



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 09:00 PM GMT

PDB ID : 1N4A  
Title : The Ligand Bound Structure of E.coli BtuF, the Periplasmic Binding Protein for Vitamin B12  
Authors : Karpowich, N.K; Smith, P.C.; Hunt, J.F.; Northeast Structural Genomics Consortium (NESG)  
Deposited on : 2002-10-30  
Resolution : 2.00 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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  
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
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) : trunk26865

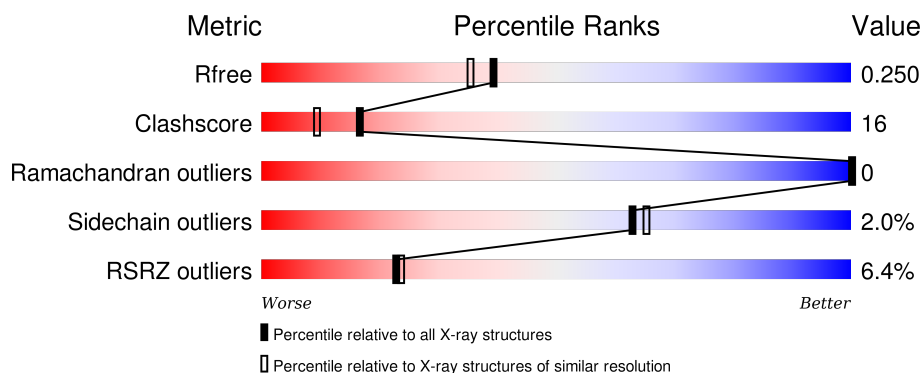
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.00 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	6249 (2.00-2.00)
Clashscore	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (2.00-2.00)
RSRZ outliers	91569	6262 (2.00-2.00)

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. 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  $\leq 5\%$ . 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	252	<div> <div>4%</div> <div>71%</div> <div>24%</div> <div>• •</div> </div>
1	B	252	<div> <div>9%</div> <div>71%</div> <div>26%</div> <div>•</div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4539 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.

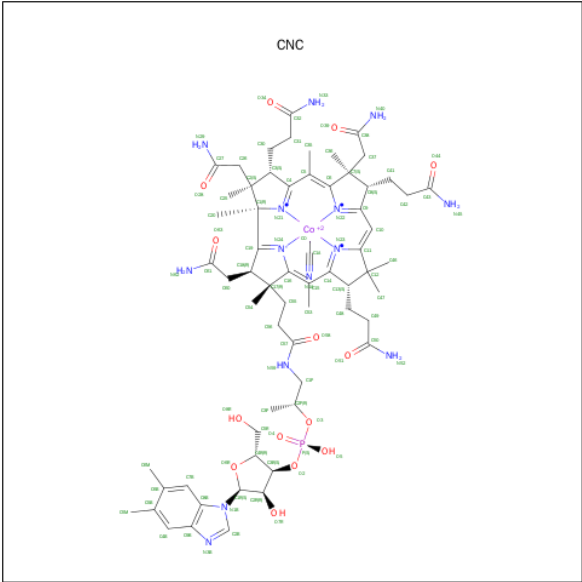
- Molecule 1 is a protein called Vitamin B12 transport protein btuF.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	244	Total	C	N	O	S	Se	0	0	0
			1902	1213	331	354	2	2			
1	B	244	Total	C	N	O	S	Se	0	0	0
			1902	1213	331	354	2	2			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	47	MSE	MET	MODIFIED RESIDUE	UNP P37028
A	83	MSE	MET	MODIFIED RESIDUE	UNP P37028
A	245	LEU	-	EXPRESSION TAG	UNP P37028
A	246	GLU	-	EXPRESSION TAG	UNP P37028
A	247	HIS	-	EXPRESSION TAG	UNP P37028
A	248	HIS	-	EXPRESSION TAG	UNP P37028
A	249	HIS	-	EXPRESSION TAG	UNP P37028
A	250	HIS	-	EXPRESSION TAG	UNP P37028
A	251	HIS	-	EXPRESSION TAG	UNP P37028
A	252	HIS	-	EXPRESSION TAG	UNP P37028
B	5047	MSE	MET	MODIFIED RESIDUE	UNP P37028
B	5083	MSE	MET	MODIFIED RESIDUE	UNP P37028
B	5245	LEU	-	EXPRESSION TAG	UNP P37028
B	5246	GLU	-	EXPRESSION TAG	UNP P37028
B	5247	HIS	-	EXPRESSION TAG	UNP P37028
B	5248	HIS	-	EXPRESSION TAG	UNP P37028
B	5249	HIS	-	EXPRESSION TAG	UNP P37028
B	5250	HIS	-	EXPRESSION TAG	UNP P37028
B	5251	HIS	-	EXPRESSION TAG	UNP P37028
B	5252	HIS	-	EXPRESSION TAG	UNP P37028

