



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 4, 2017 – 05:37 PM EDT

PDB ID : 5EMO
Title : Structure of the star domain of T-STAR in complex with AUUAAA RNA
Authors : Dominguez, C.; Feracci, M.
Deposited on : unknown
Resolution : 3.03 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
Xtriage (Phenix) : 1.9-1692
EDS : rb-20029824
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : rb-20029824

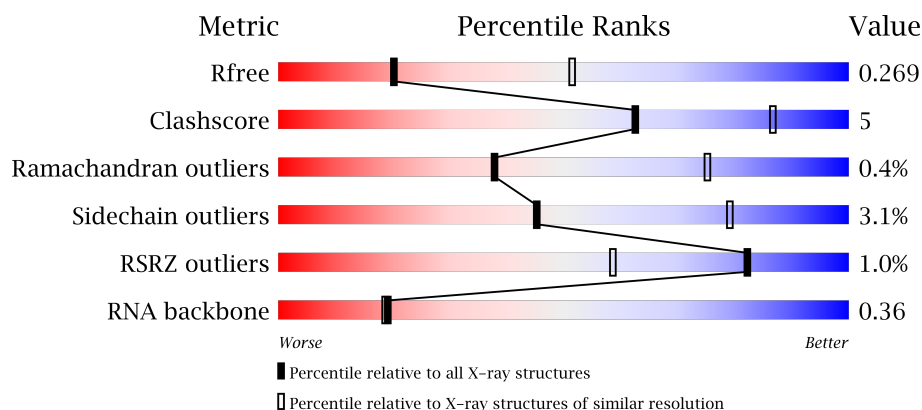
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.03 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}	100719	2176 (3.08-3.00)
Clashscore	112137	2542 (3.08-3.00)
Ramachandran outliers	110173	2458 (3.08-3.00)
Sidechain outliers	110143	2461 (3.08-3.00)
RSRZ outliers	101464	2202 (3.08-3.00)
RNA backbone	2435	1033 (3.40-2.68)

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	185	
1	B	185	
2	E	6	
2	F	6	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2606 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 KH domain-containing, RNA-binding, signal transduction-associated protein 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	144	Total	C	N	O	S	0	0	0
			1159	745	197	212	5			
1	B	147	Total	C	N	O	S	0	0	0
			1191	769	202	215	5			

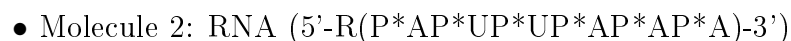
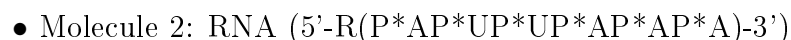
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP O75525
A	0	ALA	-	expression tag	UNP O75525
B	-1	GLY	-	expression tag	UNP O75525
B	0	ALA	-	expression tag	UNP O75525

- Molecule 2 is a RNA chain called RNA (5'-R(P*AP*UP*UP*AP*AP*A)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	6	Total	C	N	O	P	0	0	0
			128	58	24	40	6			
2	F	6	Total	C	N	O	P	0	0	0
			128	58	24	40	6			

- Molecule 1: KH domain-containing, RNA-binding, signal transduction-associated protein 3



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	51.60 Å 79.97 Å 53.83 Å 90.00° 101.05° 90.00°	Depositor
Resolution (Å)	28.51 – 3.03 28.51 – 3.03	Depositor EDS
% Data completeness (in resolution range)	93.6 (28.51-3.03) 86.1 (28.51-3.03)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.51 (at 3.05 Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.221 , 0.269 0.217 , 0.269	Depositor DCC
R_{free} test set	723 reflections (9.96%)	DCC
Wilson B-factor (Å ²)	49.8	Xtriage
Anisotropy	0.516	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 55.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.042 for l,-k,h	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	2606	wwPDB-VP
Average B, all atoms (Å ²)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.52% 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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

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	A	0.26	0/1180	0.44	0/1583
1	B	0.26	0/1213	0.48	0/1624
2	E	0.18	0/143	0.66	0/220
2	F	0.20	0/143	0.71	0/220
All	All	0.25	0/2679	0.49	0/3647

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	1159	0	1191	9	0
1	B	1191	0	1232	17	0
2	E	128	0	65	3	0
2	F	128	0	65	2	0
All	All	2606	0	2553	26	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 5.

