



wwPDB X-ray Structure Validation Summary Report

Feb 13, 2017 – 07:52 am GMT

PDB ID : 1SRU
Title : Crystal structure of full length E. coli SSB protein
Authors : Savvides, S.N.; Raghunathan, S.; Fuetterer, K.; Kozlov, A.G.; Lohman, T.M.;
Waksman, G.
Deposited on : 2004-03-23
Resolution : 3.30 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

<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
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : recalc28949

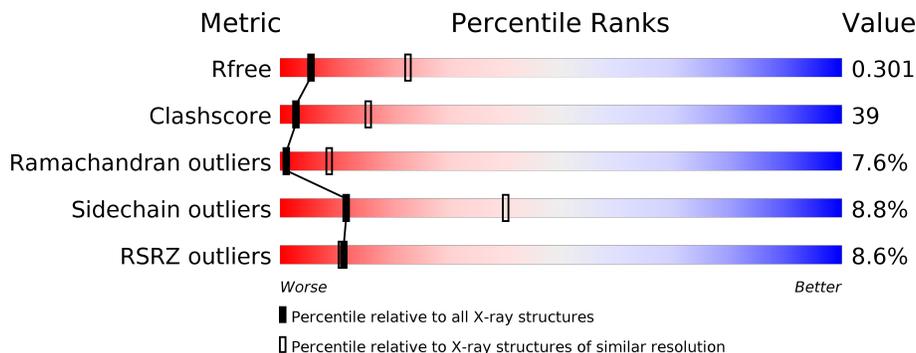
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.30 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}	100719	1034 (3.36-3.24)
Clashscore	112137	1100 (3.36-3.24)
Ramachandran outliers	110173	1081 (3.36-3.24)
Sidechain outliers	110143	1080 (3.36-3.24)
RSRZ outliers	101464	1039 (3.36-3.24)

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	113	
1	B	113	
1	C	113	
1	D	113	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 2808 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 Single-strand binding protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	100	698	440	122	134	2	0	0	0
1	B	97	688	432	121	134	1	0	0	0
1	C	96	698	443	121	133	1	0	0	0
1	D	101	724	453	125	144	2	0	0	0

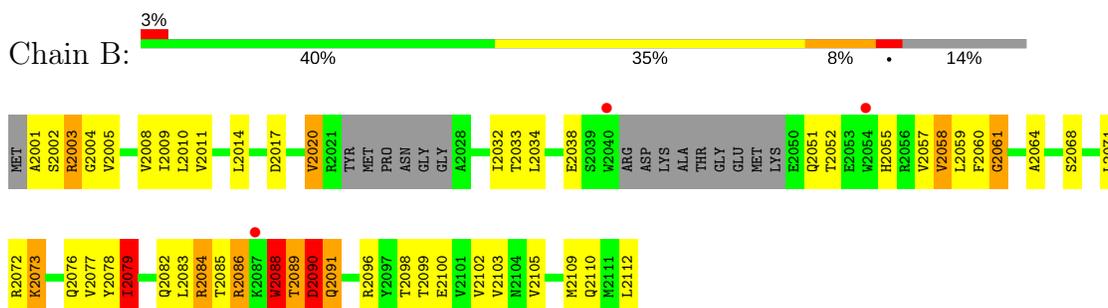
3 Residue-property plots [i](#)

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.

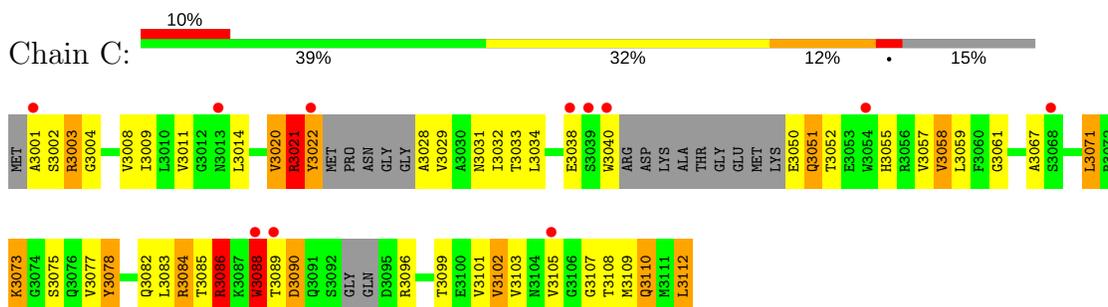
- Molecule 1: Single-strand binding protein