- Molecule 2 is CO-CYANOCOBALAMIN (three-letter code: CNC) (formula:  $C_{63}H_{88}CoN_{14}O_{14}P$ ).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	Co	N	O	P	0	0
			93	63	1	14	14	1		
2	B	1	Total	C	Co	N	O	P	0	0
			93	63	1	14	14	1		

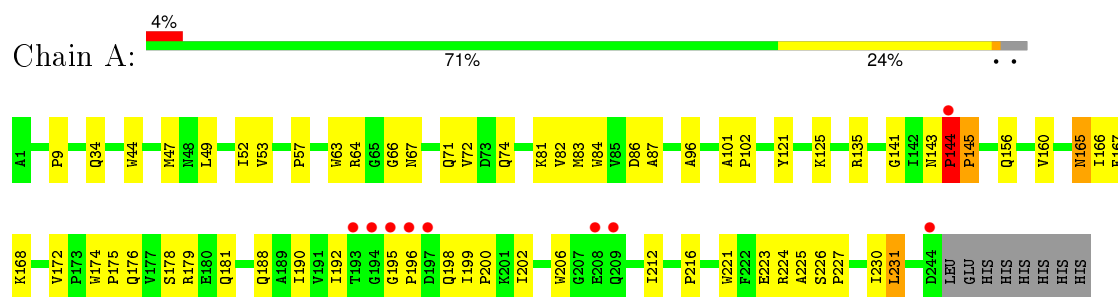
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	296	Total	O	0	0
			296	296		
3	B	253	Total	O	0	0
			253	253		

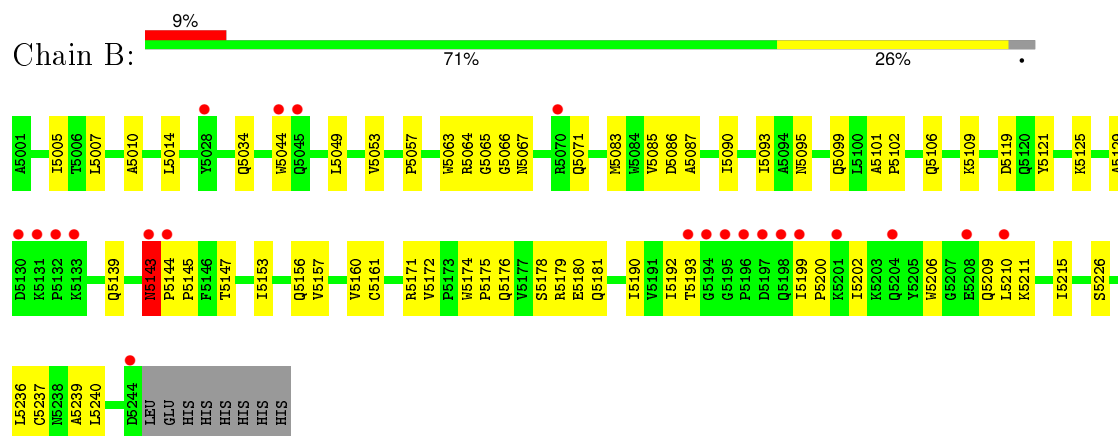
### 3 Residue-property plots [i](#)

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 ( $\text{RSRZ} > 2$ ). 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: Vitamin B12 transport protein btuF



