



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 06:06 PM UTC

PDB ID : 6B15 / pdb_00006b15
Title : Crystal structure of CBMbc (family CBM26) from Eubacterium rectale Amy13K
Authors : Cockburn, D.W.; Wawrzak, Z.; Perez Medina, K.; Koropatkin, N.M.
Deposited on : 2017-09-16
Resolution : 2.10 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

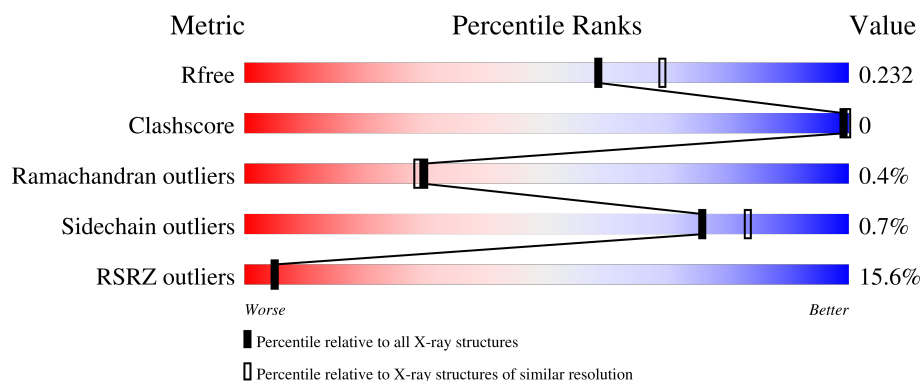
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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}	180053	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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 $\leq 5\%$. 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	209	 2% 100%
1	B	209	 2% 97%
1	C	209	 26% 96%
1	D	209	 33% 98%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 13009 atoms, of which 5874 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 Amy13K.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	209	Total	C	H	N	O	S	0	0	0
			3112	1016	1495	259	336	6			
1	B	209	Total	C	H	N	O	S	0	0	0
			3112	1016	1495	259	336	6			
1	C	209	Total	C	H	N	O	S	0	0	0
			3113	1016	1496	259	336	6			
1	D	209	Total	C	H	N	O	S	0	0	0
			2912	961	1370	250	327	4			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	179	MET	-	initiating methionine	UNP D6DYI9
B	179	MET	-	initiating methionine	UNP D6DYI9
C	179	MET	-	initiating methionine	UNP D6DYI9
D	179	MET	-	initiating methionine	UNP D6DYI9

- Molecule 2 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	H	O	0	0
			10	2	6	2		
2	B	1	Total	C	H	O	0	0
			10	2	6	2		
2	B	1	Total	C	H	O	0	0
			10	2	6	2		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	256	Total	O	0	0
			256	256		
3	B	218	Total	O	0	0
			218	218		
3	C	138	Total	O	0	0
			138	138		
3	D	118	Total	O	0	0
			118	118		

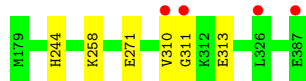
3 Residue-property plots [i](#)

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.

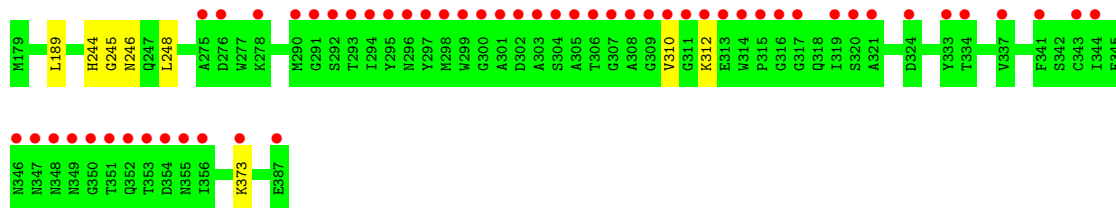
- Molecule 1: Amy13K



- Molecule 1: Amy13K



- Molecule 1: Amy13K



- Molecule 1: Amy13K



4 Data and refinement statistics

Property	Value	Source
Space group	P 31 1 2	Depositor
Cell constants a, b, c, α , β , γ	131.73Å 131.73Å 151.87Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	36.02 – 2.10 36.02 – 2.10	Depositor EDS
% Data completeness (in resolution range)	98.5 (36.02-2.10) 98.5 (36.02-2.10)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.91 (at 2.10Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.200 , 0.229 0.209 , 0.232	Depositor DCC
R_{free} test set	1994 reflections (2.27%)	wwPDB-VP
Wilson B-factor (Å ²)	35.6	Xtriage
Anisotropy	0.091	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 47.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.028 for -h,-k,l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	13009	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.08% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: EDO

