



Full wwPDB X-ray Structure Validation Report ⓘ

May 29, 2020 – 03:34 am BST

PDB ID : 3QK6
Title : Crystal structure of Escherichia coli PhnD
Authors : Alicea, I.; Schreiter, E.R.
Deposited on : 2011-01-31
Resolution : 2.40 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 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

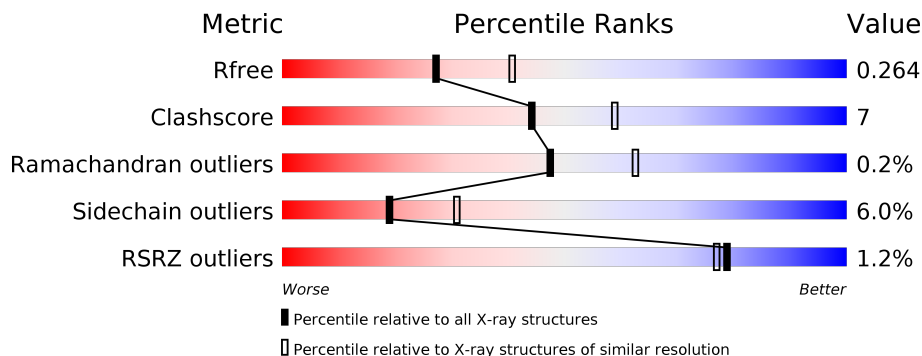
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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}	130704	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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 ≥ 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	321	
1	B	321	

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	UNL	A	313	-	-	X	-
2	UNL	B	313	-	-	X	-

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 4828 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 PhnD, subunit of alkylphosphonate ABC transporter.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	Se			
1	A	304	2380	1512	407	455	6	0	0	0
1	B	308	2409	1530	413	460	6	0	0	0

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-8	MSE	-	EXPRESSION TAG	UNP Q1R3F7
A	-7	HIS	-	EXPRESSION TAG	UNP Q1R3F7
A	-6	HIS	-	EXPRESSION TAG	UNP Q1R3F7
A	-5	HIS	-	EXPRESSION TAG	UNP Q1R3F7
A	-4	HIS	-	EXPRESSION TAG	UNP Q1R3F7
A	-3	HIS	-	EXPRESSION TAG	UNP Q1R3F7
A	-2	HIS	-	EXPRESSION TAG	UNP Q1R3F7
A	-1	GLY	-	EXPRESSION TAG	UNP Q1R3F7
A	0	SER	-	EXPRESSION TAG	UNP Q1R3F7
B	-8	MSE	-	EXPRESSION TAG	UNP Q1R3F7
B	-7	HIS	-	EXPRESSION TAG	UNP Q1R3F7
B	-6	HIS	-	EXPRESSION TAG	UNP Q1R3F7
B	-5	HIS	-	EXPRESSION TAG	UNP Q1R3F7
B	-4	HIS	-	EXPRESSION TAG	UNP Q1R3F7
B	-3	HIS	-	EXPRESSION TAG	UNP Q1R3F7
B	-2	HIS	-	EXPRESSION TAG	UNP Q1R3F7
B	-1	GLY	-	EXPRESSION TAG	UNP Q1R3F7
B	0	SER	-	EXPRESSION TAG	UNP Q1R3F7

- Molecule 2 is UNKNOWN LIGAND (three-letter code: UNL) (formula:).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	X	0	0
			5	5		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total X 5 5	0	0


- Molecule 3 is water.

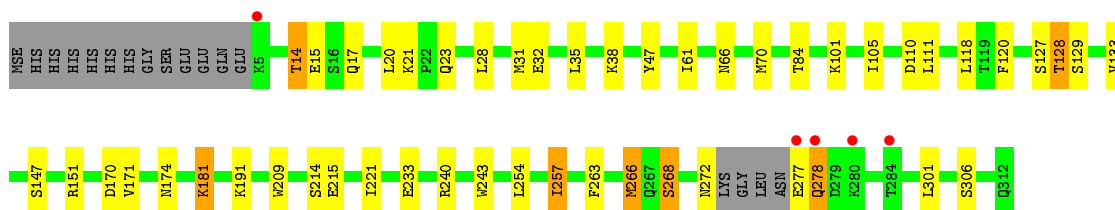
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	13	Total O 13 13	0	0
3	B	16	Total O 16 16	0	0

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 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.

