



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 01:42 AM UTC

PDB ID : 6S3U / pdb_00006s3u
Title : Adhesin P140 from Mycoplasma Genitalium
Authors : Fita, I.; Aparicio, D.
Deposited on : 2019-06-26
Resolution : 3.24 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:

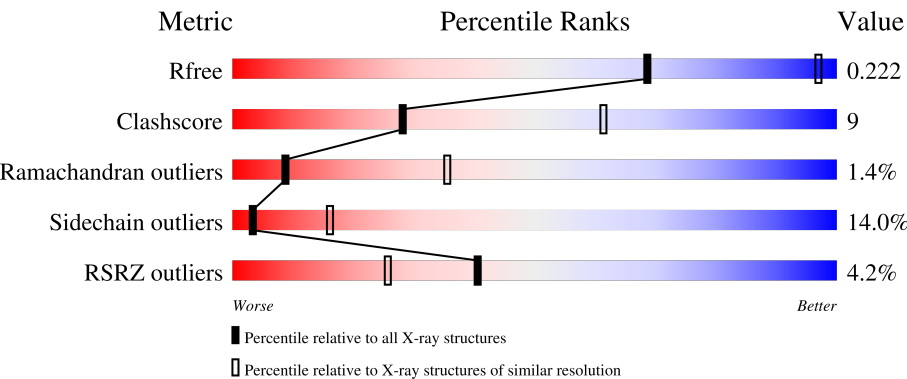
MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.24 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	2153 (3.28-3.20)
Clashscore	190562	2275 (3.28-3.20)
Ramachandran outliers	187476	2233 (3.28-3.20)
Sidechain outliers	187428	2232 (3.28-3.20)
RSRZ outliers	180081	2153 (3.28-3.20)

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	1304	% 66% 27% 5% . .
1	B	1304	2% 65% 27% 5% .
1	C	1304	% 66% 26% 5% .
1	D	1304	% 66% 27% 5% . .
1	E	1304	10% 67% 25% 5% .

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	F	1304	9% 67% 25%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 59767 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 Adhesin P1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1278	Total	C	N	O	S	0	0	0
			10016	6351	1692	1960	13			
1	B	1275	Total	C	N	O	S	0	0	0
			9999	6340	1689	1957	13			
1	C	1274	Total	C	N	O	S	0	0	0
			9993	6339	1688	1953	13			
1	D	1271	Total	C	N	O	S	0	0	0
			9976	6328	1685	1950	13			
1	E	1262	Total	C	N	O	S	0	0	0
			9886	6272	1666	1935	13			
1	F	1262	Total	C	N	O	S	0	0	0
			9897	6281	1668	1935	13			

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1352	HIS	-	expression tag	UNP P20796
A	1353	HIS	-	expression tag	UNP P20796
A	1354	HIS	-	expression tag	UNP P20796
A	1355	HIS	-	expression tag	UNP P20796
A	1356	HIS	-	expression tag	UNP P20796
A	1357	HIS	-	expression tag	UNP P20796
B	1352	HIS	-	expression tag	UNP P20796
B	1353	HIS	-	expression tag	UNP P20796
B	1354	HIS	-	expression tag	UNP P20796
B	1355	HIS	-	expression tag	UNP P20796
B	1356	HIS	-	expression tag	UNP P20796
B	1357	HIS	-	expression tag	UNP P20796
C	1352	HIS	-	expression tag	UNP P20796
C	1353	HIS	-	expression tag	UNP P20796
C	1354	HIS	-	expression tag	UNP P20796
C	1355	HIS	-	expression tag	UNP P20796
C	1356	HIS	-	expression tag	UNP P20796

Continued on next page...