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	0.25	0/1660	0.59	0/2268
1	B	0.26	0/1660	0.58	0/2268
1	C	0.36	0/1660	0.62	2/2268 (0.1%)
1	D	0.27	0/1578	0.61	0/2158
All	All	0.29	0/6558	0.60	2/8962 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	245	GLY	N-CA-C	7.79	123.59	114.16
1	C	246	ASN	N-CA-C	5.06	117.65	108.69

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	1617	1495	1492	0	0
1	B	1617	1495	1492	2	0
1	C	1617	1496	1492	1	1
1	D	1542	1370	1371	1	1
2	A	4	6	6	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	8	12	12	0	0
3	A	256	0	0	0	0
3	B	218	0	0	0	0
3	C	138	0	0	0	0
3	D	118	0	0	0	0
All	All	7135	5874	5865	4	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 0.

All (4) 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:258:LYS:NZ	1:B:271:GLU:OE1	2.41	0.54
1:B:310:VAL:HA	1:B:311:GLY:HA2	1.88	0.42
1:D:387:GLU:OE1	1:D:387:GLU:N	2.54	0.41
1:C:189:LEU:HD11	1:C:248:LEU:HD13	2.03	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)
1:C:373:LYS:O	1:D:351:THR:OG1[5_455]	2.18	0.02

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	207/209 (99%)	200 (97%)	7 (3%)	0	100	100
1	B	207/209 (99%)	198 (96%)	8 (4%)	1 (0%)	24	22

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	207/209 (99%)	196 (95%)	10 (5%)	1 (0%)	24	22
1	D	207/209 (99%)	197 (95%)	9 (4%)	1 (0%)	24	22
All	All	828/836 (99%)	791 (96%)	34 (4%)	3 (0%)	30	28

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	244	HIS
1	C	244	HIS
1	D	244	HIS

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	172/172 (100%)	171 (99%)	1 (1%)	78	86
1	B	172/172 (100%)	171 (99%)	1 (1%)	78	86
1	C	172/172 (100%)	170 (99%)	2 (1%)	63	72
1	D	153/172 (89%)	152 (99%)	1 (1%)	76	83
All	All	669/688 (97%)	664 (99%)	5 (1%)	76	83

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

Mol	Chain	Res	Type
1	A	326	LEU
1	B	313	GLU
1	C	310	VAL
1	C	312	LYS
1	D	342	SER

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

Mol	Chain	Res	Type
1	A	339	GLN
1	A	352	GLN
1	C	246	ASN
1	D	219	HIS

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 oligosaccharides 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	EDO	A	401	-	3,3,3	0.41	0	2,2,2	0.41	0
2	EDO	B	401	-	3,3,3	0.41	0	2,2,2	0.32	0
2	EDO	B	402	-	3,3,3	0.42	0	2,2,2	0.34	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	EDO	A	401	-	-	0/1/1/1	-
2	EDO	B	401	-	-	1/1/1/1	-
2	EDO	B	402	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	401	EDO	O1-C1-C2-O2

There are no ring outliers.

No monomer is involved in short contacts.

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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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	209/209 (100%)	-0.16	4 (1%) 66 69	26, 36, 54, 70	0
1	B	209/209 (100%)	0.03	4 (1%) 66 69	26, 37, 57, 74	0
1	C	209/209 (100%)	1.19	54 (25%) 1 2	33, 52, 89, 106	0
1	D	209/209 (100%)	1.99	68 (32%) 1 1	32, 53, 107, 153	0
All	All	836/836 (100%)	0.76	130 (15%) 5 5	26, 44, 88, 153	0

All (130) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	315	PRO	13.4
1	D	314	TRP	11.2
1	D	343	CYS	10.7
1	D	356	ILE	9.5
1	D	299	TRP	9.3
1	D	355	ASN	9.0
1	D	348	ASN	8.9
1	D	301	ALA	8.3
1	D	311	GLY	8.1
1	C	314	TRP	8.0
1	D	297	TYR	7.9
1	D	341	PHE	7.9
1	D	310	VAL	7.9
1	D	312	LYS	7.8
1	D	298	MET	7.4
1	D	351	THR	7.4
1	C	310	VAL	7.2
1	D	309	GLY	7.1
1	C	315	PRO	7.0
1	D	344	ILE	7.0
1	D	313	GLU	6.9

