



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 06:32 PM GMT

PDB ID : 1B7F
Title : SXL-LETHAL PROTEIN/RNA COMPLEX
Authors : Handa, N.; Nureki, O.; Kurimoto, K.; Kim, I.; Sakamoto, H.; Shimura, Y.;
Muto, Y.; Yokoyama, S.; RIKEN Structural Genomics/Proteomics Initiative
(RSGI)
Deposited on : 1999-01-23
Resolution : 2.60 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) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

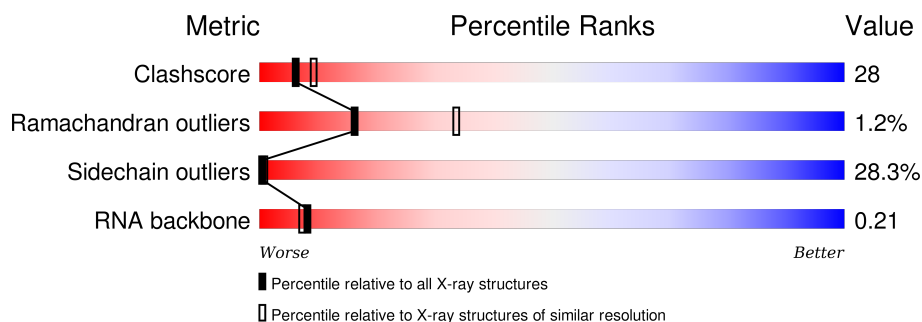
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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))
Clashscore	102246	2679 (2.60-2.60)
Ramachandran outliers	100387	2635 (2.60-2.60)
Sidechain outliers	100360	2635 (2.60-2.60)
RNA backbone	2183	1022 (3.00-2.20)

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 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	P	12	<div> <div>17%</div> <div>25%</div> <div>25%</div> <div>33%</div> </div>
1	Q	12	<div> <div>25%</div> <div>8%</div> <div>25%</div> <div>42%</div> </div>
2	A	168	<div> <div>52%</div> <div>35%</div> <div>11%</div> <div>..</div> </div>
2	B	168	<div> <div>48%</div> <div>40%</div> <div>11%</div> <div>.</div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3236 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 RNA chain called RNA (5'-R(P*GP*UP*UP*GP*UP*UP*UP*UP*UP*UP*U)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	P	12	Total	C	N	O	P	0	0	0
			247	110	30	95	12			
1	Q	12	Total	C	N	O	P	0	0	0
			247	110	30	95	12			

- Molecule 2 is a protein called PROTEIN (SXL-LETHAL PROTEIN).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	167	Total	C	N	O	S	0	0	0
			1329	834	239	252	4			
2	B	167	Total	C	N	O	S	0	0	0
			1329	834	239	252	4			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	166	TYR	PHE	ENGINEERED	UNP P19339
B	166	TYR	PHE	ENGINEERED	UNP P19339

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	36	Total	O	0	0
			36	36		
3	B	33	Total	O	0	0
			33	33		
3	P	7	Total	O	0	0
			7	7		
3	Q	8	Total	O	0	0
			8	8		

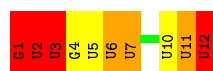
3 Residue-property plots

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.

Note EDS was not executed.

- Molecule 1: RNA (5'-R(P*GP*UP*UP*GP*UP*UP*UP*UP*UP*UP*UP*U)-3')

Chain P: 



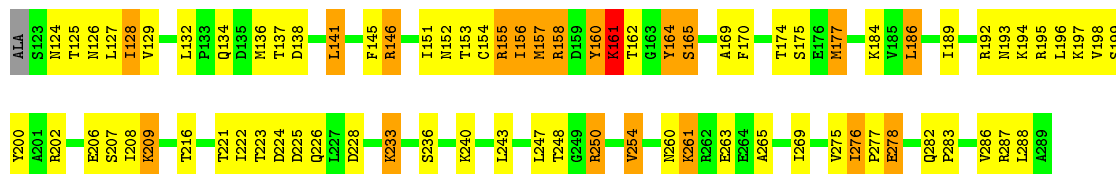
- Molecule 1: RNA (5'-R(P*GP*UP*UP*GP*UP*UP*UP*UP*UP*UP*UP*U)-3')

Chain Q: 



