



# Full wwPDB X-ray Structure Validation Report ⓘ

May 29, 2020 – 05:05 pm BST

PDB ID : 2Y3E  
Title : Traptavidin, apo-form  
Authors : Chivers, C.E.; Koner, A.L.; Lowe, E.D.; Howarth, M.  
Deposited on : 2010-12-20  
Resolution : 1.45 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](mailto: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.

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

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.11  
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) : 2.11

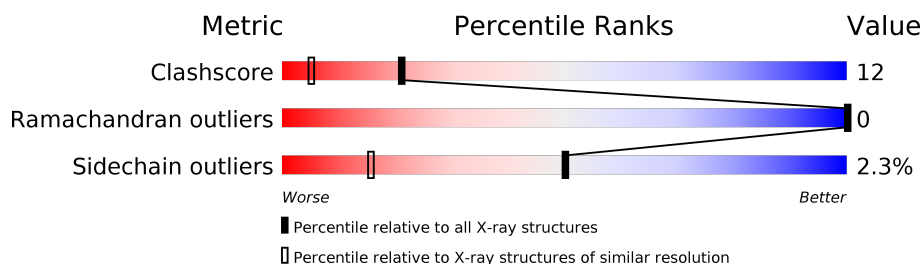
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.45 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))
Clashscore	141614	2086 (1.46-1.42)
Ramachandran outliers	138981	2047 (1.46-1.42)
Sidechain outliers	138945	2047 (1.46-1.42)

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  $\geq 3$ , 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  $\leq 5\%$ .

Mol	Chain	Length	Quality of chain
1	A	134	<div> <div style="width: 72%; background-color: green;"></div> <div style="width: 17%; background-color: yellow;"></div> <div style="width: 10%; background-color: red;"></div> <div style="width: 3%; background-color: grey;"></div> </div> <div>72% 17% 10%</div>
1	B	134	<div> <div style="width: 69%; background-color: green;"></div> <div style="width: 21%; background-color: yellow;"></div> <div style="width: 10%; background-color: red;"></div> <div style="width: 0%; background-color: grey;"></div> </div> <div>69% 21% 10%</div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	GOL	B	1137	-	-	X	-

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 2191 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 STREPTAVIDIN.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	A	120	Total	C	N	O	0	3	0
			916	571	157	188			
1	B	120	Total	C	N	O	0	5	0
			939	593	158	188			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	12	MET	-	expression tag	UNP P22629
A	52	GLY	SER	engineered mutation	UNP P22629
A	53	ASP	ARG	engineered mutation	UNP P22629
A	140	HIS	-	expression tag	UNP P22629
A	141	HIS	-	expression tag	UNP P22629
A	142	HIS	-	expression tag	UNP P22629
A	143	HIS	-	expression tag	UNP P22629
A	144	HIS	-	expression tag	UNP P22629
A	145	HIS	-	expression tag	UNP P22629
B	12	MET	-	expression tag	UNP P22629
B	52	GLY	SER	engineered mutation	UNP P22629
B	53	ASP	ARG	engineered mutation	UNP P22629
B	140	HIS	-	expression tag	UNP P22629
B	141	HIS	-	expression tag	UNP P22629
B	142	HIS	-	expression tag	UNP P22629
B	143	HIS	-	expression tag	UNP P22629
B	144	HIS	-	expression tag	UNP P22629
B	145	HIS	-	expression tag	UNP P22629

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			6	3	3		
2	B	1	Total	C	O	0	0
			6	3	3		
2	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 3 is water.

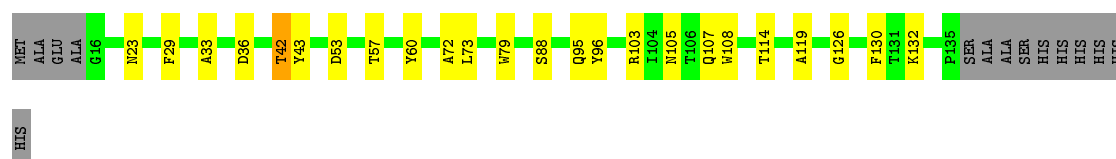
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	148	Total	O	0	0
			148	148		
3	B	170	Total	O	0	0
			170	170		

### 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 the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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. 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.

