wwPDB X-ray Structure Validation Summary Report (i)

Aug 22, 2023 – 03:54 PM EDT

PDB ID	:	2RB9
Title	:	Crystal structure of E.coli HypE
Authors	:	Asinas, A.E.; Rangarajan, E.S.; Min, T.; Matte, A.; Proteau, A.; Munger, C.; Cygler, M.; Montreal-Kingston Bacterial Structural Genomics Initiative (BSGI)
Deposited on	:	2007-09-18
Resolution	:	2.00 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 (i) 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 (1)) were used in the production of this report:

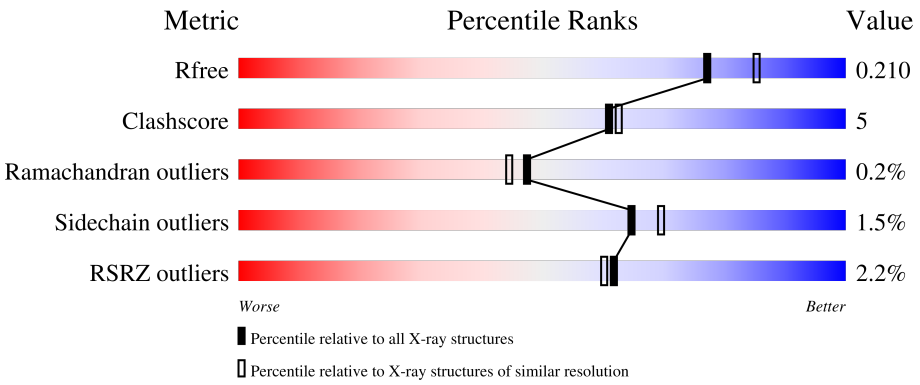
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.35
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

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 2.00 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}	130704	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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 <=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	334	2% 89% 7% •
1	B	334	2% 88% 8% •
1	C	334	3% 85% 11% •
1	D	334	% 87% 10% •

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 10568 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 HypE protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	322	2452	1561	417	461	13	5	15	0
1	B	322	2453	1557	424	459	13	0	14	0
1	C	322	2475	1576	421	464	14	0	19	0
1	D	323	2474	1570	420	468	16	0	16	0

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	3	MET	-	expression tag	UNP Q7ABB2
A	4	GLY	-	expression tag	UNP Q7ABB2
A	5	SER	-	expression tag	UNP Q7ABB2
A	6	SER	-	expression tag	UNP Q7ABB2
A	7	HIS	-	expression tag	UNP Q7ABB2
A	8	HIS	-	expression tag	UNP Q7ABB2
A	9	HIS	-	expression tag	UNP Q7ABB2
A	10	HIS	-	expression tag	UNP Q7ABB2
A	11	HIS	-	expression tag	UNP Q7ABB2
A	12	HIS	-	expression tag	UNP Q7ABB2
A	13	GLY	-	expression tag	UNP Q7ABB2
A	14	SER	-	expression tag	UNP Q7ABB2
B	3	MET	-	expression tag	UNP Q7ABB2
B	4	GLY	-	expression tag	UNP Q7ABB2
B	5	SER	-	expression tag	UNP Q7ABB2
B	6	SER	-	expression tag	UNP Q7ABB2
B	7	HIS	-	expression tag	UNP Q7ABB2
B	8	HIS	-	expression tag	UNP Q7ABB2
B	9	HIS	-	expression tag	UNP Q7ABB2
B	10	HIS	-	expression tag	UNP Q7ABB2
B	11	HIS	-	expression tag	UNP Q7ABB2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	12	HIS	-	expression tag	UNP Q7ABB2
B	13	GLY	-	expression tag	UNP Q7ABB2
B	14	SER	-	expression tag	UNP Q7ABB2
C	3	MET	-	expression tag	UNP Q7ABB2
C	4	GLY	-	expression tag	UNP Q7ABB2
C	5	SER	-	expression tag	UNP Q7ABB2
C	6	SER	-	expression tag	UNP Q7ABB2
C	7	HIS	-	expression tag	UNP Q7ABB2
C	8	HIS	-	expression tag	UNP Q7ABB2
C	9	HIS	-	expression tag	UNP Q7ABB2
C	10	HIS	-	expression tag	UNP Q7ABB2
C	11	HIS	-	expression tag	UNP Q7ABB2
C	12	HIS	-	expression tag	UNP Q7ABB2
C	13	GLY	-	expression tag	UNP Q7ABB2
C	14	SER	-	expression tag	UNP Q7ABB2
D	3	MET	-	expression tag	UNP Q7ABB2
D	4	GLY	-	expression tag	UNP Q7ABB2
D	5	SER	-	expression tag	UNP Q7ABB2
D	6	SER	-	expression tag	UNP Q7ABB2
D	7	HIS	-	expression tag	UNP Q7ABB2
D	8	HIS	-	expression tag	UNP Q7ABB2
D	9	HIS	-	expression tag	UNP Q7ABB2
D	10	HIS	-	expression tag	UNP Q7ABB2
D	11	HIS	-	expression tag	UNP Q7ABB2
D	12	HIS	-	expression tag	UNP Q7ABB2
D	13	GLY	-	expression tag	UNP Q7ABB2
D	14	SER	-	expression tag	UNP Q7ABB2

