



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 01:39 PM GMT

PDB ID : 3UJZ
Title : Crystal structure of enterohemorrhagic E. coli StcE
Authors : Yu, A.C.Y.; Strynadka, N.C.J.
Deposited on : 2011-11-08
Resolution : 2.50 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
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

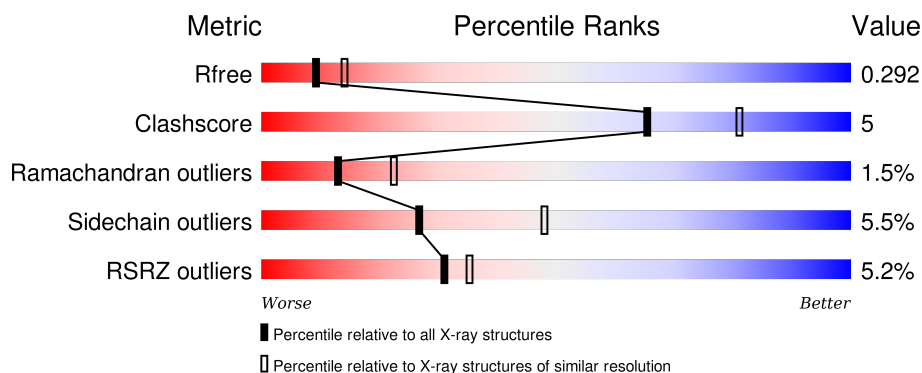
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION


The reported resolution of this entry is 2.50 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}	91344	3553 (2.50-2.50)
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (2.50-2.50)

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. 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	869	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4868 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 Metalloprotease stcE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	604	Total	C	N	O	S	Se	0	0	0
			4695	2962	817	900	4	12			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	30	GLY	-	EXPRESSION TAG	UNP O82882
A	31	SER	-	EXPRESSION TAG	UNP O82882
A	32	HIS	-	EXPRESSION TAG	UNP O82882
A	33	MSE	-	EXPRESSION TAG	UNP O82882
A	34	ALA	-	EXPRESSION TAG	UNP O82882
A	35	SER	-	EXPRESSION TAG	UNP O82882
A	318	ALA	LYS	ENGINEERED MUTATION	UNP O82882
A	320	ALA	LYS	ENGINEERED MUTATION	UNP O82882
A	321	ALA	GLU	ENGINEERED MUTATION	UNP O82882
A	447	ASP	GLU	ENGINEERED MUTATION	UNP O82882

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Zn	0	0
			1	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	172	Total	O	0	0
			172	172		

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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 ($\text{RSRZ} > 2$). 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.

[illegible]

4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	76.53Å 186.00Å 188.76Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.17 – 2.50 48.17 – 2.50	Depositor EDS
% Data completeness (in resolution range)	(Not available) (48.17-2.50) 100.0 (48.17-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.15 (at 2.51Å)	Xtriage
Refinement program	BUSTER 2.8.0	Depositor
R, R_{free}	0.211 , 0.253 0.246 , 0.292	Depositor DCC
R_{free} test set	2349 reflections (5.26%)	DCC
Wilson B-factor (Å ²)	51.0	Xtriage
Anisotropy	0.954	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 63.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	1 of 47012 reflections (0.002%)	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	4868	wwPDB-VP
Average B, all atoms (Å ²)	84.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.30% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: ZN

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	0.51	0/4806	0.72	1/6512 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	881	ASN	N-CA-C	-5.41	96.40	111.00

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	4695	0	4503	46	0
2	A	1	0	0	0	0
3	A	172	0	0	0	0
All	All	4868	0	4503	46	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 5.

