

wwPDB X-ray Structure Validation Summary Report (i)

Jul 11, 2021 – 07:08 pm BST

PDB ID : 7BAY

Title: Crystal structure of CbpF from Streptococcus pneumoniae complexed with a

Ytterbium derivative

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Deposited on : 2020-12-16

Resolution : 2.65 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
A user guide is available at

https://www.wwpdb.org/validation/2017/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 : 1.8.5 (274361), CSD as541be (2020)

Xtriage (Phenix) : 1.13 EDS : 2.22

buster-report : 1.1.7 (2018)

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)

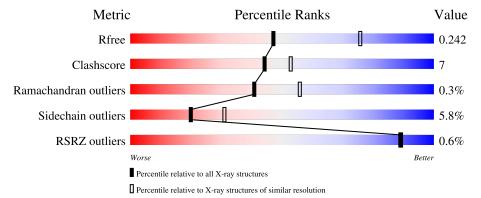
Validation Pipeline (wwPDB-VP) : 2.22

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 2.65 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	Similar resolution			
Metric	$(\# \mathrm{Entries})$	$(\# ext{Entries}, ext{resolution range}(ext{Å}))$			
R_{free}	130704	1332 (2.68-2.64)			
Clashscore	141614	1374 (2.68-2.64)			
Ramachandran outliers	138981	1349 (2.68-2.64)			
Sidechain outliers	138945	1349 (2.68-2.64)			
RSRZ outliers	127900	1318 (2.68-2.64)			

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 of the lower bar indicate the fraction of residues that contain outliers for >=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 <=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	
			<u>%</u>	
1	AA	311	82%	18%



2 Entry composition (i)

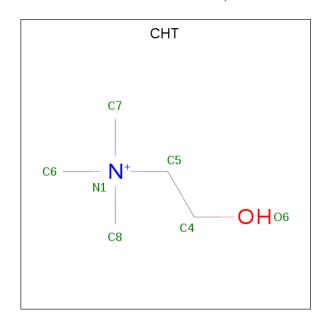
There are 6 unique types of molecules in this entry. The entry contains 2849 atoms, of which 122 are hydrogens and 0 are deuteriums.

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 Choline-binding protein F.

\mathbf{Mol}	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	AA	311	Total 2580	C 1672	N 416	O 486	S 6	0	0	0

• Molecule 2 is CHOLINE ION (three-letter code: CHT) (formula: C₅H₁₄NO).



Mol	Chain	Residues		Atoms					AltConf	
2	Α Α	1	Total	С	Н	Ν	О	0	0	
2	AA	1	21	5	14	1	1	0	U	
2	AA	1	Total	С	Н	N	О	0	0	
2	AA	1	21	5	14	1	1	0	U	
2	AA	1	Total	С	Н	N	О	0	0	
	AA	1	21	5	14	1	1	0	U	
2	Λ Λ	1	Total	С	Н	N	О	0	0	
2	AA	1	21	5	14	1	1	U	U	
2	AA	1	Total	С	Н	N	О	0	0	
		1	21	5	14	1	1		U	

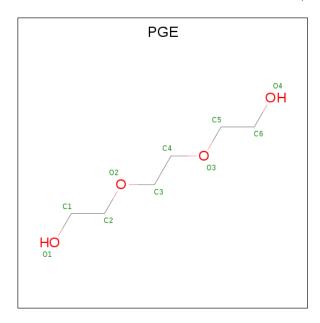
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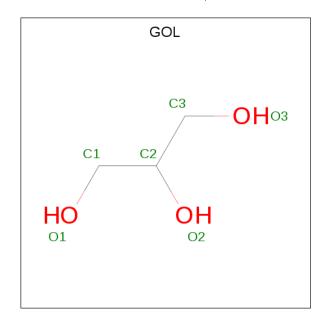
\mathbf{Mol}	Chain	Residues	${f Atoms}$				ZeroOcc	AltConf	
າ	Α Α	1	Total	С	Н	N	О	0	0
2	AA	1	21	5	14	1	1	0	U

• Molecule 3 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula: C₆H₁₄O₄).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	Λ Λ	1	Total	С	Н	О	0	0
J	$\Lambda\Lambda$	1	24	6	14	4	U	0

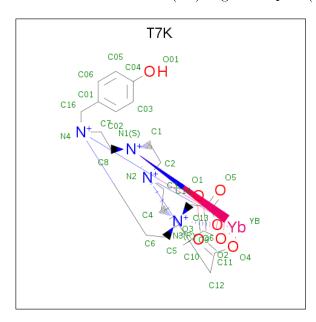
• Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).





Mol	Chain	Residues	${f Atoms}$				ZeroOcc	AltConf
4	AA	1	Total 14	C 3		O 3	0	0
4	AA	1	Total 14	C 3		O 3	0	0
4	AA	1	Total 14	C 3	H 8	O 3	0	0

 $\bullet \ \ \mathrm{Molecule} \ 5 \ \mathrm{is} \ \mathrm{neutral} \ \mathrm{Yb(III)} \text{-} \mathrm{caged} \ \mathrm{complex} \ (\mathrm{three-letter} \ \mathrm{code} \colon \ \mathrm{T7K}) \ (\mathrm{formula} \colon \ \mathrm{C}_{21}\mathrm{H}_{29}\mathrm{N}_4\mathrm{O}_7\mathrm{Yb}).$



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf		
5	AA	1	Total 33	C 21	N 4	O 7	Yb 1	0	0

 $\bullet\,$ Molecule 6 is water.