- Molecule 1: Single-strand binding protein

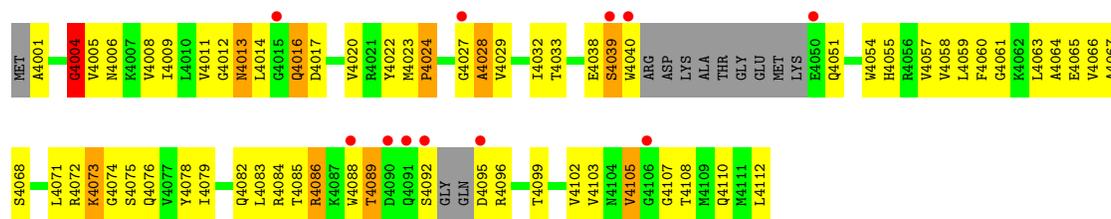


- Molecule 1: Single-strand binding protein



- Molecule 1: Single-strand binding protein





4 Data and refinement statistics

Property	Value	Source
Space group	P 31 1 2	Depositor
Cell constants a, b, c, α , β , γ	60.85Å 60.85Å 348.92Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	19.92 – 3.30 19.92 – 3.29	Depositor EDS
% Data completeness (in resolution range)	97.9 (19.92-3.30) 97.8 (19.92-3.29)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.26 (at 3.29Å)	Xtrriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.288 , 0.309 0.286 , 0.301	Depositor DCC
R_{free} test set	1166 reflections (10.31%)	DCC
Wilson B-factor (Å ²)	106.9	Xtrriage
Anisotropy	0.335	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 118.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	0.075 for -h,-k,l	Xtrriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	2808	wwPDB-VP
Average B, all atoms (Å ²)	102.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.66% 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

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	0.76	0/707	0.88	0/966
1	B	1.57	12/696 (1.7%)	1.48	15/950 (1.6%)
1	C	1.65	13/707 (1.8%)	1.42	12/963 (1.2%)
1	D	0.82	0/733	0.93	3/999 (0.3%)
All	All	1.26	25/2843 (0.9%)	1.21	30/3878 (0.8%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	C	0	1
All	All	0	2

The worst 5 of 25 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	2088	TRP	CG-CD1	-16.84	1.13	1.36
1	C	3088	TRP	CG-CD1	-16.16	1.14	1.36
1	C	3058	VAL	CB-CG2	-14.08	1.23	1.52
1	C	3020	VAL	CB-CG2	-13.34	1.24	1.52
1	B	2058	VAL	CB-CG2	-12.11	1.27	1.52

The worst 5 of 30 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	2086	ARG	NE-CZ-NH2	12.02	126.31	120.30
1	C	3058	VAL	CG1-CB-CG2	-11.69	92.20	110.90
1	C	3071	LEU	CD1-CG-CD2	-11.09	77.22	110.50
1	B	2071	LEU	CD1-CG-CD2	-10.92	77.74	110.50
1	C	3020	VAL	CG1-CB-CG2	-10.79	93.63	110.90

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1078	TYR	Sidechain
1	C	3078	TYR	Sidechain

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	698	0	632	52	0
1	B	688	0	628	54	0
1	C	698	0	635	64	0
1	D	724	0	661	77	0
All	All	2808	0	2556	207	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 39.

The worst 5 of 207 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:2089:THR:O	1:B:2090:ASP:HB3	1.53	1.09
1:D:4020:VAL:HG21	1:D:4068:SER:HB2	1.37	1.06
1:C:3014:LEU:HD23	1:C:3034:LEU:HD23	1.42	0.97
1:C:3077:VAL:HG23	1:C:3110:GLN:O	1.63	0.97
1:C:3011:VAL:O	1:D:4004:GLY:HA3	1.63	0.97

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	94/113 (83%)	77 (82%)	9 (10%)	8 (8%)	1	6
1	B	91/113 (80%)	78 (86%)	6 (7%)	7 (8%)	1	8
1	C	88/113 (78%)	74 (84%)	8 (9%)	6 (7%)	1	10
1	D	95/113 (84%)	78 (82%)	10 (10%)	7 (7%)	1	9
All	All	368/452 (81%)	307 (83%)	33 (9%)	28 (8%)	1	9

5 of 28 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1003	ARG
1	A	1024	PRO
1	A	1073	LYS
1	A	1105	VAL
1	B	2051	GLN

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	63/94 (67%)	59 (94%)	4 (6%)	21	56
1	B	64/94 (68%)	60 (94%)	4 (6%)	21	56
1	C	64/94 (68%)	55 (86%)	9 (14%)	4	19
1	D	69/94 (73%)	63 (91%)	6 (9%)	12	41
All	All	260/376 (69%)	237 (91%)	23 (9%)	12	40

5 of 23 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	3022	TYR
1	C	3086	ARG
1	D	4089	THR

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Mol	Chain	Res	Type
1	C	3082	GLN
1	C	3088	TRP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	2110	GLN
1	C	3055	HIS
1	D	4031	ASN
1	B	2051	GLN
1	D	4016	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 carbohydrates 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	100/113 (88%)	0.24	9 (9%) 10 10	49, 97, 168, 200	0
1	B	97/113 (85%)	0.06	3 (3%) 49 48	51, 99, 164, 192	0
1	C	96/113 (84%)	0.28	11 (11%) 5 4	50, 106, 173, 200	0
1	D	101/113 (89%)	0.30	11 (10%) 6 5	38, 92, 169, 200	0
All	All	394/452 (87%)	0.22	34 (8%) 11 11	38, 98, 169, 200	0

The worst 5 of 34 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	4095	ASP	5.9
1	A	1095	ASP	5.4
1	A	1096	ARG	4.6
1	C	3039	SER	4.5
1	A	1088	TRP	4.3

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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.