All (26) 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:104:ARG:NH2	2:F:3:U:OP1	2.22	0.73
1:B:62:ILE:HD12	1:B:72:PHE:HB2	1.78	0.65
1:B:76:LEU:HD23	1:B:154:PHE:HD1	1.62	0.64
1:B:104:ARG:NH2	2:E:3:U:OP1	2.39	0.55
1:B:50:ILE:HD12	1:B:52:LYS:H	1.72	0.55
1:B:6:LEU:HD21	1:B:34:PHE:HD2	1.72	0.55
1:B:69:LYS:HB3	2:E:1:A:N6	2.25	0.51
2:E:1:A:H5''	2:E:2:U:H5'	1.93	0.50
1:A:89:GLU:O	1:A:92:LEU:HD23	2.12	0.49
1:B:51:ASN:ND2	1:B:51:ASN:O	2.46	0.49
1:B:156:ILE:O	1:B:156:ILE:HD12	2.14	0.48
1:A:5:TYR:HB3	1:A:7:PRO:HD2	1.95	0.48
1:B:119:LYS:HD2	1:B:120:TYR:CZ	2.49	0.47
1:B:76:LEU:HD23	1:B:154:PHE:CD1	2.48	0.45
1:B:46:ILE:HD12	1:B:137:PRO:HG3	2.00	0.44
1:A:62:ILE:HD12	1:A:127:LEU:HG	2.00	0.44
1:A:46:ILE:HG22	1:B:59:LYS:O	2.18	0.44
1:A:85:LYS:HA	1:A:88:GLN:HE21	1.83	0.43
2:F:1:A:H4'	2:F:2:U:OP1	2.17	0.43
1:A:138:ALA:HB1	1:B:149:GLU:HG3	1.99	0.43
1:A:81:GLY:O	1:A:85:LYS:HG3	2.19	0.43
1:B:85:LYS:HA	1:B:88:GLN:HE21	1.83	0.43
1:A:54:MET:N	1:A:135:ALA:O	2.50	0.43
1:B:93:THR:HG22	1:B:133:VAL:HB	2.00	0.42
1:B:57:GLY:HA2	1:B:131:ILE:O	2.20	0.42
1:B:46:ILE:HD11	1:B:54:MET:HE3	2.03	0.40

There are no symmetry-related clashes.

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
1	A	140/185 (76%)	136 (97%)	3 (2%)	1 (1%)	25 64

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	143/185 (77%)	140 (98%)	3 (2%)	0	100	100
All	All	283/370 (76%)	276 (98%)	6 (2%)	1 (0%)	38	75

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	7	PRO

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	
1	A	127/160 (79%)	124 (98%)	3 (2%)	54	83
1	B	130/160 (81%)	125 (96%)	5 (4%)	38	74
All	All	257/320 (80%)	249 (97%)	8 (3%)	45	79

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	14	ASP
1	A	71	ASN
1	A	106	LYS
1	B	14	ASP
1	B	45	TYR
1	B	71	ASN
1	B	113	ARG
1	B	134	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	58	GLN
1	A	82	ASN

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Mol	Chain	Res	Type
1	B	35	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	E	5/6 (83%)	1 (20%)	0
2	F	6/6 (100%)	1 (16%)	1 (16%)
All	All	11/12 (91%)	2 (18%)	1 (9%)

All (2) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	E	2	U
2	F	2	U

All (1) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	F	1	A

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

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	144/185 (77%)	-0.40	0 100 100	29, 49, 72, 97	0
1	B	147/185 (79%)	-0.09	3 (2%) 65 36	28, 57, 94, 114	0
2	E	6/6 (100%)	-0.22	0 100 100	42, 49, 66, 69	2 (33%)
2	F	6/6 (100%)	-0.31	0 100 100	39, 49, 72, 86	0
All	All	303/382 (79%)	-0.25	3 (0%) 82 58	28, 52, 86, 114	2 (0%)

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	116	GLY	4.3
1	B	115	SER	2.7
1	B	112	LEU	2.7

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.