Full wwPDB X-ray Structure Validation Report (i)

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PDB ID	:	5CLZ
Title	:	X-ray structure of TTR mutant - T119M at 1.22A resolution
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Deposited on	:	2015-07-16
Resolution	:	1.22 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:

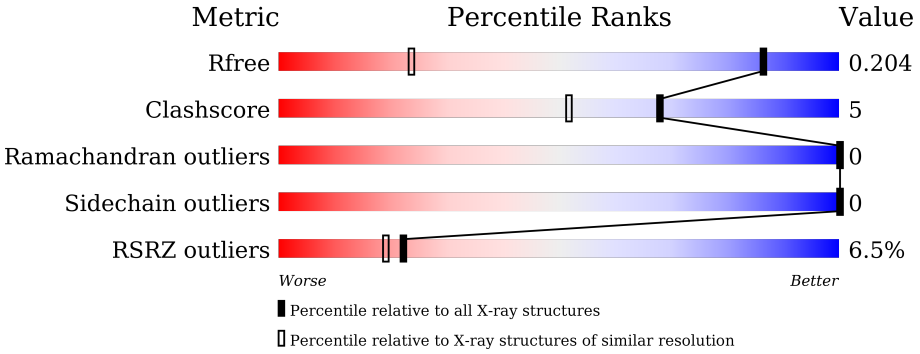
MolProbity	:	4.02b-467
Mogul	:	unknown
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20027790
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20027790

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 1.22 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	1197 (1.26-1.18)
Clashscore	102246	1295 (1.26-1.18)
Ramachandran outliers	100387	1239 (1.26-1.18)
Sidechain outliers	100360	1237 (1.26-1.18)
RSRZ outliers	91569	1201 (1.26-1.18)

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	130	2% 82% 8% 11%
1	B	130	9% 81% 8% 11%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 2039 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 Transthyretin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	116	935	598	151	183	3	0	8	0
1	B	116	917	584	150	180	3	0	4	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP P02766
A	-1	ALA	-	expression tag	UNP P02766
A	0	MET	-	expression tag	UNP P02766
A	119	MET	THR	engineered mutation	UNP P02766
B	-2	GLY	-	expression tag	UNP P02766
B	-1	ALA	-	expression tag	UNP P02766
B	0	MET	-	expression tag	UNP P02766
B	119	MET	THR	engineered mutation	UNP P02766

- Molecule 2 is water.

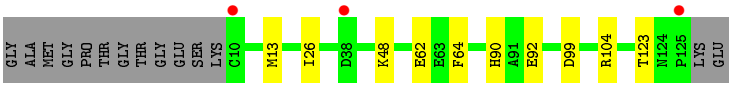
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
2	A	101	106	106	0	5
2	B	79	81	81	0	2

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.

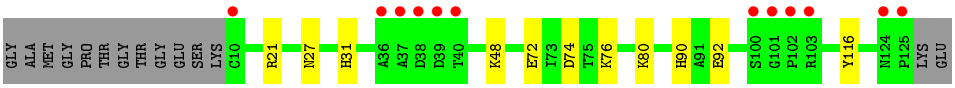
- Molecule 1: Transthyretin

Chain A:



- Molecule 1: Transthyretin

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α, β, γ	42.91Å 85.72Å 63.36Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.37 – 1.22 35.53 – 1.22	Depositor EDS
% Data completeness (in resolution range)	98.5 (38.37-1.22) 98.5 (35.53-1.22)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.04	Depositor
$< I/\sigma(I) >$ [1]	1.50 (at 1.22Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.162 , 0.197 0.170 , 0.204	Depositor DCC
R_{free} test set	3482 reflections (5.29%)	DCC
Wilson B-factor (Å^2)	16.3	Xtriage
Anisotropy	0.085	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.39 , 49.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	2039	wwPDB-VP
Average B, all atoms (Å^2)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 33.47 % of the origin peak, indicating pseudo translational symmetry.The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 7.9593e-04.*

