Full wwPDB X-ray Structure Validation Report (i)

Feb 19, 2016 – 08:35 PM GMT

PDB ID	:	4YVQ
Title	:	Crystal Structure of FLU-TPR in Complex with the C-terminal Region of GluTR
Authors	:	Zhang, M.; Zhang, F.; Liu, L.
Deposited on	:	2015-03-20
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:

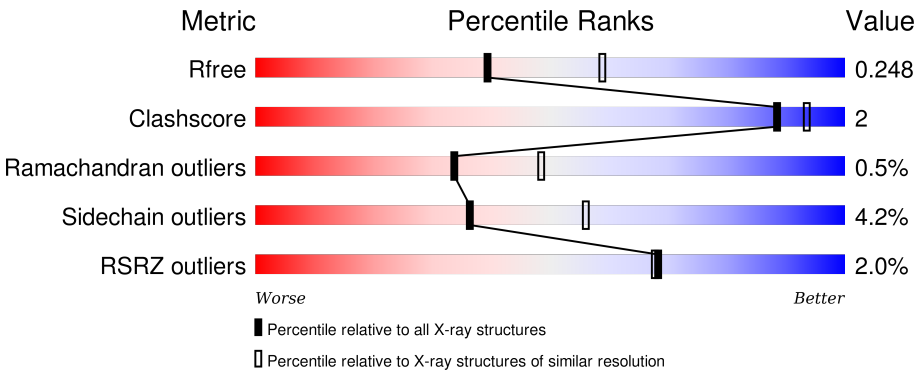
MolProbity	:	4.02b-467
Mogul	:	unknown
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026982
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20026982

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	105	3%, 72%, 7%, •, 20%
2	C	159	%, 68%, 5%, •, 25%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 1691 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 Glutamyl-tRNA reductase 1, chloroplastic.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	84	661	409	125	120	7	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	439	MET	-	expression tag	UNP P42804

- Molecule 2 is a protein called Protein FLUORESCENT IN BLUE LIGHT, chloroplastic.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	C	119	949	598	163	186	2	2	1	0

There are 37 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	158	MET	-	expression tag	UNP Q940U6
C	159	LYS	-	expression tag	UNP Q940U6
C	160	TYR	-	expression tag	UNP Q940U6
C	161	LEU	-	expression tag	UNP Q940U6
C	162	LEU	-	expression tag	UNP Q940U6
C	163	PRO	-	expression tag	UNP Q940U6
C	164	THR	-	expression tag	UNP Q940U6
C	165	ALA	-	expression tag	UNP Q940U6
C	166	ALA	-	expression tag	UNP Q940U6
C	167	ALA	-	expression tag	UNP Q940U6
C	168	GLY	-	expression tag	UNP Q940U6
C	169	LEU	-	expression tag	UNP Q940U6
C	170	LEU	-	expression tag	UNP Q940U6
C	171	LEU	-	expression tag	UNP Q940U6
C	172	LEU	-	expression tag	UNP Q940U6

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Chain	Residue	Modelled	Actual	Comment	Reference
C	173	ALA	-	expression tag	UNP Q940U6
C	174	ALA	-	expression tag	UNP Q940U6
C	175	GLN	-	expression tag	UNP Q940U6
C	176	PRO	-	expression tag	UNP Q940U6
C	177	ALA	-	expression tag	UNP Q940U6
C	178	MET	-	expression tag	UNP Q940U6
C	179	ALA	-	expression tag	UNP Q940U6
C	180	MET	-	expression tag	UNP Q940U6
C	181	ASP	-	expression tag	UNP Q940U6
C	182	ILE	-	expression tag	UNP Q940U6
C	183	GLY	-	expression tag	UNP Q940U6
C	184	ILE	-	expression tag	UNP Q940U6
C	185	ASN	-	expression tag	UNP Q940U6
C	186	SER	-	expression tag	UNP Q940U6
C	187	ASP	-	expression tag	UNP Q940U6
C	188	PRO	-	expression tag	UNP Q940U6
C	189	HIS	-	expression tag	UNP Q940U6
C	190	HIS	-	expression tag	UNP Q940U6
C	191	HIS	-	expression tag	UNP Q940U6
C	192	HIS	-	expression tag	UNP Q940U6
C	193	HIS	-	expression tag	UNP Q940U6
C	194	HIS	-	expression tag	UNP Q940U6

- Molecule 3 is water.

