



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 2IEE / pdb_00002iee
Title : Crystal Structure of YCKB_BACSU from Bacillus subtilis. Northeast Structural Genomics Consortium target SR574.
Authors : Kuzin, A.P.; Su, M.; Jayaraman, S.; Chen, X.C.; Jang, M.; Cunningham, K.; Ma, C.; Xiao, R.; Liu, J.; Baran, M.C.; Acton, T.B.; Rost, B.; Montelione, G.T.; Tong, L.; Hunt, J.F.; Northeast Structural Genomics Consortium (NESG)
Deposited on : 2006-09-18
Resolution : 2.20 Å(reported)

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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)

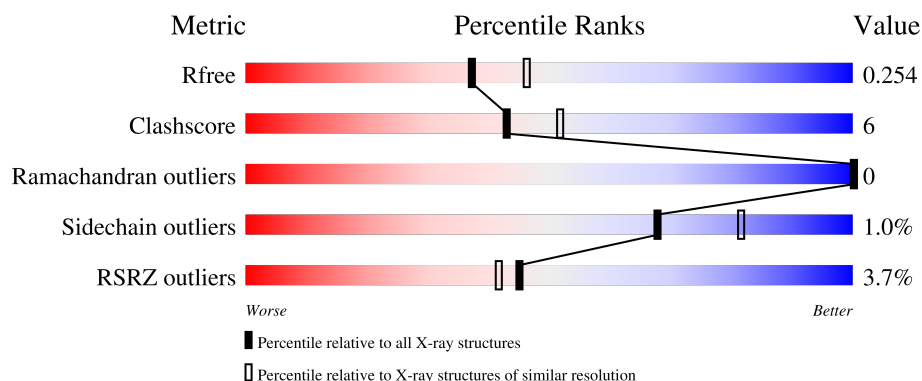
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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	271	4% 76% 16% 7%
1	B	271	3% 74% 15% 10%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4048 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 Probable ABC transporter extracellular-binding protein yckB.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	251	Total	C	N	O	Se	0	0	0
			1949	1229	325	388	7			
1	B	244	Total	C	N	O	Se	0	0	0
			1909	1208	318	376	7			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	-	cloning artifact	UNP P42400
A	70	MSE	MET	modified residue	UNP P42400
A	75	MSE	MET	modified residue	UNP P42400
A	144	MSE	MET	modified residue	UNP P42400
A	205	MSE	MET	modified residue	UNP P42400
A	213	MSE	MET	modified residue	UNP P42400
A	224	MSE	MET	modified residue	UNP P42400
A	231	MSE	MET	modified residue	UNP P42400
A	264	LEU	-	cloning artifact	UNP P42400
A	265	GLU	-	cloning artifact	UNP P42400
A	266	HIS	-	cloning artifact	UNP P42400
A	267	HIS	-	cloning artifact	UNP P42400
A	268	HIS	-	cloning artifact	UNP P42400
A	269	HIS	-	cloning artifact	UNP P42400
A	270	HIS	-	cloning artifact	UNP P42400
A	271	HIS	-	cloning artifact	UNP P42400
B	1	MSE	-	cloning artifact	UNP P42400
B	70	MSE	MET	modified residue	UNP P42400
B	75	MSE	MET	modified residue	UNP P42400
B	144	MSE	MET	modified residue	UNP P42400
B	205	MSE	MET	modified residue	UNP P42400
B	213	MSE	MET	modified residue	UNP P42400
B	224	MSE	MET	modified residue	UNP P42400
B	231	MSE	MET	modified residue	UNP P42400
B	264	LEU	-	cloning artifact	UNP P42400

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Chain	Residue	Modelled	Actual	Comment	Reference
B	265	GLU	-	cloning artifact	UNP P42400
B	266	HIS	-	cloning artifact	UNP P42400
B	267	HIS	-	cloning artifact	UNP P42400
B	268	HIS	-	cloning artifact	UNP P42400
B	269	HIS	-	cloning artifact	UNP P42400
B	270	HIS	-	cloning artifact	UNP P42400
B	271	HIS	-	cloning artifact	UNP P42400

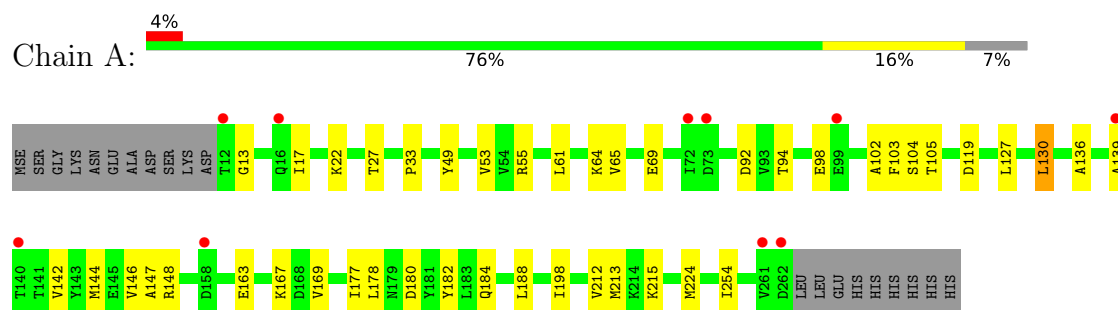
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	89	Total O 89 89	0	0
2	B	101	Total O 101 101	0	0

