0.50
4:D:174:GLN:O	4:D:178:ILE:HD13	2.12	0.49
2:B:195:ILE:O	2:B:198:ARG:N	2.46	0.48
4:D:197:GLN:O	4:D:201:LYS:CB	2.62	0.48
2:B:244:VAL:O	2:B:248:VAL:HG23	2.15	0.47
1:A:42:VAL:HA	1:A:45:ILE:HD13	1.97	0.46
2:B:213:HIS:CB	3:C:35:LEU:HD22	2.46	0.46
4:D:161:ARG:CG	4:D:165:LEU:HD11	2.46	0.46
1:A:46:MET:HB3	2:B:215:MET:CE	2.40	0.46
4:D:147:ASP:HA	4:D:150:LEU:HD12	1.96	0.46
1:A:41:GLU:O	1:A:45:ILE:CD1	2.64	0.45
4:D:153:VAL:O	4:D:156:ILE:N	2.50	0.45
1:A:51:ASP:O	1:A:52:LYS:C	2.53	0.45
1:A:46:MET:C	2:B:215:MET:HE1	2.36	0.45
4:D:161:ARG:O	4:D:162:HIS:C	2.54	0.45
3:C:40:LYS:O	3:C:41:ASP:C	2.54	0.45
2:B:219:MET:HG2	4:D:167:MET:HE1	1.98	0.45
2:B:203:ILE:H	2:B:203:ILE:HD12	1.81	0.45
2:B:195:ILE:O	2:B:196:GLU:C	2.56	0.44
3:C:47:LEU:O	3:C:48:VAL:C	2.56	0.44
2:B:200:SER:HA	2:B:203:ILE:HD13	1.99	0.44
1:A:46:MET:CB	2:B:215:MET:CE	2.95	0.44
2:B:224:GLU:HA	3:C:49:MET:SD	2.58	0.43
3:C:36:VAL:CG1	4:D:156:ILE:HG21	2.44	0.43
1:A:36:GLN:NE2	2:B:208:SER:OG	2.50	0.43
4:D:140:SER:O	4:D:144:ASN:CG	2.57	0.43
2:B:211:GLU:O	2:B:212:LEU:C	2.55	0.43
1:A:36:GLN:O	1:A:37:ALA:C	2.56	0.43
5:E:66:ILE:CD1	5:E:67:ARG:N	2.72	0.42
4:D:153:VAL:O	4:D:157:ILE:HD13	2.19	0.42
5:E:62:VAL:O	5:E:66:ILE:HG23	2.20	0.42
3:C:36:VAL:CG1	4:D:156:ILE:CG2	2.98	0.42
4:D:157:ILE:O	4:D:158:GLY:C	2.58	0.42
2:B:206:GLU:OE1	3:C:28:SER:OG	2.22	0.42
3:C:27:GLU:OE2	3:C:30:ARG:NH1	2.51	0.42
5:E:66:ILE:HD12	5:E:67:ARG:CA	2.49	0.42
1:A:60:LEU:HB3	2:B:229:MET:HE2	2.02	0.42
3:C:71:MET:HE3	4:D:191:ARG:HG3	2.01	0.42
4:D:151:GLU:O	4:D:152:GLN:C	2.58	0.42
4:D:171:ILE:O	4:D:172:ASP:C	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:149:ASN:O	4:D:153:VAL:HG23	2.19	0.41
1:A:59:LYS:HB3	4:D:178:ILE:HG21	2.03	0.41
2:B:230:ILE:HG22	2:B:231:ASP:N	2.35	0.41
1:A:41:GLU:HG2	1:A:45:ILE:CD1	2.50	0.41
1:A:45:ILE:CG2	4:D:164:ALA:HB1	2.50	0.41
4:D:157:ILE:N	4:D:157:ILE:HD12	2.35	0.41
5:E:27:LEU:N	5:E:28:PRO:CD	2.83	0.41
5:E:66:ILE:O	5:E:67:ARG:C	2.59	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	32/37 (86%)	28 (88%)	4 (12%)	0	100	100
2	B	60/65 (92%)	45 (75%)	14 (23%)	1 (2%)	11	54
3	C	63/81 (78%)	60 (95%)	3 (5%)	0	100	100
4	D	63/65 (97%)	55 (87%)	8 (13%)	0	100	100
5	E	48/63 (76%)	43 (90%)	5 (10%)	0	100	100
All	All	266/311 (86%)	231 (87%)	34 (13%)	1 (0%)	39	81

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	195	ILE

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	32/34 (94%)	32 (100%)	0	100	100
2	B	56/59 (95%)	56 (100%)	0	100	100
3	C	58/72 (81%)	58 (100%)	0	100	100
4	D	55/56 (98%)	55 (100%)	0	100	100
5	E	38/48 (79%)	37 (97%)	1 (3%)	54	83
All	All	239/269 (89%)	238 (100%)	1 (0%)	93	98

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	E	66	ILE

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

Mol	Chain	Res	Type
1	A	36	GLN
4	D	149	ASN
4	D	152	GLN
4	D	177	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(Å²)	Q<0.9	
1	A	34/37 (91%)	-0.81	0	100	100	21, 59, 100, 110	0
2	B	62/65 (95%)	-0.60	0	100	100	30, 74, 166, 187	0
3	C	65/81 (80%)	-0.70	0	100	100	33, 86, 147, 152	1 (1%)
4	D	65/65 (100%)	-0.51	0	100	100	35, 77, 173, 179	1 (1%)
5	E	50/63 (79%)	-0.21	1 (2%)	68	59	58, 150, 185, 189	2 (4%)
All	All	276/311 (88%)	-0.56	1 (0%)	93	90	21, 89, 179, 189	4 (1%)

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
5	E	24	GLY	2.6

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.