Full wwPDB X-ray Structure Validation Report ⓘ

Jun 23, 2024 – 10:23 AM EDT

PDB ID	:	6SQT
Title	:	Structure of the U1A variant A1-98 Y31H/Q36R/F56W triple mutant
Authors	:	Rosenbach, H.; Span, I.
Deposited on	:	2019-09-04
Resolution	:	1.84 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
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references ⓘ) were used in the production of this report:

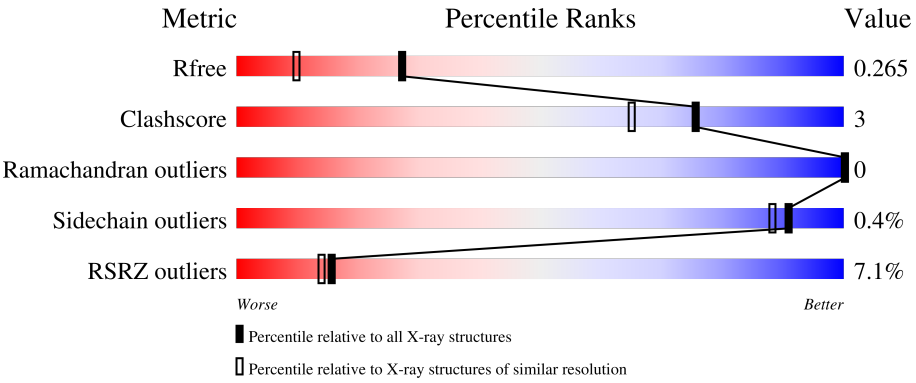
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

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 1.84 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}	130704	4003 (1.86-1.82)
Clashscore	141614	4233 (1.86-1.82)
Ramachandran outliers	138981	4185 (1.86-1.82)
Sidechain outliers	138945	4186 (1.86-1.82)
RSRZ outliers	127900	3957 (1.86-1.82)

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	AAA	98	6% 95%
1	BBB	98	6% 80% 9% 11%
1	CCC	98	7% 86% 12%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 4556 atoms, of which 2285 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 U1 small nuclear ribonucleoprotein A.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	AAA	95	Total	C	H	N	O	S	37	0	0
			1581	497	806	137	137	4			
1	BBB	87	Total	C	H	N	O	S	36	0	0
			1459	460	744	128	124	3			
1	CCC	86	Total	C	H	N	O	S	36	0	0
			1443	455	735	127	123	3			

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AAA	31	HIS	TYR	engineered mutation	UNP P09012
AAA	36	ARG	GLN	engineered mutation	UNP P09012
AAA	56	TRP	PHE	engineered mutation	UNP P09012
BBB	31	HIS	TYR	engineered mutation	UNP P09012
BBB	36	ARG	GLN	engineered mutation	UNP P09012
BBB	56	TRP	PHE	engineered mutation	UNP P09012
CCC	31	HIS	TYR	engineered mutation	UNP P09012
CCC	36	ARG	GLN	engineered mutation	UNP P09012
CCC	56	TRP	PHE	engineered mutation	UNP P09012

- Molecule 2 is water.

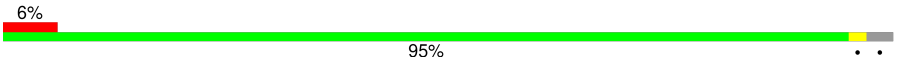
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	AAA	29	Total	O	0	0
			29	29		
2	BBB	22	Total	O	0	0
			22	22		
2	CCC	22	Total	O	0	0
			22	22		

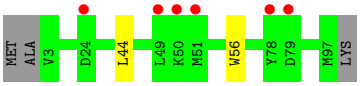
3 Residue-property plots (i)

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: U1 small nuclear ribonucleoprotein A

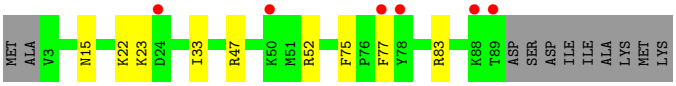
Chain AAA:





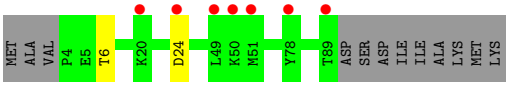
• Molecule 1: U1 small nuclear ribonucleoprotein A

Chain BBB:



• Molecule 1: U1 small nuclear ribonucleoprotein A

Chain CCC:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α, β, γ	89.81Å 89.81Å 86.56Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	38.89 – 1.84 38.89 – 1.84	Depositor EDS
% Data completeness (in resolution range)	82.0 (38.89-1.84) 82.0 (38.89-1.84)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.17 (at 1.84Å)	Xtriage
Refinement program	REFMAC 5.8.0253	Depositor
R, R_{free}	0.213 , 0.245 0.228 , 0.265	Depositor DCC
R_{free} test set	1474 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å^2)	32.0	Xtriage
Anisotropy	0.264	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.43 , 39.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.029 for -h,-k,l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	4556	wwPDB-VP
Average B, all atoms (Å^2)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.98% of the height of the origin peak. No significant pseudotranslation is detected.*

[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	AAA	0.74	0/790	0.88	0/1060
1	BBB	0.70	0/730	0.87	0/980
1	CCC	0.72	0/723	0.85	0/969
All	All	0.72	0/2243	0.87	0/3009

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	AAA	775	806	803	1	0
1	BBB	715	744	741	13	0
1	CCC	708	735	733	2	0
2	AAA	29	0	0	0	0
2	BBB	22	0	0	0	0
2	CCC	22	0	0	0	0
All	All	2271	2285	2277	14	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 (14) 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:BBB:33:ILE:HD11	1:BBB:77:PHE:CE1	2.24	0.73
1:BBB:15:ASN:OD1	1:BBB:83:ARG:HB2	1.91	0.71
1:BBB:33:ILE:CD1	1:BBB:77:PHE:CE1	2.86	0.58
1:BBB:75:PHE:CE1	1:CCC:6:THR:HG22	2.42	0.55
1:BBB:22:LYS:CG	1:BBB:23:LYS:H	2.23	0.51
1:BBB:22:LYS:HG3	1:BBB:23:LYS:H	1.79	0.47
1:AAA:44:LEU:HB2	1:AAA:56:TRP:HB2	1.98	0.45
1:BBB:22:LYS:HG3	1:BBB:23:LYS:N	2.33	0.44
1:BBB:22:LYS:HD2	1:BBB:23:LYS:H	1.82	0.44
1:BBB:22:LYS:CD	1:BBB:23:LYS:H	2.32	0.42
1:BBB:75:PHE:CZ	1:CCC:6:THR:HG22	2.53	0.42
1:BBB:33:ILE:HD11	1:BBB:77:PHE:CD1	2.54	0.42
1:BBB:22:LYS:CG	1:BBB:23:LYS:N	2.84	0.41
1:BBB:47:ARG:O	1:BBB:52:ARG:CZ	2.69	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	AAA	93/98 (95%)	92 (99%)	1 (1%)	0	100	100
1	BBB	85/98 (87%)	83 (98%)	2 (2%)	0	100	100
1	CCC	84/98 (86%)	83 (99%)	1 (1%)	0	100	100
All	All	262/294 (89%)	258 (98%)	4 (2%)	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	AAA	86/88 (98%)	86 (100%)	0	100 100
1	BBB	79/88 (90%)	79 (100%)	0	100 100
1	CCC	78/88 (89%)	77 (99%)	1 (1%)	69 58
All	All	243/264 (92%)	242 (100%)	1 (0%)	91 88

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

Mol	Chain	Res	Type
1	CCC	24	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 monosaccharides 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

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, 95^{th} 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	AAA	95/98 (96%)	0.35	6 (6%)	20	17	27, 37, 72, 91	0
1	BBB	87/98 (88%)	0.38	6 (6%)	16	15	28, 40, 64, 74	0
1	CCC	86/98 (87%)	0.57	7 (8%)	12	11	28, 38, 71, 78	0
All	All	268/294 (91%)	0.43	19 (7%)	16	14	27, 39, 70, 91	0

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	CCC	49	LEU	7.2
1	CCC	50	LYS	4.3
1	AAA	49	LEU	4.2
1	CCC	51	MET	3.7
1	BBB	89	THR	3.6
1	AAA	78	TYR	3.1
1	CCC	89	THR	3.0
1	BBB	88	LYS	3.0
1	CCC	78	TYR	2.8
1	CCC	20	LYS	2.7
1	AAA	50	LYS	2.7
1	BBB	50	LYS	2.7
1	CCC	24	ASP	2.4
1	AAA	79	ASP	2.3
1	BBB	78	TYR	2.2
1	AAA	24	ASP	2.1
1	BBB	77	PHE	2.1
1	BBB	24	ASP	2.1
1	AAA	51	MET	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 monosaccharides 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.