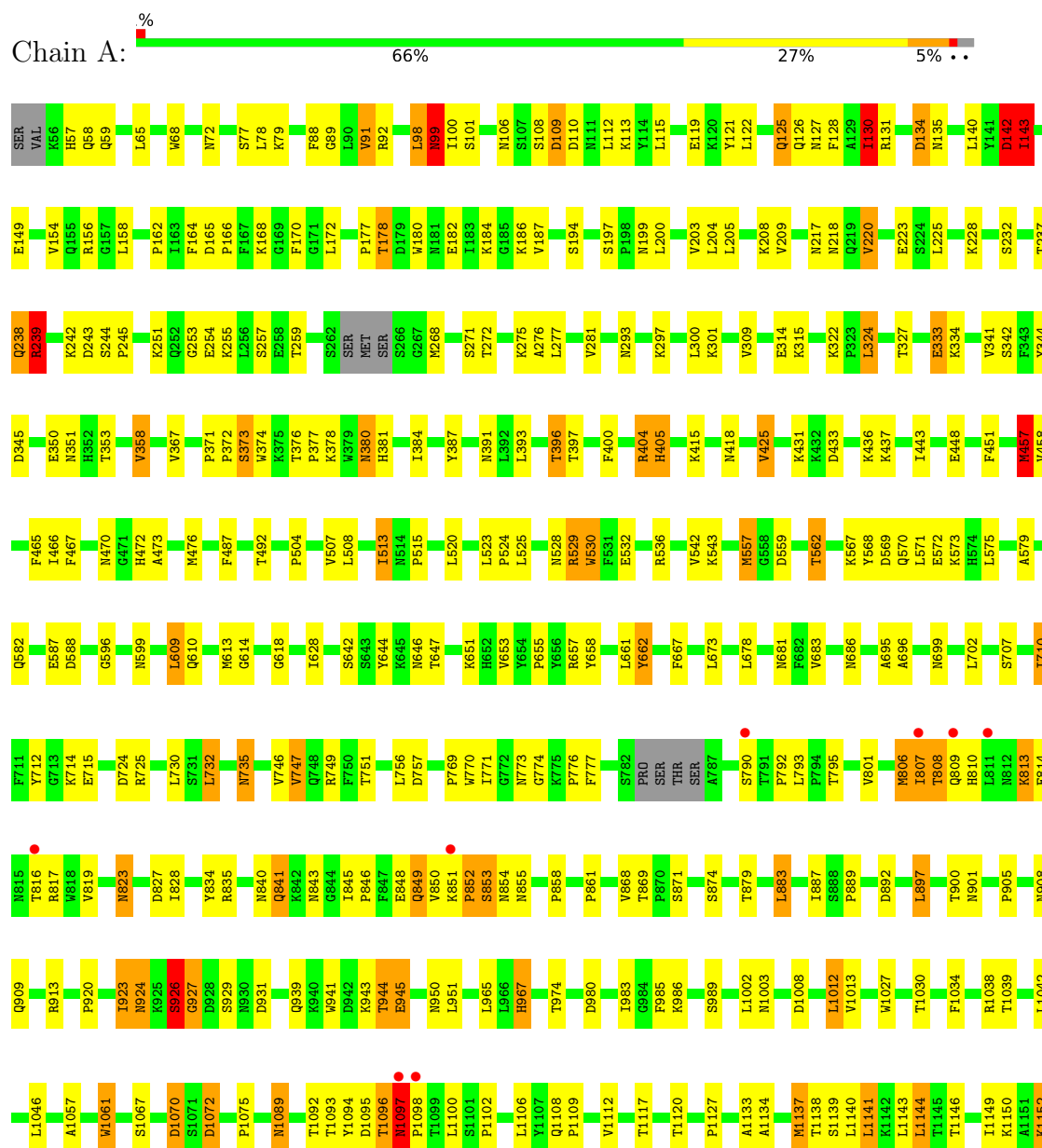
Continued from previous page...