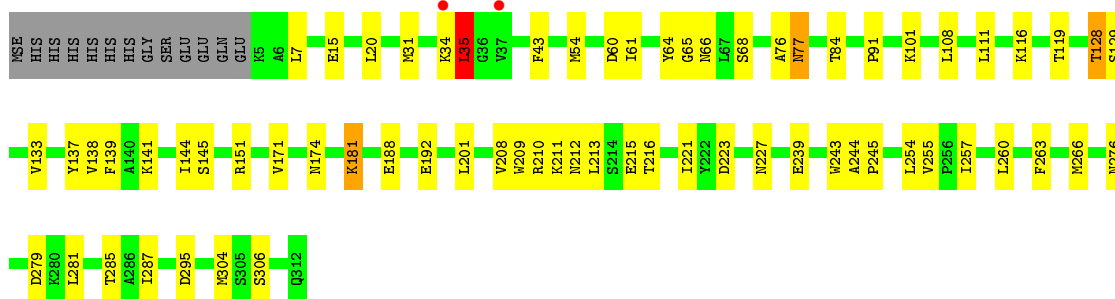
- Molecule 1: PhnD, subunit of alkylphosphonate ABC transporter

Chain A: 



- Molecule 1: PhnD, subunit of alkylphosphonate ABC transporter

Chain B: 



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	145.74Å 82.98Å 66.14Å 90.00° 103.20° 90.00°	Depositor
Resolution (Å)	43.00 – 2.40 41.49 – 2.40	Depositor EDS
% Data completeness (in resolution range)	93.9 (43.00-2.40) 93.9 (41.49-2.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.13 (at 2.39Å)	Xtrriage
Refinement program	REFMAC 5.5.0072	Depositor
R, R_{free}	0.206 , 0.267 0.204 , 0.264	Depositor DCC
R_{free} test set	1435 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	43.0	Xtrriage
Anisotropy	0.628	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 45.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4828	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.58% 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: UNL

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	0.82	0/2420	0.82	0/3266
1	B	0.82	2/2450 (0.1%)	0.80	1/3307 (0.0%)
All	All	0.82	2/4870 (0.0%)	0.81	1/6573 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	43	PHE	CE2-CZ	5.71	1.48	1.37
1	B	43	PHE	CG-CD1	5.39	1.46	1.38

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	35	LEU	CA-CB-CG	5.14	127.13	115.30

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	2380	0	2384	31	0
1	B	2409	0	2418	33	0
2	A	5	0	0	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	5	0	0	5	0
3	A	13	0	0	0	0
3	B	16	0	0	0	0
All	All	4828	0	4802	63	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.

