



wwPDB X-ray Structure Validation Summary Report i

Feb 26, 2014 – 04:56 PM GMT

PDB ID : 3V89
Title : The crystal structure of transferrin binding protein A (TbpA) from *Neisseria meningitidis* serogroup B in complex with the C-lobe of human transferrin
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Deposited on : 2011-12-22
Resolution : 3.10 Å (reported)

This is a wwPDB 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/ValidationPDFNotes.html>

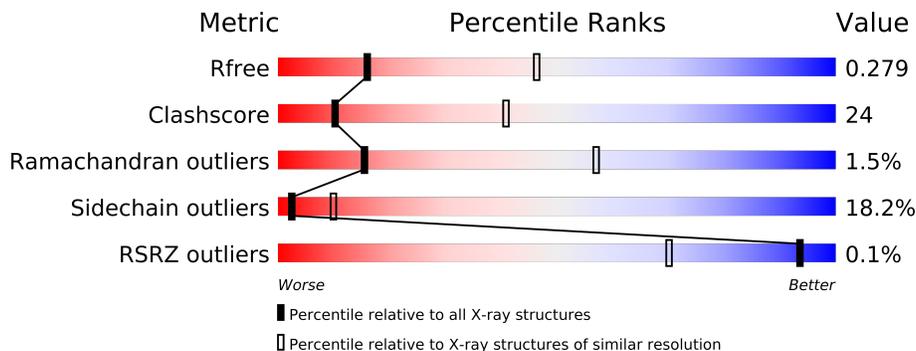
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 3.10 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}	66092	1007 (3.18-3.02)
Clashscore	79885	1078 (3.16-3.04)
Ramachandran outliers	78287	1044 (3.16-3.04)
Sidechain outliers	78261	1044 (3.16-3.04)
RSRZ outliers	66119	1008 (3.18-3.02)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	904	
2	B	343	

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 9110 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Transferrin-binding protein A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	853	6558	4091	1182	1274	11	0	0	0

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	12	MET	-	EXPRESSION TAG	UNP Q9JPJ0
A	13	ASP	-	EXPRESSION TAG	UNP Q9JPJ0
A	14	ILE	-	EXPRESSION TAG	UNP Q9JPJ0
A	15	HIS	-	EXPRESSION TAG	UNP Q9JPJ0
A	16	HIS	-	EXPRESSION TAG	UNP Q9JPJ0
A	17	HIS	-	EXPRESSION TAG	UNP Q9JPJ0
A	18	HIS	-	EXPRESSION TAG	UNP Q9JPJ0
A	19	HIS	-	EXPRESSION TAG	UNP Q9JPJ0
A	20	HIS	-	EXPRESSION TAG	UNP Q9JPJ0
A	21	HIS	-	EXPRESSION TAG	UNP Q9JPJ0
A	22	HIS	-	EXPRESSION TAG	UNP Q9JPJ0
A	23	HIS	-	EXPRESSION TAG	UNP Q9JPJ0
A	24	HIS	-	EXPRESSION TAG	UNP Q9JPJ0

- Molecule 2 is a protein called Serotransferrin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	339	2552	1587	436	503	26	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	429	VAL	ILE	VARIANT	UNP P02787

R632	I641	N645	E648	E653	Y656	K657	T667	C674	PHE	ARG	ARG	PRD
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4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	58.05Å 107.59Å 130.72Å 90.00° 94.48° 90.00°	Depositor
Resolution (Å)	29.96 – 3.10 41.69 – 3.09	Depositor EDS
% Data completeness (in resolution range)	96.8 (29.96-3.10) 91.6 (41.69-3.09)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.14 (at 3.06Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.2_865)	Depositor
R, R_{free}	0.224 , 0.287 0.221 , 0.279	Depositor DCC
R_{free} test set	1345 reflections (4.99%)	DCC
Wilson B-factor (Å ²)	59.2	Xtriage
Anisotropy	0.406	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 35.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 28386 reflections	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	9110	wwPDB-VP
Average B, all atoms (Å ²)	73.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.07% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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	A	0.31	0/6701	0.57	0/9081
2	B	0.28	0/2605	0.50	0/3535
All	All	0.30	0/9306	0.55	0/12616

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	A	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	289	VAL	Peptide
1	A	743	ASP	Peptide

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	6558	0	37	190	1
2	B	2552	0	0	28	1
All	All	9110	0	37	215	1

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 24.

The worst 5 of 215 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:75:ASN:ND2	1:A:77:ARG:N	1.95	1.14
1:A:854:TYR:CE1	1:A:856:VAL:CG1	2.30	1.13
1:A:52:ASP:CB	1:A:53:ASN:CB	2.30	1.09
1:A:854:TYR:CD1	1:A:856:VAL:CG1	2.40	1.05
1:A:855:THR:CG2	1:A:861:THR:CB	2.37	1.03

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	Distance(Å)	Clash(Å)
1:A:290:SER:OG	2:B:438:ASP:O[2_454]	2.02	0.18

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	847/904 (94%)	757 (89%)	72 (8%)	18 (2%)	11	48
2	B	337/343 (98%)	311 (92%)	26 (8%)	0	100	100
All	All	1184/1247 (95%)	1068 (90%)	98 (8%)	18 (2%)	15	57

5 of 18 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	52	ASP
1	A	55	VAL
1	A	56	THR

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Mol	Chain	Res	Type
1	A	58	LEU
1	A	800	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	662/741 (89%)	530 (80%)	132 (20%)	2	8
2	B	271/292 (93%)	233 (86%)	38 (14%)	5	21
All	All	933/1033 (90%)	763 (82%)	170 (18%)	2	10

5 of 170 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	508	SER
1	A	625	SER
2	B	611	ASN
1	A	524	TYR
1	A	566	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	75	ASN

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

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	853/904 (94%)	-0.18	1 (0%) 93 70	24, 73, 122, 160	0
2	B	339/343 (98%)	-0.26	0 100 100	31, 69, 112, 126	0
All	All	1192/1247 (95%)	-0.20	1 (0%) 93 70	24, 72, 118, 160	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	621	HIS	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.