#### • Molecule 1: Vitamin B12 transport protein btuF



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 2 <sub>1</sub> 2 <sub>1</sub> 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	131.73 Å   92.02 Å   44.69 Å 90.00°   90.00°   90.00°	Depositor
Resolution (Å)	20.00 – 2.00 20.10 – 1.98	Depositor EDS
% Data completeness (in resolution range)	24.4 (20.00-2.00) 90.9 (20.10-1.98)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	33.49 (at 1.99 Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.234   ,   0.261 0.208   ,   0.250	Depositor DCC
$R_{free}$ test set	1732 reflections (5.27%)	DCC
Wilson B-factor (Å <sup>2</sup> )	31.8	Xtriage
Anisotropy	0.427	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 67.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 34910 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	4539	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.11% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: CNC

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	0.33	0/1944	0.61	3/2648 (0.1%)
1	B	0.32	0/1944	0.60	1/2648 (0.0%)
All	All	0.32	0/3888	0.60	4/5296 (0.1%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	5143	ASN	C-N-CD	-9.21	100.34	120.60
1	A	143	ASN	C-N-CD	-6.97	105.27	120.60
1	A	144	PRO	N-CA-C	6.66	129.41	112.10
1	A	144	PRO	C-N-CD	-5.43	108.65	120.60

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	1902	0	1922	53	0
1	B	1902	0	1921	61	0
2	A	93	0	87	20	0
2	B	93	0	87	14	0
3	A	296	0	0	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	253	0	0	18	0
All	All	4539	0	4017	131	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 16.

The worst 5 of 131 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:135:ARG:H	1:A:188:GLN:HE21	1.18	0.92
1:A:145:PRO:HA	3:A:7442:HOH:O	1.72	0.88
1:B:5063:TRP:H	1:B:5067:ASN:HD22	1.23	0.86
1:B:5139:GLN:HE22	1:B:5206:TRP:HE1	1.21	0.85
1:A:82:VAL:H	1:B:5095:ASN:HD21	1.24	0.85

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	242/252 (96%)	238 (98%)	4 (2%)	0	100	100
1	B	242/252 (96%)	237 (98%)	5 (2%)	0	100	100
All	All	484/504 (96%)	475 (98%)	9 (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	205/211 (97%)	200 (98%)	5 (2%)	57	58
1	B	205/211 (97%)	202 (98%)	3 (2%)	72	75
All	All	410/422 (97%)	402 (98%)	8 (2%)	63	65

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	226	SER
1	B	5226	SER
1	B	5007	LEU
1	A	165	ASN
1	A	231	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	198	GLN
1	B	5045	GLN
1	B	5143	ASN
1	A	188	GLN
1	B	5181	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules 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

2 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	CNC	A	501	-	75,103,103	0.86	3 (4%)	107,171,171	1.57	19 (17%)
2	CNC	B	5501	-	75,103,103	0.72	1 (1%)	107,171,171	1.48	21 (19%)

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	CNC	A	501	-	-	0/51/235/235	0/3/11/11
2	CNC	B	5501	-	-	0/51/235/235	0/3/11/11

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	CNC	C8B-N1B	2.06	1.41	1.38
2	B	5501	CNC	C41-C8	2.10	1.57	1.54
2	A	501	CNC	C41-C8	2.11	1.57	1.54
2	A	501	CNC	C1-C19	2.56	1.54	1.51

The worst 5 of 40 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	CNC	C20-C1-N21	-4.05	106.62	110.47
2	B	5501	CNC	C20-C1-N21	-3.92	106.74	110.47
2	A	501	CNC	C48-C13-C12	-3.49	106.96	116.53
2	A	501	CNC	C18-C19-N24	-3.26	101.99	109.30
2	B	5501	CNC	O34-C32-C31	-3.20	111.72	121.05

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 34 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501	CNC	20	0
2	B	5501	CNC	14	0

## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	242/252 (96%)	-0.00	9 (3%) 45 47	11, 23, 57, 111	0
1	B	242/252 (96%)	0.27	22 (9%) 11 12	11, 24, 68, 139	0
All	All	484/504 (96%)	0.13	31 (6%) 23 24	11, 24, 65, 139	0

The worst 5 of 31 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	5130	ASP	7.6
1	A	195	GLY	5.8
1	B	5144	PRO	5.1
1	A	244	ASP	4.3
1	B	5195	GLY	4.3

### 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](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	CNC	B	5501	93/93	0.88	0.19	0.58	13,36,52,55	0
2	CNC	A	501	93/93	0.94	0.13	0.11	11,18,29,35	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.