[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 (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	1.18	1/981 (0.1%)	1.09	2/1339 (0.1%)
1	B	1.17	3/949 (0.3%)	1.04	3/1294 (0.2%)
All	All	1.18	4/1930 (0.2%)	1.07	5/2633 (0.2%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	72	GLU	CD-OE2	-6.01	1.19	1.25
1	B	72	GLU	CB-CG	-5.22	1.42	1.52
1	A	62	GLU	CD-OE2	5.10	1.31	1.25
1	B	116	TYR	CE2-CZ	-5.04	1.32	1.38

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	104	ARG	NE-CZ-NH1	9.63	125.12	120.30
1	A	64	PHE	CB-CG-CD2	-5.57	116.90	120.80
1	B	72	GLU	CG-CD-OE1	5.47	129.23	118.30
1	B	21	ARG	NE-CZ-NH2	-5.46	117.57	120.30
1	B	72	GLU	CG-CD-OE2	-5.24	107.81	118.30

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	935	0	913	9	0
1	B	917	0	885	8	0
2	A	106	0	0	8	1
2	B	81	0	0	4	0
All	All	2039	0	1798	17	1

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 (17) 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:92:GLU:HB2	2:A:230:HOH:O	1.67	0.94
1:A:99:ASP:OD1	2:A:202:HOH:O	1.93	0.86
1:B:90:HIS:CD2	1:B:92:GLU:HG3	2.22	0.74
1:B:74[B]:ASP:OD1	2:B:202:HOH:O	2.08	0.70
1:B:74[A]:ASP:OD1	2:B:201:HOH:O	0.67	0.67
1:A:48:LYS:CD	2:A:203:HOH:O	2.44	0.64
1:B:74[B]:ASP:CG	2:B:202:HOH:O	2.36	0.62
1:A:99:ASP:O	2:A:204:HOH:O	2.16	0.60
1:B:90:HIS:HD2	1:B:92:GLU:HG3	1.67	0.59
1:A:123:THR:HG22	2:A:268:HOH:O	2.07	0.54
1:B:76:LYS:HG2	1:B:80:LYS:HD3	1.92	0.52
1:A:48:LYS:HD2	2:A:203:HOH:O	2.08	0.51
1:B:31:HIS:HD2	2:B:269:HOH:O	1.94	0.50
1:B:27[A]:ASN:OD1	1:B:48:LYS:HD3	2.13	0.48
1:A:90[A]:HIS:NE2	1:A:92:GLU:OE1	2.50	0.44
1:A:13:MET:HB2	2:A:298:HOH:O	2.20	0.42
1:A:26:ILE:HD11	2:A:214:HOH:O	2.20	0.41

All (1) 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)
2:A:204:HOH:O	2:A:263:HOH:O[4_445]	2.15	0.05

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	122/130 (94%)	121 (99%)	1 (1%)	0	100	100
1	B	118/130 (91%)	116 (98%)	2 (2%)	0	100	100
All	All	240/260 (92%)	237 (99%)	3 (1%)	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	A	105/106 (99%)	105 (100%)	0	100	100
1	B	101/106 (95%)	101 (100%)	0	100	100
All	All	206/212 (97%)	206 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

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	116/130 (89%)	0.07	3 (2%) 59 55	11, 17, 41, 50	0
1	B	116/130 (89%)	0.38	12 (10%) 9 8	12, 19, 54, 83	0
All	All	232/260 (89%)	0.22	15 (6%) 22 19	11, 19, 48, 83	0

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	125	PRO	6.3
1	B	102	PRO	5.8
1	B	37	ALA	5.0
1	B	38	ASP	4.3
1	B	101	GLY	4.2
1	B	39	ASP	3.7
1	B	10	CYS	3.4
1	B	124	ASN	3.0
1	B	40	THR	3.0
1	A	125	PRO	2.8
1	B	36	ALA	2.6
1	A	10	CYS	2.5
1	B	103	ARG	2.2
1	B	100	SER	2.2
1	A	38	ASP	2.0

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.