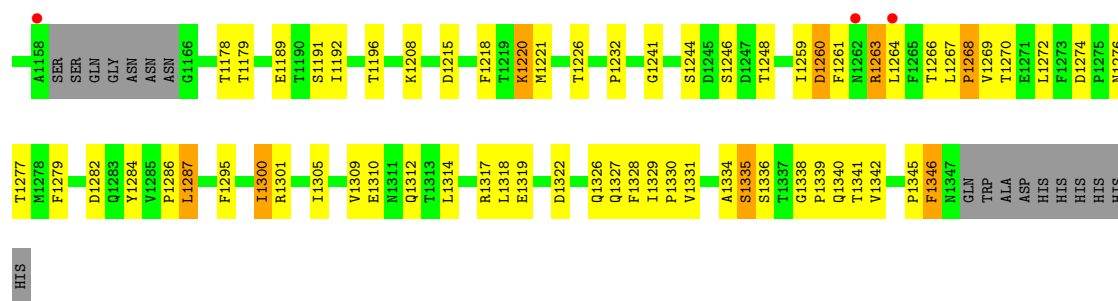
Chain	Residue	Modelled	Actual	Comment	Reference
C	1357	HIS	-	expression tag	UNP P20796
D	1352	HIS	-	expression tag	UNP P20796
D	1353	HIS	-	expression tag	UNP P20796
D	1354	HIS	-	expression tag	UNP P20796
D	1355	HIS	-	expression tag	UNP P20796
D	1356	HIS	-	expression tag	UNP P20796
D	1357	HIS	-	expression tag	UNP P20796
E	1352	HIS	-	expression tag	UNP P20796
E	1353	HIS	-	expression tag	UNP P20796
E	1354	HIS	-	expression tag	UNP P20796
E	1355	HIS	-	expression tag	UNP P20796
E	1356	HIS	-	expression tag	UNP P20796
E	1357	HIS	-	expression tag	UNP P20796
F	1352	HIS	-	expression tag	UNP P20796
F	1353	HIS	-	expression tag	UNP P20796
F	1354	HIS	-	expression tag	UNP P20796
F	1355	HIS	-	expression tag	UNP P20796
F	1356	HIS	-	expression tag	UNP P20796
F	1357	HIS	-	expression tag	UNP P20796

3 Residue-property plots

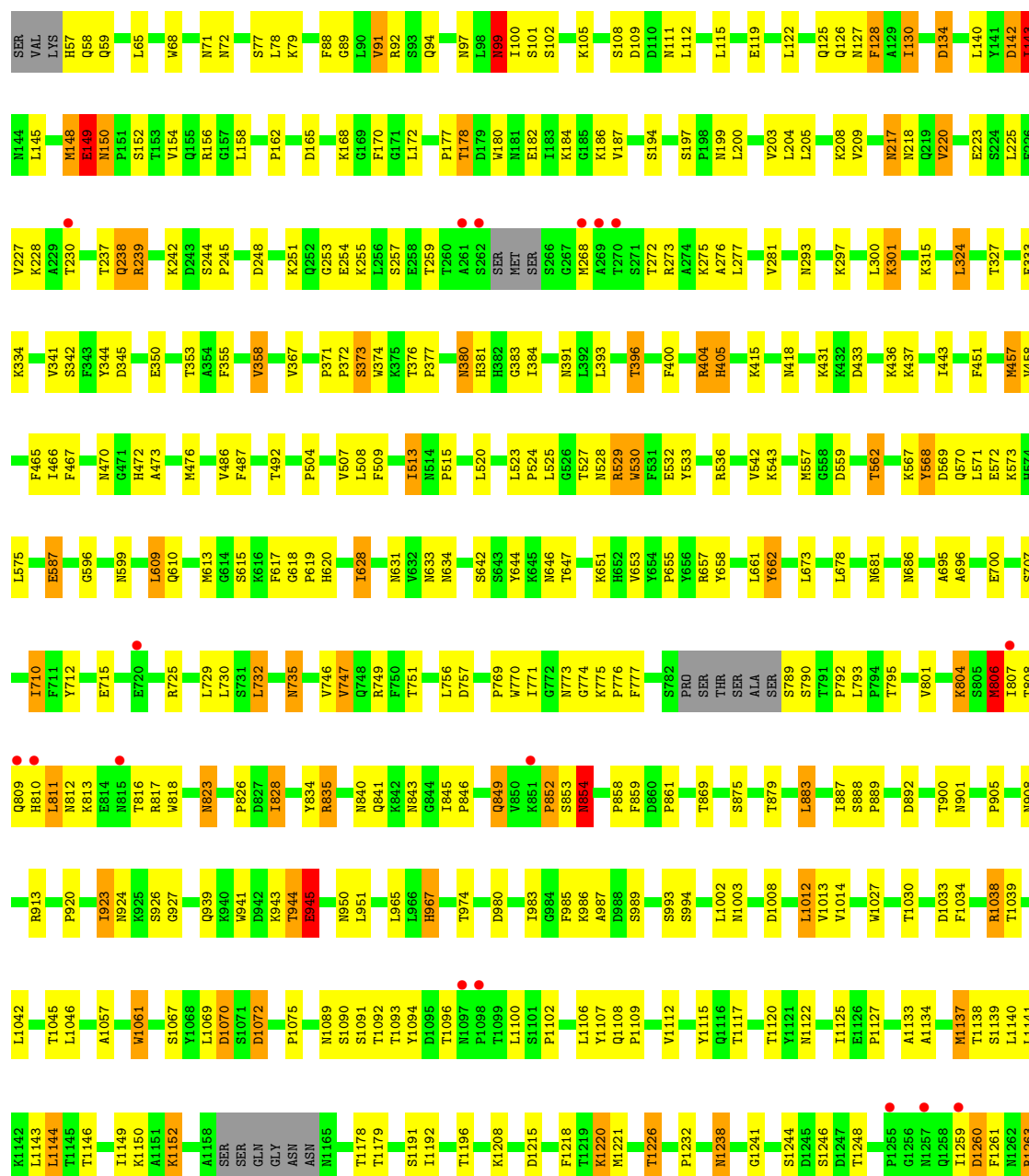
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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.