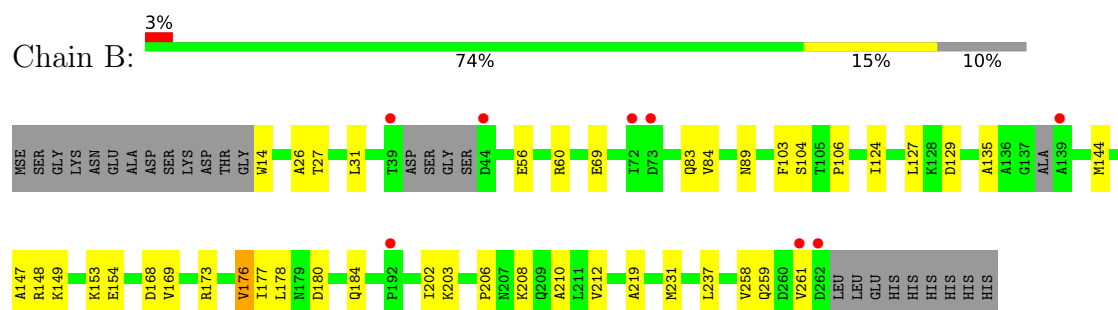
3 Residue-property plots

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: Probable ABC transporter extracellular-binding protein yckB



- Molecule 1: Probable ABC transporter extracellular-binding protein yckB



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	55.28Å 49.92Å 106.77Å 90.00° 99.73° 90.00°	Depositor
Resolution (Å)	19.95 – 2.20 19.95 – 2.20	Depositor EDS
% Data completeness (in resolution range)	83.8 (19.95-2.20) 87.2 (19.95-2.20)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.46 (at 2.20Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.202 , 0.241 0.212 , 0.254	Depositor DCC
R_{free} test set	2444 reflections (4.87%)	wwPDB-VP
Wilson B-factor (Å ²)	19.2	Xtriage
Anisotropy	0.068	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 46.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	4048	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.04% 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

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	0.36	0/1969	0.85	5/2639 (0.2%)
1	B	0.36	0/1927	0.87	4/2579 (0.2%)
All	All	0.36	0/3896	0.86	9/5218 (0.2%)

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	139	ALA	N-CA-C	6.93	118.62	111.14
1	B	104	SER	N-CA-C	-6.64	100.96	110.59
1	B	83	GLN	N-CA-C	-5.80	105.09	111.82
1	B	176	VAL	N-CA-C	5.69	115.74	107.88
1	A	105	THR	N-CA-C	-5.57	102.09	109.84
1	A	104	SER	N-CA-C	-5.54	101.77	110.36
1	B	169	VAL	N-CA-C	-5.47	105.38	110.53
1	A	169	VAL	N-CA-C	-5.23	105.62	110.53
1	A	119	ASP	N-CA-C	5.02	116.83	111.36

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-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 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	1949	0	1971	22	0
1	B	1909	0	1937	27	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	89	0	0	2	0
2	B	101	0	0	0	0
All	All	4048	0	3908	48	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 6.