All (46) 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:809:ILE:HG12	1:A:893:MSE:HE1	1.31	1.07
1:A:357:THR:O	1:A:358:ASP:HB2	1.60	1.01
1:A:83:THR:HG22	1:A:542:GLN:HE21	1.34	0.93
1:A:83:THR:HG22	1:A:542:GLN:NE2	1.97	0.79
1:A:300:HIS:HD1	1:A:338:ASN:HD22	1.29	0.76
1:A:516:ASP:OD2	1:A:518:MSE:N	2.22	0.72
1:A:349:MSE:HE1	1:A:353:GLY:HA2	1.70	0.72
1:A:897:TYR:O	1:A:898:LYS:HB2	1.91	0.69
1:A:700:THR:HA	1:A:701:LEU:HB3	1.74	0.68
1:A:105:VAL:HG22	1:A:277:ILE:HG12	1.78	0.65
1:A:130:ILE:HG12	1:A:527:ALA:HB1	1.79	0.64
1:A:822:VAL:HG11	1:A:897:TYR:CD2	2.35	0.62
1:A:93:ARG:HB2	1:A:259:ILE:HG12	1.81	0.62
1:A:357:THR:O	1:A:358:ASP:CB	2.40	0.61
1:A:334:ARG:HD3	1:A:798:GLN:O	2.02	0.60
1:A:501:ASN:O	1:A:502:ASN:HB2	2.03	0.59
1:A:347:GLU:HB3	1:A:355:LEU:HD11	1.84	0.58
1:A:64:ALA:HB3	1:A:89:LEU:HB3	1.85	0.57
1:A:130:ILE:HD11	1:A:482:LYS:HD3	1.88	0.55
1:A:809:ILE:CG1	1:A:893:MSE:HE1	2.22	0.53
1:A:296:GLU:HB2	1:A:550:VAL:HG22	1.91	0.52
1:A:56:SER:HB3	1:A:283:SER:H	1.76	0.51
1:A:881:ASN:O	1:A:883:GLN:N	2.41	0.51
1:A:372:ARG:NH2	1:A:428:SER:OG	2.45	0.50
1:A:765:SER:O	1:A:766:GLN:HB2	2.11	0.50
1:A:822:VAL:CG1	1:A:897:TYR:CD2	2.96	0.49
1:A:366:TRP:O	1:A:372:ARG:NH1	2.46	0.48
1:A:40:SER:HA	1:A:252:ARG:HD2	1.95	0.47
1:A:828:TYR:CE2	1:A:855:ASP:HB3	2.51	0.46
1:A:293:ALA:HB2	1:A:562:TRP:CG	2.53	0.44
1:A:897:TYR:O	1:A:898:LYS:CB	2.60	0.44
1:A:517:ALA:HB2	1:A:531:THR:HB	2.00	0.44
1:A:685:GLY:HA3	1:A:713:TYR:CE1	2.53	0.44
1:A:517:ALA:HB2	1:A:531:THR:CG2	2.48	0.43
1:A:68:ILE:HD12	1:A:476:TRP:HB2	2.01	0.42
1:A:121:TYR:HB3	1:A:125:SER:HB2	2.02	0.42
1:A:300:HIS:NE2	1:A:408:GLN:NE2	2.67	0.42
1:A:45:ASN:HB3	1:A:256:ALA:HB2	2.01	0.42
1:A:501:ASN:O	1:A:502:ASN:CB	2.68	0.41
1:A:414:SER:HB3	1:A:425:HIS:HD2	1.85	0.41
1:A:336:ILE:HD11	1:A:800:LEU:HD21	2.02	0.41
1:A:306:MSE:O	1:A:416:GLY:HA2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:702:SER:O	1:A:754:MSE:SE	2.89	0.40
1:A:475:THR:HG23	1:A:532:MSE:CE	2.52	0.40
1:A:311:ARG:HH11	1:A:424:VAL:HG11	1.87	0.40
1:A:822:VAL:HG11	1:A:897:TYR:CE2	2.56	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	594/869 (68%)	560 (94%)	25 (4%)	9 (2%)	13	22

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	789	GLU
1	A	882	GLY
1	A	41	ALA
1	A	358	ASP
1	A	702	SER
1	A	790	GLY
1	A	766	GLN
1	A	856	ASN
1	A	502	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	506/716 (71%)	478 (94%)	28 (6%)	27	48

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	83	THR
1	A	84	SER
1	A	110	ASP
1	A	112	ASN
1	A	114	ILE
1	A	130	ILE
1	A	134	ASP
1	A	263	GLU
1	A	308	THR
1	A	313	ARG
1	A	314	PHE
1	A	324	ARG
1	A	354	GLU
1	A	357	THR
1	A	366	TRP
1	A	404	TYR
1	A	414	SER
1	A	422	ILE
1	A	467	ARG
1	A	550	VAL
1	A	692	VAL
1	A	701	LEU
1	A	758	HIS
1	A	789	GLU
1	A	832	ASP
1	A	851	LEU
1	A	881	ASN
1	A	894	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	323	HIS
1	A	408	GLN
1	A	423	GLN

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Mol	Chain	Res	Type
1	A	528	ASN
1	A	536	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 1 ligands modelled in this entry, 1 is monoatomic - 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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	592/869 (68%)	0.41	31 (5%) 31 35	24, 83, 120, 167	0

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	779	LEU	6.9
1	A	700	THR	6.1
1	A	898	LYS	5.9
1	A	697	PRO	5.2
1	A	698	GLU	4.9
1	A	576	ILE	4.6
1	A	259	ILE	4.1
1	A	260	TRP	3.9
1	A	514	GLY	3.7
1	A	695	TYR	3.6
1	A	897	TYR	3.6
1	A	94	PRO	3.2
1	A	759	ILE	3.1
1	A	862	ILE	3.1
1	A	286	LEU	3.0
1	A	575	THR	3.0
1	A	896	VAL	2.8
1	A	137	PRO	2.8
1	A	253	ILE	2.8
1	A	249	GLU	2.7
1	A	391	LEU	2.6
1	A	854	TRP	2.6
1	A	830	LEU	2.5
1	A	767	PRO	2.5
1	A	41	ALA	2.4
1	A	694	TYR	2.2
1	A	57	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	677	GLU	2.2
1	A	133	LEU	2.0
1	A	784	LEU	2.0
1	A	102	PRO	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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
2	ZN	A	1	1/1	0.98	0.15	-	53,53,53,53	0

6.5 Other polymers [i](#)

There are no such residues in this entry.