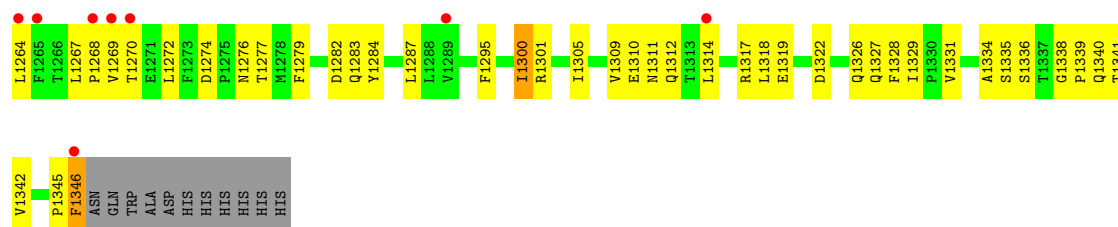
• Molecule 1: Adhesin P1



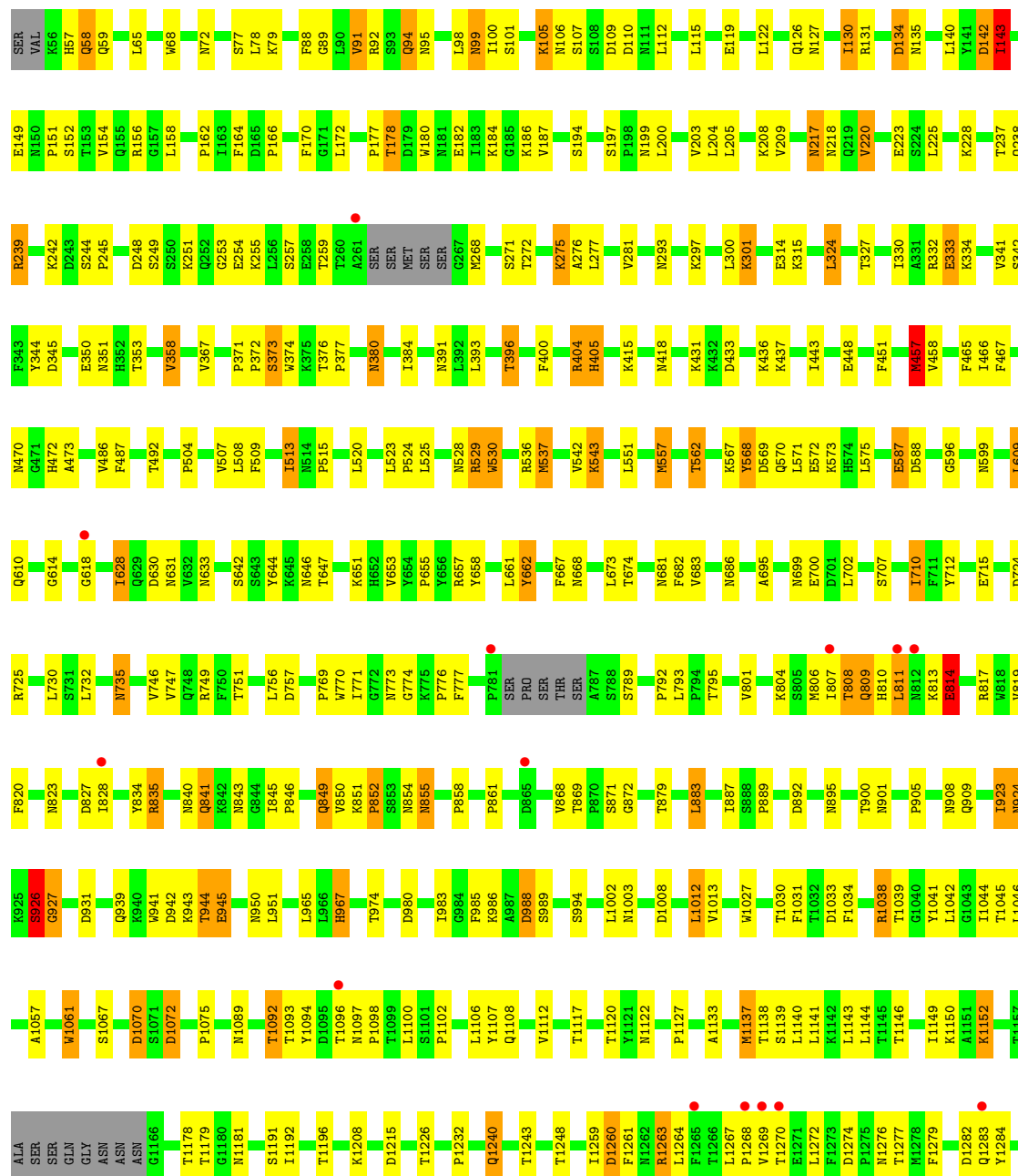


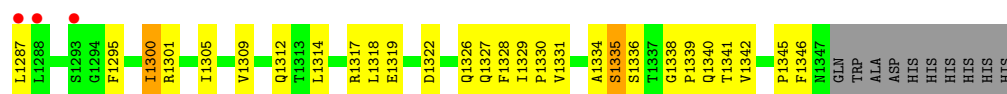
• Molecule 1: Adhesin P1



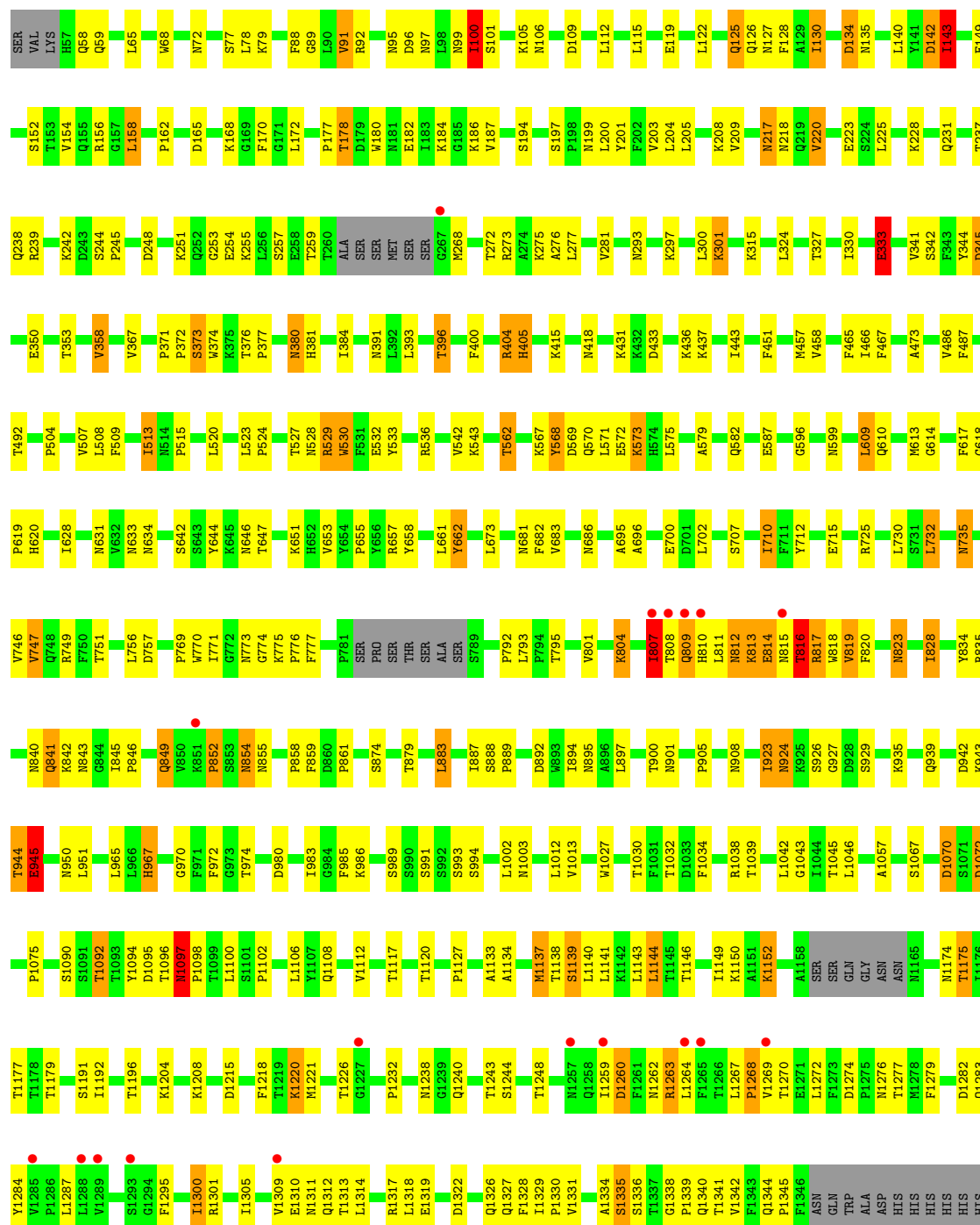


• Molecule 1: Adhesin P1

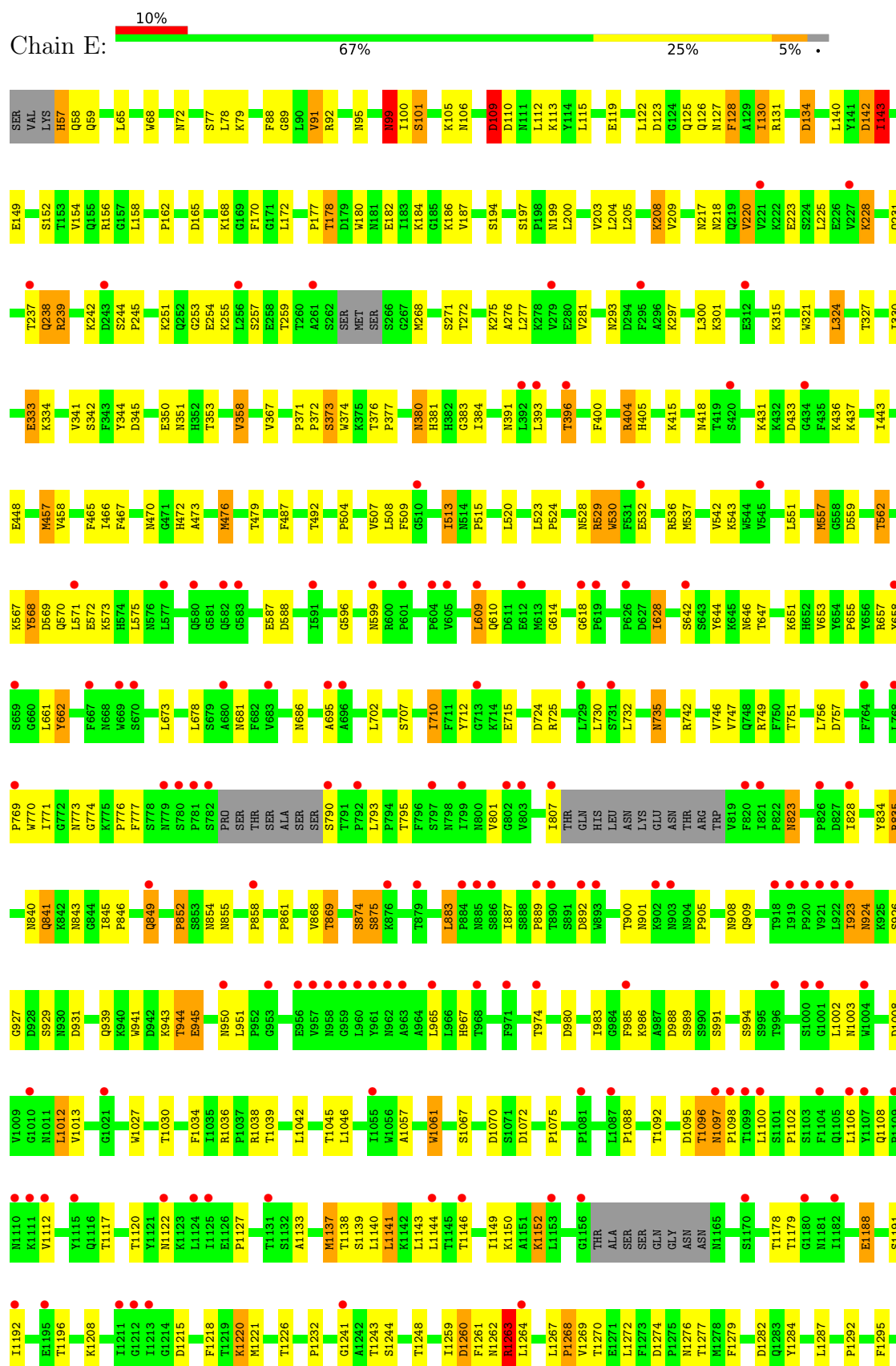




• Molecule 1: Adhesin P1

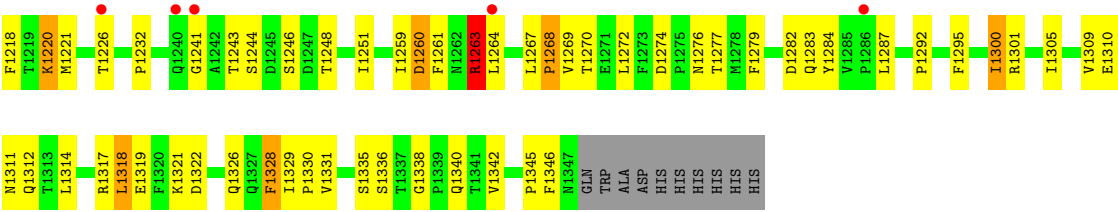


• Molecule 1: Adhesin P1



Chain F: 9% 67% 25% . .