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Mol	Chain	Res	Type	RSRZ
1	D	340	ASN	6.4
1	D	347	ASN	6.3
1	C	316	GLY	6.2
1	D	308	ALA	5.8
1	C	295	TYR	5.7
1	D	337	VAL	5.3
1	D	358	VAL	5.2
1	C	344	ILE	5.2
1	D	300	GLY	5.2
1	D	339	GLN	5.1
1	D	316	GLY	5.1
1	C	297	TYR	4.9
1	D	342	SER	4.9
1	C	348	ASN	4.8
1	D	295	TYR	4.8
1	D	346	ASN	4.7
1	D	353	THR	4.7
1	C	317	GLY	4.5
1	D	357	ASP	4.5
1	D	352	GLN	4.5
1	C	308	ALA	4.4
1	D	302	ASP	4.4
1	C	307	GLY	4.3
1	C	346	ASN	4.3
1	D	305	ALA	4.3
1	D	349	ASN	4.2
1	B	311	GLY	4.2
1	C	347	ASN	4.2
1	C	355	ASN	4.2
1	B	310	VAL	4.2
1	C	298	MET	4.0
1	D	354	ASP	4.0
1	C	311	GLY	4.0
1	D	307	GLY	3.9
1	A	311	GLY	3.9
1	D	376	THR	3.9
1	C	333	TYR	3.8
1	D	303	ALA	3.7
1	C	296	ASN	3.7
1	C	349	ASN	3.7
1	C	293	THR	3.6
1	C	306	THR	3.6

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Mol	Chain	Res	Type	RSRZ
1	D	359	SER	3.6
1	C	299	TRP	3.5
1	D	306	THR	3.5
1	D	319	ILE	3.5
1	C	350	GLY	3.5
1	C	312	LYS	3.4
1	C	351	THR	3.4
1	C	304	SER	3.3
1	D	318	GLN	3.3
1	D	373	LYS	3.3
1	C	309	GLY	3.3
1	C	294	ILE	3.2
1	D	296	ASN	3.2
1	A	310	VAL	3.2
1	C	319	ILE	3.2
1	C	356	ILE	3.2
1	D	304	SER	3.2
1	C	301	ALA	3.1
1	D	375	ASP	3.1
1	D	293	THR	3.1
1	D	374	GLY	3.1
1	D	279	TYR	3.1
1	C	343	CYS	3.0
1	D	350	GLY	3.0
1	D	336	ASP	3.0
1	C	321	ALA	3.0
1	C	373	LYS	3.0
1	D	335	GLN	2.9
1	D	360	VAL	2.8
1	D	333	TYR	2.8
1	D	377	THR	2.8
1	D	372	THR	2.8
1	D	294	ILE	2.7
1	D	378	VAL	2.7
1	C	300	GLY	2.7
1	C	313	GLU	2.5
1	C	387	GLU	2.5
1	D	317	GLY	2.5
1	C	276	ASP	2.4
1	D	345	PHE	2.4
1	B	387	GLU	2.4
1	C	334	THR	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	326	LEU	2.4
1	C	320	SER	2.4
1	D	275	ALA	2.4
1	C	354	ASP	2.4
1	C	292	SER	2.4
1	C	353	THR	2.4
1	D	277	TRP	2.4
1	A	326	LEU	2.3
1	C	324	ASP	2.3
1	C	341	PHE	2.3
1	D	387	GLU	2.2
1	C	352	GLN	2.2
1	C	305	ALA	2.2
1	C	291	GLY	2.2
1	D	292	SER	2.1
1	D	334	THR	2.1
1	C	275	ALA	2.1
1	D	361	THR	2.1
1	C	278	LYS	2.1
1	C	290	MET	2.1
1	C	302	ASP	2.1
1	C	337	VAL	2.1
1	D	272	THR	2.0
1	A	387	GLU	2.0
1	C	303	ALA	2.0

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

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

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

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, 95th 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	B-factors($\text{\AA}^2$)	Q<0.9
2	EDO	B	401	4/4	0.85	0.15	48,57,67,71	0
2	EDO	B	402	4/4	0.85	0.22	33,48,71,71	0
2	EDO	A	401	4/4	0.90	0.17	54,65,69,70	0

6.5 Other polymers [i](#)

There are no such residues in this entry.