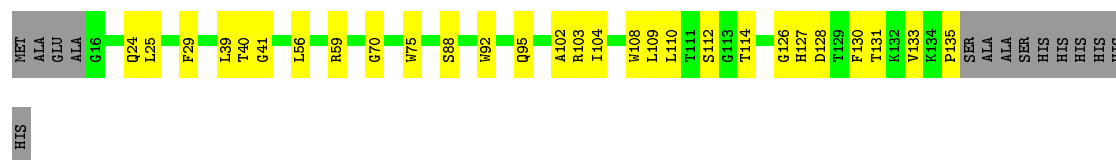
#### • Molecule 1: STREPTAVIDIN

Chain A: 



#### • Molecule 1: STREPTAVIDIN

Chain B: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	I 41	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	57.59Å 57.59Å 183.35Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	27.47 – 1.45 27.47 – 1.45	Depositor EDS
% Data completeness (in resolution range)	92.8 (27.47-1.45) 92.8 (27.47-1.45)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.04 (at 1.45Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, $R_{free}$	0.134 , 0.178 (Not available) , (Not available)	Depositor DCC
$R_{free}$ test set	2633 reflections (5.11%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	14.1	Xtriage
Anisotropy	0.458	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 33.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.44$ , $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	0.477 for -h,k,-l	Xtriage
Reported twinning fraction	0.497 for -H,K,-L	Depositor
Outliers	0 of 51525 reflections	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	2191	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.69% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup> Intensities estimated from amplitudes.

<sup>2</sup> Theoretical 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL

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	0.30	0/939	0.51	0/1286
1	B	0.30	0/964	0.53	0/1321
All	All	0.30	0/1903	0.52	0/2607

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	916	0	846	20	0
1	B	939	0	875	31	0
2	A	6	0	8	0	0
2	B	12	0	16	6	0
3	A	148	0	0	3	0
3	B	170	0	0	1	0
All	All	2191	0	1745	44	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 12.