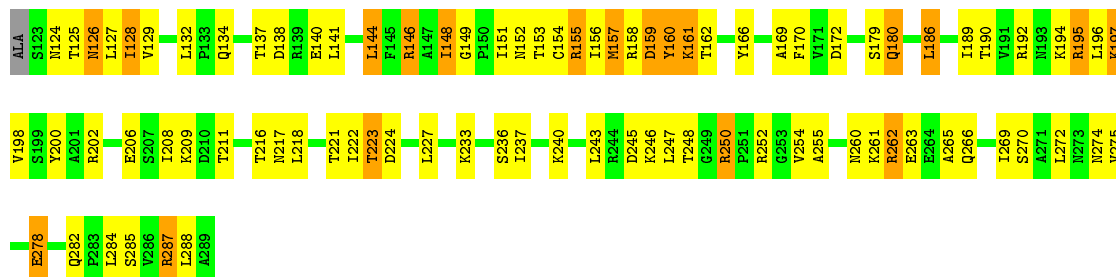
- Molecule 2: PROTEIN (SXL-LETHAL PROTEIN)

Chain A: 



- Molecule 2: PROTEIN (SXL-LETHAL PROTEIN)

Chain B: 



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	77.90 Å 86.80 Å 160.40 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 2.60	Depositor
% Data completeness (in resolution range)	98.5 (15.00-2.60)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
Refinement program	X-PLOR 3.851	Depositor
R, R_{free}	0.201 , 0.294	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3236	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

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	P	1.52	0/272	1.81	9/418 (2.2%)
1	Q	1.66	0/272	1.84	9/418 (2.2%)
2	A	0.43	0/1350	0.68	0/1823
2	B	0.48	0/1350	0.68	0/1823
All	All	0.78	0/3244	1.00	18/4482 (0.4%)

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	Q	1	0

There are no bond length outliers.

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	P	3	U	O4'-C1'-N1	9.04	115.44	108.20
1	P	1	G	O4'-C1'-N9	7.60	114.28	108.20
1	Q	6	U	O4'-C1'-N1	6.75	113.60	108.20
1	P	2	U	O4'-C1'-N1	6.34	113.28	108.20
1	P	10	U	O4'-C1'-N1	6.19	113.16	108.20

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	Q	2	U	C1'

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	P	247	0	123	16	3
1	Q	247	0	123	20	3
2	A	1329	0	1345	73	1
2	B	1329	0	1345	76	1
3	A	36	0	0	9	0
3	B	33	0	0	8	0
3	P	7	0	0	10	1
3	Q	8	0	0	7	1
All	All	3236	0	2936	171	5

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 28.

The worst 5 of 171 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:Q:1:G:H4'	3:Q:143:HOH:O	1.30	1.22
1:Q:2:U:C6	3:Q:145:HOH:O	2.09	1.03
1:P:1:G:H4'	3:P:59:HOH:O	1.61	0.99
2:B:154:CYS:HB3	3:B:319:HOH:O	1.63	0.97
2:A:160:TYR:O	2:A:161:LYS:HB2	1.65	0.94

All (5) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:4:G:N7	1:Q:2:U:O4[2_665]	1.88	0.32
1:P:3:U:OP2	1:Q:2:U:O4[2_665]	1.97	0.23
1:P:2:U:O2	1:Q:4:G:O6[2_665]	2.11	0.09
2:A:206:GLU:OE2	2:B:154:CYS:SG[1_565]	2.13	0.07
3:P:42:HOH:O	3:Q:20:HOH:O[2_665]	2.19	0.01

5.3 Torsion angles

5.3.1 Protein backbone

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	
2	A	165/168 (98%)	155 (94%)	8 (5%)	2 (1%)	16	33
2	B	165/168 (98%)	154 (93%)	9 (6%)	2 (1%)	16	33
All	All	330/336 (98%)	309 (94%)	17 (5%)	4 (1%)	16	33

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	161	LYS
2	A	157	MET
2	B	161	LYS
2	B	157	MET

5.3.2 Protein sidechains

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	
2	A	145/145 (100%)	100 (69%)	45 (31%)	0	0
2	B	145/145 (100%)	108 (74%)	37 (26%)	1	1
All	All	290/290 (100%)	208 (72%)	82 (28%)	0	1

5 of 82 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	254	VAL
2	B	126	ASN

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Mol	Chain	Res	Type
2	B	263	GLU
2	A	261	LYS
2	A	276	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
2	A	241	ASN
2	B	134	GLN
2	B	124	ASN
2	A	134	GLN
2	B	126	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	P	12/12 (100%)	6 (50%)	4 (33%)
1	Q	12/12 (100%)	7 (58%)	5 (41%)
All	All	24/24 (100%)	13 (54%)	9 (37%)

5 of 13 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	P	2	U
1	P	3	U
1	P	6	U
1	P	7	U
1	P	11	U

5 of 9 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	Q	1	G
1	Q	11	U
1	Q	3	U
1	P	6	U
1	Q	2	U

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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.