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	459.19Å 116.66Å 285.64Å 90.00° 124.20° 90.00°	Depositor
Resolution (Å)	37.36 – 3.24 37.36 – 3.24	Depositor EDS
% Data completeness (in resolution range)	61.7 (37.36-3.24) 61.9 (37.36-3.24)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.62 (at 3.26Å)	Xtriage
Refinement program	BUSTER 2.10.3	Depositor
R, R_{free}	0.184 , 0.205 (Not available) , 0.222	Depositor DCC
R_{free} test set	6155 reflections (3.08%)	wwPDB-VP
Wilson B-factor (Å ²)	59.0	Xtriage
Anisotropy	0.038	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 99.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	59767	wwPDB-VP
Average B, all atoms (Å ²)	91.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.81% 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

5.1 Standard geometry

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	0.87	8/10269 (0.1%)	1.39	82/13978 (0.6%)
1	B	0.83	5/10252 (0.0%)	1.37	81/13956 (0.6%)
1	C	0.83	6/10246 (0.1%)	1.36	86/13947 (0.6%)
1	D	0.83	4/10229 (0.0%)	1.37	89/13925 (0.6%)
1	E	0.78	4/10135 (0.0%)	1.34	77/13795 (0.6%)
1	F	0.77	6/10147 (0.1%)	1.34	72/13812 (0.5%)
All	All	0.82	33/61278 (0.1%)	1.36	487/83413 (0.6%)

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 33 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	557	MET	SD-CE	-10.72	1.52	1.79
1	A	1137	MET	SD-CE	-10.60	1.53	1.79
1	A	1097	ASN	CA-C	7.49	1.62	1.52
1	B	1137	MET	SD-CE	-7.12	1.61	1.79
1	F	143	ILE	CA-C	6.99	1.61	1.52