All (48) 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:22:LYS:HG2	1:A:64:LYS:HB3	1.69	0.74
1:B:206:PRO:HB3	1:B:258:VAL:HG21	1.74	0.67
1:B:127:LEU:HD11	1:B:202:ILE:HG23	1.76	0.67
1:A:148:ARG:HD2	1:B:153:LYS:HD3	1.76	0.66
1:B:14:TRP:HB2	1:B:219:ALA:HB1	1.79	0.65
1:A:102:ALA:HB2	1:A:215:LYS:HA	1.81	0.62
1:B:149:LYS:HZ3	1:B:261:VAL:HG12	1.63	0.62
1:A:13:GLY:O	1:A:17:ILE:HG12	2.01	0.60
1:B:127:LEU:HD13	1:B:259:GLN:NE2	2.17	0.60
1:B:27:THR:O	1:B:69:GLU:HA	2.02	0.60
1:A:148:ARG:HD3	2:A:345:HOH:O	2.00	0.59
1:B:144:MSE:HE3	1:B:147:ALA:HB3	1.83	0.59
1:B:149:LYS:NZ	1:B:261:VAL:HG12	2.18	0.58
1:B:203:LYS:HB3	1:B:258:VAL:HG12	1.86	0.57
1:A:61:LEU:HD12	1:A:224:MSE:HE2	1.87	0.55
1:A:144:MSE:HE3	1:A:147:ALA:HB3	1.89	0.54
1:B:103:PHE:CE1	1:B:212:VAL:HG22	2.43	0.53
1:A:103:PHE:CE1	1:A:212:VAL:HG22	2.44	0.52
1:A:136:ALA:HB3	1:A:177:ILE:CD1	2.42	0.49
1:A:142:VAL:O	1:A:146:VAL:HG23	2.13	0.49
1:A:27:THR:O	1:A:69:GLU:HA	2.14	0.48
1:B:180:ASP:O	1:B:184:GLN:HG3	2.14	0.48
1:B:106:PRO:HG2	1:B:208:LYS:HD2	1.95	0.47
1:B:231:MSE:HB3	1:B:237:LEU:HD13	1.97	0.46
1:A:94:THR:O	1:A:98:GLU:HG3	2.15	0.45
1:B:124:ILE:HG23	1:B:129:ASP:HB2	1.99	0.45
1:A:127:LEU:O	1:A:130:LEU:HB2	2.17	0.45
1:A:163:GLU:CG	1:A:167:LYS:HE2	2.47	0.45
1:A:61:LEU:CD1	1:A:224:MSE:HE2	2.47	0.44
1:B:135:ALA:HB3	1:B:144:MSE:HE1	1.99	0.44
1:A:49:TYR:O	1:A:53:VAL:HG23	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:180:ASP:O	1:A:184:GLN:HG3	2.17	0.44
1:B:127:LEU:CD1	1:B:202:ILE:HG23	2.44	0.44
1:B:176:VAL:HG22	1:B:177:ILE:N	2.33	0.44
1:B:168:ASP:CG	1:B:173:ARG:HD3	2.43	0.43
1:B:127:LEU:HD13	1:B:259:GLN:HE22	1.82	0.43
1:A:188:LEU:CD2	1:A:198:ILE:HG13	2.49	0.42
1:A:55:ARG:HA	1:A:65:VAL:HG21	2.01	0.42
1:B:147:ALA:HB2	1:B:178:LEU:HD22	2.01	0.42
1:B:26:ALA:HB2	1:B:84:VAL:HG11	2.02	0.42
1:B:31:LEU:HD12	1:B:89:ASN:ND2	2.35	0.42
1:A:182:TYR:OH	1:A:254:ILE:HD11	2.20	0.42
1:B:149:LYS:HB2	1:B:149:LYS:HE3	1.87	0.42
1:B:106:PRO:HA	1:B:210:ALA:HB2	2.02	0.42
1:B:56:GLU:O	1:B:60:ARG:HG3	2.19	0.41
1:A:92:ASP:HB3	2:A:325:HOH:O	2.21	0.41
1:A:188:LEU:HD21	1:A:198:ILE:HG13	2.03	0.41
1:B:148:ARG:HD3	1:B:154:GLU:OE1	2.22	0.40

There are no symmetry-related clashes.

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	249/271 (92%)	239 (96%)	10 (4%)	0	100	100
1	B	238/271 (88%)	231 (97%)	7 (3%)	0	100	100
All	All	487/542 (90%)	470 (96%)	17 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	209/219 (95%)	205 (98%)	4 (2%)	50	66
1	B	205/219 (94%)	205 (100%)	0	100	100
All	All	414/438 (94%)	410 (99%)	4 (1%)	68	81

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	33	PRO
1	A	130	LEU
1	A	178	LEU
1	A	213	MSE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	80	ASN
1	A	171	ASN
1	B	80	ASN
1	B	83	GLN
1	B	89	ASN
1	B	164	GLN
1	B	217	ASN
1	B	221	GLN
1	B	243	GLN
1	B	259	GLN

5.3.3 RNA ⓘ

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](#)

There are no ligands in this entry.

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, 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	244/271 (90%)	-0.02	10 (4%) 41 38	10, 19, 42, 55	0
1	B	237/271 (87%)	-0.04	8 (3%) 48 45	8, 19, 41, 60	0
All	All	481/542 (88%)	-0.03	18 (3%) 45 42	8, 19, 42, 60	0

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	139	ALA	3.9
1	B	39	THR	3.6
1	B	262	ASP	3.5
1	A	262	ASP	3.4
1	A	158	ASP	3.1
1	A	73	ASP	3.1
1	B	44	ASP	3.0
1	A	139	ALA	3.0
1	B	73	ASP	2.9
1	B	72	ILE	2.9
1	A	12	THR	2.6
1	B	261	VAL	2.6
1	B	192	PRO	2.4
1	A	16	GLN	2.2
1	A	140	THR	2.2
1	A	99	GLU	2.1
1	A	261	VAL	2.0
1	A	72	ILE	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 oligosaccharides 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.