All (63) 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:128:THR:H	2:B:313:UNL:X3	1.92	0.82
1:A:151:ARG:HH11	1:A:151:ARG:HG2	1.51	0.75
1:A:128:THR:H	2:A:313:UNL:X2	2.03	0.70
1:B:128:THR:OG1	2:B:313:UNL:X3	2.44	0.65
1:B:139:PHE:HB3	1:B:144:ILE:O	1.95	0.65
1:A:268:SER:O	1:A:272:ASN:HB2	1.96	0.65
1:A:47:TYR:OH	2:A:313:UNL:X3	2.45	0.64
1:A:101:LYS:HE3	1:A:191:LYS:O	1.98	0.62
1:B:263:PHE:O	1:B:266:MSE:HB3	2.01	0.60
1:A:15:GLU:OE1	1:A:181:LYS:HG2	2.02	0.59
1:B:108:LEU:HD11	1:B:138:VAL:HG13	1.85	0.59
1:A:240:ARG:HG2	1:A:240:ARG:O	2.03	0.58
1:A:61:ILE:HD11	1:A:221:ILE:CD1	2.33	0.58
1:A:32:GLU:OE2	1:A:38:LYS:HA	2.04	0.58
1:A:17:GLN:O	1:A:21:LYS:HG3	2.06	0.56
1:B:129:SER:H	2:B:313:UNL:X5	2.18	0.56
1:B:64:TYR:HD1	1:B:68:SER:HG	1.53	0.56
1:B:31:MSE:HG2	1:B:35:LEU:HD22	1.88	0.55
1:B:60:ASP:OD1	1:B:210:ARG:NH2	2.38	0.55
1:B:111:LEU:HD11	1:B:171:VAL:HG11	1.89	0.55
1:B:119:THR:HG22	1:B:151:ARG:HB3	1.89	0.54
1:A:61:ILE:HD11	1:A:221:ILE:HD13	1.91	0.53
1:A:151:ARG:HG2	1:A:151:ARG:NH1	2.22	0.53
1:B:66:ASN:HB3	1:B:257:ILE:HG12	1.91	0.52
1:B:61:ILE:HD11	1:B:221:ILE:CD1	2.41	0.50
1:B:15:GLU:OE1	1:B:181:LYS:HG2	2.11	0.50
1:B:101:LYS:HD3	1:B:192:GLU:HA	1.94	0.50
1:B:137:TYR:HA	1:B:141:LYS:HG3	1.93	0.49
1:A:128:THR:O	1:A:133:VAL:HG23	2.13	0.48
1:B:129:SER:OG	2:B:313:UNL:X5	2.62	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:66:ASN:HB3	1:A:257:ILE:HG13	1.95	0.48
1:A:32:GLU:OE2	1:A:38:LYS:HD2	2.13	0.48
1:A:263:PHE:O	1:A:266:MSE:HB3	2.14	0.47
1:B:60:ASP:OD1	1:B:210:ARG:NE	2.46	0.47
1:B:84:THR:HG21	1:B:243:TRP:CZ2	2.49	0.47
1:B:281:LEU:O	1:B:285:THR:HG23	2.15	0.47
1:A:129:SER:OG	2:A:313:UNL:X4	2.63	0.47
1:A:120:PHE:HD1	1:A:171:VAL:HG13	1.79	0.46
1:A:14:THR:HG22	1:A:20:LEU:HD21	1.98	0.46
1:A:23:GLN:HA	1:A:240:ARG:CD	2.46	0.46
1:B:133:VAL:HG22	1:B:260:LEU:HD21	1.97	0.45
1:B:76:ALA:O	1:B:77:ASN:CB	2.61	0.45
1:A:105:ILE:HG23	1:A:110:ASP:HB2	1.99	0.45
1:B:266:MSE:HE2	1:B:287:ILE:HG22	1.99	0.45
1:B:276:ASN:HB2	1:B:279:ASP:H	1.81	0.45
1:A:278:GLN:H	1:A:278:GLN:HG2	1.69	0.44
1:A:28:LEU:O	1:A:32:GLU:HG3	2.19	0.43
1:B:91:PRO:HG2	1:B:201:LEU:HD21	2.00	0.42
1:B:15:GLU:O	1:B:20:LEU:HD11	2.19	0.42
1:B:65:GLY:HA3	2:B:313:UNL:X3	2.49	0.42
1:A:70:MSE:HA	1:A:254:LEU:HD13	2.00	0.42
1:A:84:THR:HG21	1:A:243:TRP:CZ2	2.55	0.42
1:A:127:SER:OG	2:A:313:UNL:X3	2.67	0.42
1:B:54:MSE:HE1	1:B:208:VAL:HG12	2.01	0.42
1:A:111:LEU:HD11	1:A:171:VAL:HG11	2.02	0.42
1:A:118:LEU:HD22	1:A:170:ASP:HB3	2.02	0.42
1:B:211:LYS:C	1:B:213:LEU:H	2.24	0.41
1:A:301:LEU:HD22	1:B:304:MSE:HE1	2.01	0.41
1:A:31:MSE:HG2	1:A:35:LEU:HD22	2.01	0.41
1:B:254:LEU:O	1:B:255:VAL:C	2.59	0.41
1:B:244:ALA:HB1	1:B:245:PRO:HD2	2.02	0.41
1:B:223:ASP:OD2	1:B:227:ASN:ND2	2.54	0.40
1:A:23:GLN:HA	1:A:240:ARG:HD3	2.02	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	300/321 (94%)	290 (97%)	10 (3%)	0	100	100
1	B	306/321 (95%)	293 (96%)	12 (4%)	1 (0%)	41	55
All	All	606/642 (94%)	583 (96%)	22 (4%)	1 (0%)	47	62

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	212	ASN

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	258/266 (97%)	243 (94%)	15 (6%)	20	32
1	B	261/266 (98%)	245 (94%)	16 (6%)	18	30
All	All	519/532 (98%)	488 (94%)	31 (6%)	19	31

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	14	THR
1	A	128	THR
1	A	147	SER
1	A	174	ASN
1	A	181	LYS

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Mol	Chain	Res	Type
1	A	209	TRP
1	A	214	SER
1	A	215	GLU
1	A	233	GLU
1	A	257	ILE
1	A	266	MSE
1	A	268	SER
1	A	277	GLU
1	A	278	GLN
1	A	306	SER
1	B	7	LEU
1	B	34	LYS
1	B	35	LEU
1	B	77	ASN
1	B	116	LYS
1	B	128	THR
1	B	145	SER
1	B	174	ASN
1	B	181	LYS
1	B	188	GLU
1	B	209	TRP
1	B	215	GLU
1	B	216	THR
1	B	239	GLU
1	B	295	ASP
1	B	306	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	57	ASN
1	B	299	ASN

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](#)

Of 2 ligands modelled in this entry, 2 are unknown - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

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 [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	298/321 (92%)	-0.15	5 (1%) 70 68	25, 41, 64, 88	0
1	B	302/321 (94%)	-0.11	2 (0%) 87 86	26, 45, 77, 102	0
All	All	600/642 (93%)	-0.13	7 (1%) 79 77	25, 43, 70, 102	0

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	278	GLN	3.6
1	A	280	LYS	2.6
1	A	5	LYS	2.6
1	B	34	LYS	2.5
1	B	37	VAL	2.2
1	A	277	GLU	2.0
1	A	284	THR	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 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. 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(\AA^2)	Q<0.9
2	UNL	B	313	5/-	0.95	0.34	28,29,30,34	0
2	UNL	A	313	5/-	0.98	0.36	30,30,33,33	0

6.5 Other polymers [i](#)

There are no such residues in this entry.