The worst 5 of 487 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	853	SER	N-CA-C	10.76	124.15	111.02
1	A	806	MET	CA-C-N	10.63	137.12	121.18
1	A	806	MET	C-N-CA	10.63	137.12	121.18

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	E	861	PRO	N-CA-C	-10.52	94.65	111.38
1	F	861	PRO	N-CA-C	-10.42	94.81	111.38

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	926	SER	Mainchain
1	C	926	SER	Mainchain

5.2 Too-close contacts

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	10016	0	9726	186	0
1	B	9999	0	9707	187	0
1	C	9993	0	9706	184	0
1	D	9976	0	9687	208	0
1	E	9886	0	9597	159	0
1	F	9897	0	9610	164	0
All	All	59767	0	58033	1046	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 9.

The worst 5 of 1046 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance ($\text{\AA}$)	Clash overlap ($\text{\AA}$)
1:D:100:ILE:CG1	1:D:100:ILE:CD1	1.76	1.57
1:D:812:ASN:ND2	1:D:815:ASN:HD22	1.28	1.31
1:F:1279:PHE:CE2	1:F:1301:ARG:HD2	1.78	1.18
1:A:1266:THR:HG21	1:C:1264:LEU:HD11	1.19	1.15
1:A:1264:LEU:HG	1:C:1283:GLN:HB2	1.30	1.09

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	1270/1304 (97%)	1128 (89%)	122 (10%)	20 (2%)	7	33
1	B	1267/1304 (97%)	1136 (90%)	114 (9%)	17 (1%)	9	37
1	C	1266/1304 (97%)	1128 (89%)	123 (10%)	15 (1%)	10	38
1	D	1263/1304 (97%)	1127 (89%)	117 (9%)	19 (2%)	8	34
1	E	1252/1304 (96%)	1118 (89%)	117 (9%)	17 (1%)	9	35
1	F	1252/1304 (96%)	1114 (89%)	119 (10%)	19 (2%)	8	34
All	All	7570/7824 (97%)	6751 (89%)	712 (9%)	107 (1%)	9	35

5 of 107 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	108	SER
1	A	1094	TYR
1	A	1097	ASN
1	A	1241	GLY
1	B	811	LEU

5.3.2 Protein sidechains

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	1121/1146 (98%)	957 (85%)	164 (15%)	3	14
1	B	1120/1146 (98%)	961 (86%)	159 (14%)	3	16
1	C	1118/1146 (98%)	961 (86%)	157 (14%)	3	16

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	1117/1146 (98%)	958 (86%)	159 (14%)	3	16
1	E	1107/1146 (97%)	957 (86%)	150 (14%)	3	17
1	F	1108/1146 (97%)	958 (86%)	150 (14%)	4	17
All	All	6691/6876 (97%)	5752 (86%)	939 (14%)	3	16

5 of 939 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	1263	ARG
1	F	924	ASN
1	D	840	ASN
1	F	835	ARG
1	F	127	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 224 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	155	GLN
1	F	1311	ASN
1	D	1235	ASN
1	F	1193	GLN
1	F	629	GLN

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 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	1278/1304 (98%)	-0.32	11 (0%) 81 64	13, 49, 106, 165	0
1	B	1275/1304 (97%)	-0.18	25 (1%) 65 45	24, 60, 127, 238	0
1	C	1274/1304 (97%)	-0.23	17 (1%) 75 56	11, 50, 128, 234	0
1	D	1271/1304 (97%)	-0.17	18 (1%) 73 54	18, 58, 132, 228	0
1	E	1262/1304 (96%)	0.81	136 (10%) 11 8	25, 156, 238, 252	0
1	F	1262/1304 (96%)	0.71	113 (8%) 15 10	21, 149, 229, 244	0
All	All	7622/7824 (97%)	0.10	320 (4%) 40 26	11, 68, 224, 252	0

The worst 5 of 320 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	295	PHE	5.9
1	C	807	ILE	5.6
1	E	920	PRO	5.6
1	E	957	VAL	5.5
1	E	604	PRO	5.2

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.