



wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 5XEU / pdb_00005xeu
Title : crystal structure of Hcp2 from Salmonella typhimurium
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Deposited on : 2017-04-06
Resolution : 3.00 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

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
Xtrriage (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

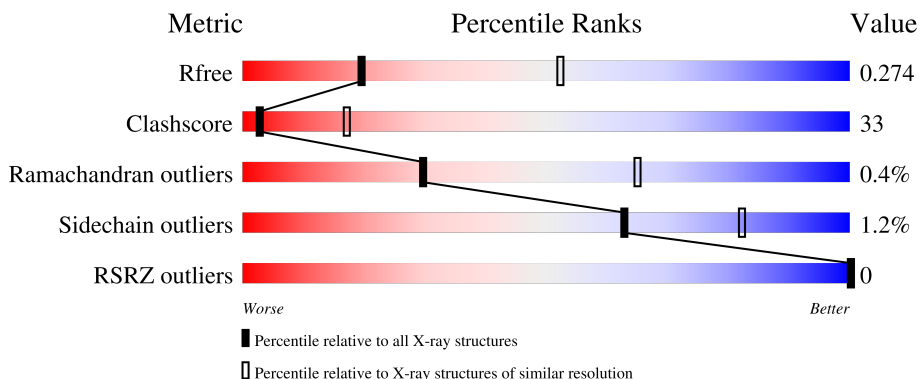
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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}	180053	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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 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	161	
1	B	161	
1	C	161	
1	D	161	
1	E	161	

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Mol	Chain	Length	Quality of chain
1	F	161	 46% 32% 20%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 5934 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 Hcp1 family type VI secretion system effector.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	128	Total 989	C 635	N 157	O 195	S 2	0	0	0
1	B	128	Total 990	C 634	N 157	O 196	S 3	0	0	0
1	C	129	Total 990	C 634	N 159	O 195	S 2	0	0	0
1	D	129	Total 992	C 634	N 159	O 197	S 2	0	0	0
1	E	128	Total 990	C 635	N 159	O 194	S 2	0	0	0
1	F	128	Total 983	C 631	N 156	O 194	S 2	0	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	102.64Å 147.79Å 85.69Å 90.00° 123.74° 90.00°	Depositor
Resolution (Å)	32.80 – 3.00 32.80 – 3.00	Depositor EDS
% Data completeness (in resolution range)	98.6 (32.80-3.00) 80.0 (32.80-3.00)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.81 (at 2.95Å)	Xtriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
R, R_{free}	0.237 , 0.280 0.249 , 0.274	Depositor DCC
R_{free} test set	1061 reflections (4.75%)	wwPDB-VP
Wilson B-factor (Å ²)	75.6	Xtriage
Anisotropy	0.483	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 285.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.53$, $\langle L^2 \rangle = 0.37$	Xtriage
Estimated twinning fraction	0.000 for $-1/2^*h+1/2^*k-1,3/2^*h+1/2^*k+1,1/2^*h-1/2^*k$ 0.000 for $1/2^*h-1/2^*k+1,-1/2^*h+1/2^*k+1,-h$ 0.000 for $1/2^*h+1/2^*k+1,1/2^*h+1/2^*k-1,-h-1$ 0.000 for $-1/2^*h-1/2^*k-1,-3/2^*h+1/2^*k-1,1/2^*h+1/2^*k$ 0.000 for $-h,-h-2^*1,1/2^*h-1/2^*k$ 0.000 for $-h,h+2^*1,1/2^*h+1/2^*k$ 0.439 for $1/2^*h+1/2^*k+1,3/2^*h-1/2^*k+1,-1$ 0.440 for $1/2^*h-1/2^*k+1,-3/2^*h-1/2^*k-1,-1$ 0.000 for $-1/2^*h+1/2^*k-1,1/2^*h-1/2^*k-1,-1/2^*h-1/2^*k$ 0.000 for $-1/2^*h-1/2^*k-1,-1/2^*h-1/2^*k+1,-1/2^*h+1/2^*k$ 0.000 for $h,-k,-h-1$	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5934	wwPDB-VP
Average B, all atoms (Å ²)	104.0	wwPDB-VP

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.