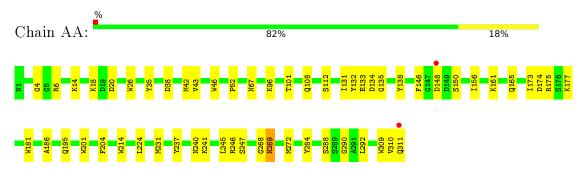
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	AA	44	Total O 44 44	0	0



3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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 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: Choline-binding protein F





4 Data and refinement statistics (i)

Property	Value	Source	
Space group	P 21 21 2	Depositor	
Cell constants	114.90Å 52.21Å 73.99Å	Donositor	
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor	
Resolution (Å)	47.53 - 2.65	Depositor	
Resolution (A)	47.53 - 2.65	EDS	
% Data completeness	99.6 (47.53-2.65)	Depositor	
(in resolution range)	99.6 (47.53-2.65)	EDS	
R_{merge}	0.10	Depositor	
R_{sym}	(Not available)	Depositor	
$< I/\sigma(I) > 1$	2.04 (at 2.65Å)	Xtriage	
Refinement program	PHENIX 1.18_3855	Depositor	
D D.	0.201 , 0.242	Depositor	
R, R_{free}	0.201 , 0.242	DCC	
R_{free} test set	614 reflections (4.56%)	wwPDB-VP	
Wilson B-factor (Å ²)	55.2	Xtriage	
Anisotropy	0.217	Xtriage	
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.33 , 30.9	EDS	
L-test for twinning ²	$ < L >=0.51, < L^2>=0.35$	Xtriage	
Estimated twinning fraction	No twinning to report.	Xtriage	
F_o, F_c correlation	0.94	EDS	
Total number of atoms	2849	wwPDB-VP	
Average B, all atoms (Å ²)	58.0	wwPDB-VP	

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.96% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical 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.



¹Intensities estimated from amplitudes.

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, CHT, T7K, PGE

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).

Mal	Chain	Bond	lengths	Bond angles		
MIOI		RMSZ	# Z >5	RMSZ	# Z > 5	
1	AA	0.25	0/2670	0.41	0/3630	

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)	$\mathbf{H}(\mathbf{added})$	Clashes	Symm-Clashes
1	AA	2580	0	2372	33	0
2	AA	42	84	84	2	0
3	AA	10	14	14	0	0
4	AA	18	24	24	1	0
5	AA	33	0	0	1	0
6	AA	44	0	0	1	0
All	All	2727	122	2494	34	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 7.

The worst 5 of 34 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.



Atom-1	Atom-2	$egin{aligned} ext{Interatomic} \ ext{distance} & (ext{Å}) \end{aligned}$	Clash overlap (Å)
1:AA:14:LYS:HD2	1:AA:42:MET:CE	2.19	0.71
1:AA:14:LYS:HD2	1:AA:42:MET:HE1	1.76	0.66
1:AA:173:ILE:HG22	1:AA:175:ARG:HD2	1.79	0.64
1:AA:132:TYR:OH	1:AA:135:GLY:HA2	1.98	0.62
1:AA:26:TRP:CD2	1:AA:52:PRO:HB3	2.41	0.56

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	AA	309/311 (99%)	292 (94%)	16 (5%)	1 (0%)	41 56

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	AA	268	GLY

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	AA	$259/259 \; (100\%)$	244 (94%)	15 (6%)	20	31

5 of 15 residues with a non-rotameric sidechain are listed below:



Mol	Chain	Res	Type
1	AA	148	ASP
1	AA	288	SER
1	AA	150	SER
1	AA	310	VAL
1	AA	247	SER

Sometimes 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 monosaccharides in this entry.

5.6 Ligand geometry (i)

11 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).

Mal	T	Chain	Chain Res Link Bond lengths		${ m ths}$	В	ond ang	cles		
Mol	Type	Chain	nes	Link	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	СНТ	AA	1405	-	6,6,6	0.40	0	8,8,8	0.12	0
2	СНТ	AA	1402	-	6,6,6	0.40	0	8,8,8	0.10	0
3	PGE	AA	1404	-	9,9,9	0.31	0	8,8,8	0.34	0
2	СНТ	AA	1408	-	6,6,6	0.41	0	8,8,8	0.11	0
2	СНТ	AA	1406	-	6,6,6	0.41	0	8,8,8	0.14	0
2	СНТ	AA	1403	-	6,6,6	0.40	0	8,8,8	0.10	0
4	GOL	AA	1409	-	5, 5, 5	0.72	0	5,5,5	1.02	0