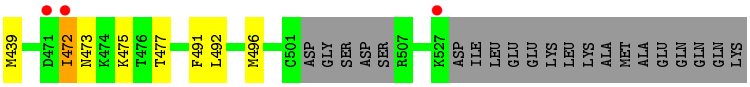
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	51	51	51	0	0
			Total	O		
3	C	30	30	30	0	0

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.

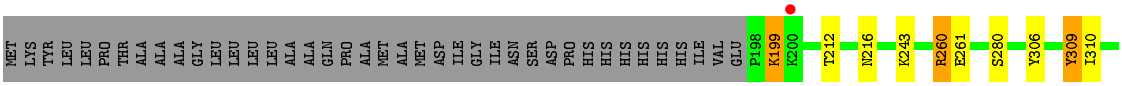
- Molecule 1: Glutamyl-tRNA reductase 1, chloroplastic

Chain A:



- Molecule 2: Protein FLUORESCENT IN BLUE LIGHT, chloroplastic

Chain C:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, α, β, γ	74.73Å 74.73Å 161.66Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	34.28 – 2.40 34.28 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.9 (34.28-2.40) 100.0 (34.28-2.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.90 (at 2.39Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.208 , 0.242 0.210 , 0.248	Depositor DCC
R_{free} test set	529 reflections (4.79%)	DCC
Wilson B-factor (Å^2)	47.9	Xtriage
Anisotropy	0.372	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 47.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Outliers	0 of 11048 reflections	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	1691	wwPDB-VP
Average B, all atoms (Å^2)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.28% 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, 0.375 respectively for untwinned datasets, and 0.333, 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	0.23	0/667	0.42	0/892
2	C	0.26	0/965	0.40	0/1290
All	All	0.25	0/1632	0.41	0/2182

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	661	0	673	3	0
2	C	949	0	963	5	0
3	A	51	0	0	1	0
3	C	30	0	0	0	0
All	All	1691	0	1636	8	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 2.

All (8) 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:439:MET:N	3:A:603:HOH:O	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:472:ILE:HG13	1:A:477:THR:OG1	2.09	0.52
2:C:306:TYR:O	2:C:310:ILE:HG12	2.12	0.50
2:C:243:LYS:NZ	2:C:280:SER:O	2.42	0.46
2:C:212:THR:O	2:C:216:ASN:ND2	2.40	0.42
1:A:492:LEU:HB3	1:A:496:MET:HE2	2.03	0.41
2:C:309:TYR:CZ	2:C:313:LEU:HD21	2.56	0.41
2:C:260:ARG:HG2	2:C:261:GLU:OE1	2.21	0.41

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	80/105 (76%)	80 (100%)	0	0	100	100
2	C	118/159 (74%)	117 (99%)	0	1 (1%)	24	35
All	All	198/264 (75%)	197 (100%)	0	1 (0%)	34	48

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	199	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	71/93 (76%)	67 (94%)	4 (6%)	26	41
2	C	98/129 (76%)	95 (97%)	3 (3%)	47	69
All	All	169/222 (76%)	162 (96%)	7 (4%)	36	57

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	472	ILE
1	A	473	ASN
1	A	475	LYS
1	A	491	PHE
2	C	199	LYS
2	C	260	ARG
2	C	309	TYR

Some 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 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(Å^2)	Q<0.9
1	A	84/105 (80%)	-0.10	3 (3%)	46	47	26, 39, 82, 103	4 (4%)
2	C	119/159 (74%)	-0.48	1 (0%)	87	87	29, 48, 80, 92	8 (6%)
All	All	203/264 (76%)	-0.32	4 (1%)	68	68	26, 44, 82, 103	12 (5%)

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	471	ASP	4.5
1	A	527	LYS	3.1
1	A	472	ILE	2.4
2	C	200	LYS	2.4

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.