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.44% of the height of the origin peak. No significant pseudotranslation is detected.*

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.43	0/1007	0.70	2/1360 (0.1%)
1	B	0.47	0/1008	0.73	0/1361
1	C	0.39	0/1008	0.65	1/1361 (0.1%)
1	D	0.42	0/1010	0.71	1/1363 (0.1%)
1	E	0.38	0/1008	0.90	7/1360 (0.5%)
1	F	0.41	0/1001	0.69	2/1351 (0.1%)
All	All	0.42	0/6042	0.73	13/8156 (0.2%)

There are no bond length outliers.

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	103	ASP	N-CA-C	11.23	127.01	111.17
1	E	157	ALA	N-CA-C	-9.55	93.77	108.96
1	A	71	LYS	N-CA-C	8.01	120.80	111.02
1	F	157	ALA	N-CA-C	-7.81	96.17	108.90
1	E	157	ALA	CB-CA-C	7.44	122.64	110.22

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	989	0	903	79	0
1	B	990	0	909	82	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	990	0	900	59	0
1	D	992	0	897	63	0
1	E	990	0	909	63	0
1	F	983	0	894	54	0
All	All	5934	0	5412	372	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 33.

The worst 5 of 372 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:101:PHE:HE1	1:A:132:VAL:CG2	1.20	1.54
1:A:101:PHE:CE1	1:A:132:VAL:CG2	1.98	1.45
1:A:101:PHE:CE1	1:A:132:VAL:HG21	1.65	1.28
1:A:21:HIS:HD2	1:A:24:GLU:HG3	1.02	1.13
1:A:21:HIS:CD2	1:A:24:GLU:HG3	1.87	1.09

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	118/161 (73%)	99 (84%)	19 (16%)	0	100	100
1	B	118/161 (73%)	106 (90%)	11 (9%)	1 (1%)	16	50
1	C	119/161 (74%)	106 (89%)	13 (11%)	0	100	100
1	D	119/161 (74%)	108 (91%)	10 (8%)	1 (1%)	16	50
1	E	118/161 (73%)	103 (87%)	14 (12%)	1 (1%)	16	50
1	F	118/161 (73%)	102 (86%)	16 (14%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	710/966 (74%)	624 (88%)	83 (12%)	3 (0%)	30 65

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	158	ASN
1	B	103	ASP
1	E	21	HIS

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	101/136 (74%)	100 (99%)	1 (1%)	68 84
1	B	101/136 (74%)	100 (99%)	1 (1%)	68 84
1	C	101/136 (74%)	101 (100%)	0	100 100
1	D	101/136 (74%)	99 (98%)	2 (2%)	48 76
1	E	101/136 (74%)	99 (98%)	2 (2%)	48 76
1	F	100/136 (74%)	99 (99%)	1 (1%)	68 84
All	All	605/816 (74%)	598 (99%)	7 (1%)	63 82

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	78	HIS
1	E	5	ILE
1	F	64	ARG
1	E	7	LEU
1	D	74	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	68	ASN
1	D	134	GLN
1	F	60	HIS
1	C	21	HIS
1	C	33	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 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	128/161 (79%)	-1.03	0 100 100	80, 106, 122, 134	0
1	B	128/161 (79%)	-1.10	0 100 100	75, 92, 112, 125	0
1	C	129/161 (80%)	-1.00	0 100 100	85, 108, 126, 132	0
1	D	129/161 (80%)	-1.09	0 100 100	74, 98, 122, 139	0
1	E	128/161 (79%)	-1.06	0 100 100	87, 115, 130, 149	0
1	F	128/161 (79%)	-1.08	0 100 100	30, 109, 125, 140	0
All	All	770/966 (79%)	-1.06	0 100 100	30, 104, 125, 149	0

There are no RSRZ outliers to report.

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.