Mol	Trino	Chain	Res	Link	Во	ond leng	ths	В	ond ang	les
10101	Type	Chain	nes	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	$\mid \# Z > 2 \mid$
4	GOL	AA	1410	-	5,5,5	0.77	0	5,5,5	1.00	0
2	CHT	AA	1401	-	6,6,6	0.41	0	8,8,8	0.13	0
4	GOL	AA	1407	-	5,5,5	0.82	0	5,5,5	0.92	0
5	T7K	AA	1411	-	18,40,40	3.69	8 (44%)	19,79,79	2.50	6 (31%)

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	СНТ	AA	1405	-	-	0/4/4/4	-
2	СНТ	AA	1402	_	-	1/4/4/4	-
3	PGE	AA	1404	_	-	3/7/7/7	-
2	CHT	AA	1408	-	-	0/4/4/4	-
2	СНТ	AA	1406	_	-	0/4/4/4	-
2	СНТ	AA	1403	-	-	1/4/4/4	-
4	GOL	AA	1409	-	-	2/4/4/4	-
4	GOL	AA	1410	-	-	2/4/4/4	-
2	CHT	AA	1401	-	-	0/4/4/4	=
4	GOL	AA	1407	-	-	1/4/4/4	-
5	T7K	AA	1411	-	-	0/2/144/144	0/1/8/8

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(\mathbf{\mathring{A}})$	$\operatorname{Ideal}(\operatorname{\AA})$
5	AA	1411	T7K	C06-C05	8.95	1.55	1.38
5	AA	1411	T7K	C02-C01	7.64	1.55	1.38
5	AA	1411	T7K	C03-C04	7.42	1.53	1.38
5	AA	1411	T7K	C06-C01	-3.51	1.31	1.38
5	AA	1411	T7K	C03-C02	-3.32	1.32	1.38

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$\operatorname{Ideal}({}^o)$
5	AA	1411	T7K	O2-C9-O1	-5.37	119.39	124.58
5	AA	1411	T7K	O2-C9-C10	5.07	123.05	116.83
5	AA	1411	T7K	O6-C13-O5	-4.83	119.90	124.58
5	AA	1411	T7K	O4-C11-O3	-4.75	119.99	124.58
5	AA	1411	T7K	O4-C11-C12	2.53	119.94	116.83



There are no chirality outliers.

5 of 10 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	AA	1410	GOL	C1-C2-C3-O3
3	AA	1404	PGE	O1-C1-C2-O2
4	AA	1407	GOL	O1-C1-C2-C3
4	AA	1409	GOL	O1-C1-C2-C3
4	AA	1410	GOL	O2-C2-C3-O3

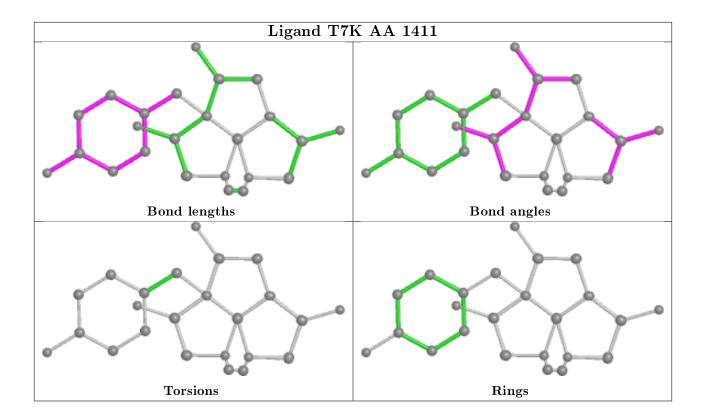
There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	AA	1406	CHT	2	0
4	AA	1409	GOL	1	0
5	AA	1411	T7K	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





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^{th} 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	$\langle { m RSRZ} \rangle$	# RSRZ > 2		$OWAB(A^2)$	Q < 0.9
1	AA	311/311 (100%)	-0.01	2 (0%) 89	89	38, 54, 88, 116	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	AA	148	ASP	3.1
1	AA	311	GLN	2.5

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 monosaccharides 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. The B-factors column lists the minimum, median, 95^{th} 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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q < 0.9
4	GOL	AA	1407	6/6	0.81	0.40	59,78,94,99	0
2	СНТ	AA	1405	7/7	0.82	0.53	55,75,96,102	0
3	PGE	AA	1404	10/10	0.86	0.19	61,78,85,92	0
2	СНТ	AA	1403	7/7	0.86	0.48	55,70,92,95	0
4	GOL	AA	1409	6/6	0.87	0.17	55,71,87,87	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	${f B-factors}({f \AA}^2)$	Q < 0.9
4	GOL	AA	1410	6/6	0.88	0.25	61,74,87,92	0
2	СНТ	AA	1406	7/7	0.89	0.27	56,71,82,85	0
2	СНТ	AA	1408	7/7	0.89	0.22	36,54,57,63	0
2	СНТ	AA	1401	7/7	0.90	0.35	52,63,87,97	0
2	СНТ	AA	1402	7/7	0.93	0.26	50,67,74,84	0
5	T7K	AA	1411	33/33	0.97	0.18	76,85,95,98	0

6.5 Other polymers (i)

There are no such residues in this entry.