- Molecule 2 is water.

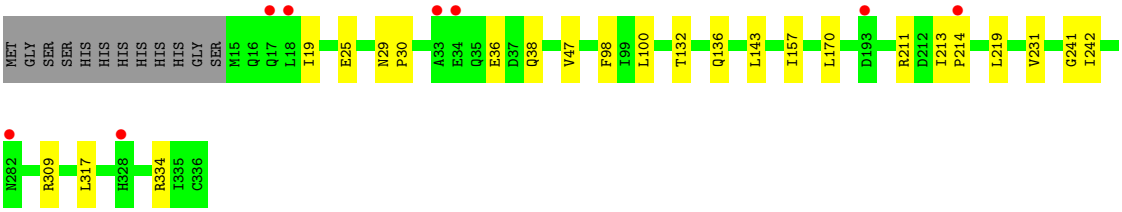
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
2	A	145	145	145	0	0
			Total	O		
2	B	144	144	144	0	0
			Total	O		
2	C	170	170	170	0	0
			Total	O		
2	D	255	255	255	0	0

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.

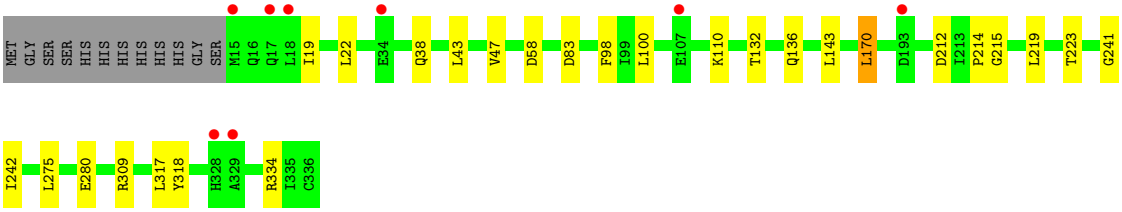
• Molecule 1: HypE protein

Chain A:



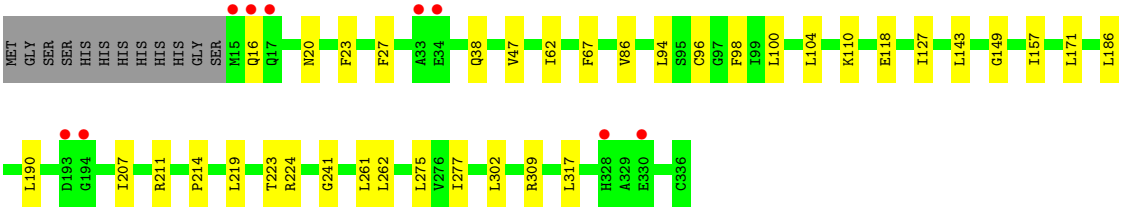
• Molecule 1: HypE protein

Chain B:



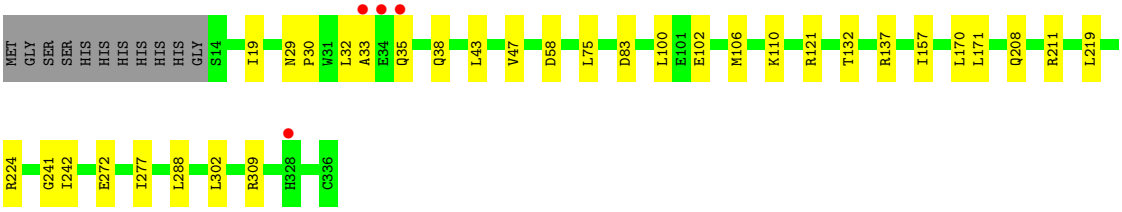
• Molecule 1: HypE protein

Chain C:



• Molecule 1: HypE protein

Chain D:


MET
GLY
SER
SER
HIS
HIS
HIS
HIS
HIS
HIS
GLY
S14
I19
N29
P30
W31
L32
A33
E34
Q35
Q38
L43
V47
D58
L75
D83
L100
E101
E102
M106
K110
R121
T132
R137
I157
L170
L171
Q208
R211
L219

R224
G241
I242
E272
I277
L288
L302
R309
H328
C336

4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	254.57Å 72.30Å 112.61Å 90.00° 115.33° 90.00°	Depositor
Resolution (Å)	43.73 – 2.00 43.72 – 2.00	Depositor EDS
% Data completeness (in resolution range)	98.7 (43.73-2.00) 98.7 (43.72-2.00)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.51 (at 2.00Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.176 , 0.208 0.179 , 0.210	Depositor DCC
R_{free} test set	6153 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å^2)	21.2	Xtriage
Anisotropy	0.044	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 54.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.012 for -h-2*l,-k,l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	10568	wwPDB-VP
Average B, all atoms (Å^2)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.89% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical 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.

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	2/2523 (0.1%)	0.54	0/3429
1	B	0.41	0/2516	0.54	0/3418
1	C	0.42	0/2557	0.57	0/3476
1	D	0.45	0/2545	0.57	0/3459
All	All	0.43	2/10141 (0.0%)	0.56	0/13782

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	219[A]	LEU	N-CA	-6.20	1.33	1.46
1	A	219[C]	LEU	N-CA	-6.20	1.33	1.46

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)	H(added)	Clashes	Symm-Clashes
1	A	2452	0	2545	20	0
1	B	2453	0	2537	23	0
1	C	2475	0	2569	34	0
1	D	2474	0	2554	28	0
2	A	145	0	0	0	0
2	B	144	0	0	0	0
2	C	170	0	0	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	255	0	0	1	1
All	All	10568	0	10205	91	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 5.

The worst 5 of 91 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:C:47[B]:VAL:HG21	1:D:47[B]:VAL:HG21	1.12	1.05
1:B:100[B]:LEU:HD23	1:B:143[B]:LEU:CD1	1.93	0.98
1:C:47[B]:VAL:HG21	1:D:47[B]:VAL:CG2	1.95	0.97
1:B:100[B]:LEU:HD23	1:B:143[B]:LEU:HD12	1.45	0.96
1:C:47[B]:VAL:CG2	1:D:47[B]:VAL:HG21	1.97	0.94

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)
2:D:371:HOH:O	2:D:585:HOH:O[4_555]	1.55	0.65

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	335/334 (100%)	324 (97%)	11 (3%)	0	100	100
1	B	334/334 (100%)	326 (98%)	7 (2%)	1 (0%)	41	37
1	C	340/334 (102%)	329 (97%)	11 (3%)	0	100	100
1	D	339/334 (102%)	328 (97%)	10 (3%)	1 (0%)	41	37
All	All	1348/1336 (101%)	1307 (97%)	39 (3%)	2 (0%)	47	49

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	223	THR
1	D	33	ALA

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	261/256 (102%)	254 (97%)	7 (3%)	44	46
1	B	259/256 (101%)	254 (98%)	5 (2%)	57	61
1	C	265/256 (104%)	261 (98%)	4 (2%)	65	69
1	D	265/256 (104%)	263 (99%)	2 (1%)	81	86
All	All	1050/1024 (102%)	1032 (98%)	18 (2%)	65	65

5 of 18 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	262	LEU
1	D	100	LEU
1	D	38	GLN
1	B	170[A]	LEU
1	C	186	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	158	HIS
1	D	208	GLN
1	B	136	GLN
1	B	158	HIS
1	C	35	GLN

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)

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	322/334 (96%)	-0.19	8 (2%)	57	56	17, 26, 42, 76	0
1	B	322/334 (96%)	-0.41	8 (2%)	57	56	12, 23, 48, 82	0
1	C	322/334 (96%)	-0.41	9 (2%)	53	51	13, 22, 43, 78	0
1	D	323/334 (96%)	-0.48	4 (1%)	79	78	10, 16, 36, 68	0
All	All	1289/1336 (96%)	-0.37	29 (2%)	62	60	10, 22, 43, 82	0

The worst 5 of 29 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	34	GLU	5.8
1	B	328	HIS	4.3
1	A	34	GLU	3.8
1	B	15	MET	3.5
1	C	330	GLU	3.4

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)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.