All (44) 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:B:29[B]:PHE:HE1	1:B:56:LEU:HD11	1.29	0.95
1:B:29[B]:PHE:CE1	1:B:56:LEU:HD11	2.12	0.84
1:A:95:GLN:HE22	1:B:114:THR:H	1.27	0.82
1:A:103:ARG:HE	1:A:105:ASN:HD21	1.27	0.81
1:B:108:TRP:CE2	2:B:1137:GOL:H11	2.18	0.78
1:A:114:THR:H	1:B:95:GLN:HE22	1.37	0.72
1:B:108:TRP:CD2	2:B:1137:GOL:H11	2.26	0.69
1:A:23:ASN:HB3	1:A:130:PHE:CE1	2.31	0.66
1:A:103:ARG:NE	1:A:105:ASN:HD21	1.98	0.61
1:B:92:TRP:HZ2	2:B:1137:GOL:O2	1.86	0.58
1:A:107:GLN:HB2	1:B:109:LEU:HD13	1.86	0.57
1:B:29[B]:PHE:CE1	1:B:56:LEU:CD1	2.86	0.56
1:B:92:TRP:CZ2	2:B:1137:GOL:O2	2.58	0.56
1:B:110:LEU:HD21	2:B:1136:GOL:H2	1.86	0.56
1:B:29[A]:PHE:CE1	1:B:56:LEU:HD11	2.39	0.56
1:A:36:ASP:HA	3:A:2031:HOH:O	2.05	0.55
1:B:24:GLN:HG2	1:B:25:LEU:HG	1.92	0.52
1:A:132:LYS:HD3	3:A:2145:HOH:O	2.10	0.51
1:B:102:ALA:O	1:B:103:ARG:HD3	2.12	0.48
1:B:29[B]:PHE:HE1	1:B:56:LEU:CD1	2.11	0.48
1:A:79:TRP:HD1	1:A:88:SER:HG	1.59	0.48
1:B:70:GLY:HA3	1:B:95:GLN:HE21	1.81	0.46
1:B:75:TRP:NE1	1:B:92:TRP:CE3	2.84	0.46
1:A:57:THR:HG22	1:B:59:ARG:HG2	1.98	0.45
1:B:104:ILE:HB	1:B:130:PHE:HB2	1.98	0.44
1:B:112:SER:O	1:B:114:THR:HG23	2.17	0.44
1:A:108:TRP:CE2	1:A:126:GLY:HA3	2.53	0.43
1:A:95:GLN:NE2	1:B:114:THR:H	2.05	0.43
1:A:42:THR:OG1	1:A:53:ASP:HB3	2.19	0.43
1:A:29:PHE:HB3	1:A:43:TYR:CD2	2.53	0.43
1:A:72:ALA:CB	1:B:88:SER:HA	2.48	0.43
1:A:33:ALA:HB1	1:A:60:TYR:CE1	2.54	0.43
1:B:29[A]:PHE:CE1	1:B:56:LEU:CD1	3.02	0.42
1:A:29:PHE:HB2	1:A:42:THR:O	2.19	0.42
1:B:88:SER:OG	2:B:1136:GOL:H32	2.20	0.42
1:B:127:HIS:O	1:B:128:ASP:OD1	2.38	0.42
1:B:108:TRP:CZ2	1:B:126:GLY:HA3	2.54	0.42
1:A:103:ARG:NH1	3:A:2117:HOH:O	2.53	0.41
1:B:88:SER:HB3	1:B:112:SER:HA	2.03	0.41
1:B:135:PRO:HD2	3:B:2017:HOH:O	2.21	0.41
1:A:114:THR:OG1	1:A:119:ALA:HA	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:114:THR:H	1:B:95:GLN:NE2	2.11	0.41
1:B:131:THR:HG23	1:B:133:VAL:O	2.21	0.40
1:B:40[A]:THR:HG22	1:B:41:GLY:N	2.36	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	A	121/134 (90%)	117 (97%)	4 (3%)	0	100	100
1	B	123/134 (92%)	122 (99%)	1 (1%)	0	100	100
All	All	244/268 (91%)	239 (98%)	5 (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	A	91/98 (93%)	88 (97%)	3 (3%)	38	7
1	B	93/98 (95%)	91 (98%)	2 (2%)	52	17
All	All	184/196 (94%)	179 (97%)	5 (3%)	50	11

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	42	THR
1	A	73	LEU
1	A	96	TYR
1	B	39[A]	LEU
1	B	39[B]	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	95	GLN
1	A	105	ASN
1	A	118	ASN
1	B	95	GLN

### 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](#)

3 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
2	GOL	B	1137	-	5,5,5	0.44	0	5,5,5	0.35	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	GOL	A	1136	-	5,5,5	0.40	0	5,5,5	0.32	0
2	GOL	B	1136	-	5,5,5	0.38	0	5,5,5	0.32	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GOL	B	1137	-	-	4/4/4/4	-
2	GOL	A	1136	-	-	2/4/4/4	-
2	GOL	B	1136	-	-	0/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1136	GOL	C1-C2-C3-O3
2	A	1136	GOL	O2-C2-C3-O3
2	B	1137	GOL	O1-C1-C2-C3
2	B	1137	GOL	O2-C2-C3-O3
2	B	1137	GOL	O1-C1-C2-O2
2	B	1137	GOL	C1-C2-C3-O3

There are no ring outliers.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1137	GOL	4	0
2	B	1136	GOL	2	0

## 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 ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.3 Carbohydrates ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.4 Ligands ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.5 Other polymers ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.