



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:20 AM UTC

PDB ID : 6E3F / pdb_00006e3f
Title : The structure of the C-terminal domains (C123) of Streptococcus intermedius antigen I/II (Pas)
Authors : Schormann, N.; Deivanayagam, C.
Deposited on : 2018-07-13
Resolution : 2.70 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

<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

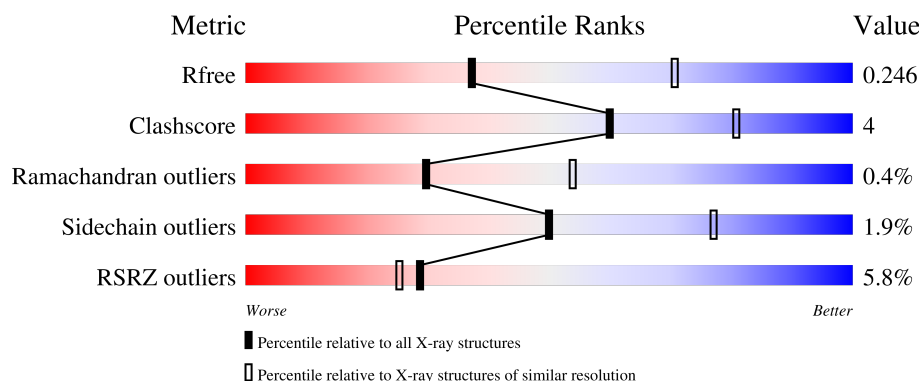
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)

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	512	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3965 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 Probable cell-surface antigen I/II.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	497	Total	C	N	O	S	0	1	0
			3890	2460	644	783	3			

There are 17 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	745	MET	-	initiating methionine	UNP Q9KW51
A	746	ALA	-	expression tag	UNP Q9KW51
A	1242	GLU	-	expression tag	UNP Q9KW51
A	1243	ASN	-	expression tag	UNP Q9KW51
A	1244	LEU	-	expression tag	UNP Q9KW51
A	1245	TYR	-	expression tag	UNP Q9KW51
A	1246	PHE	-	expression tag	UNP Q9KW51
A	1247	GLN	-	expression tag	UNP Q9KW51
A	1248	GLY	-	expression tag	UNP Q9KW51
A	1249	LEU	-	expression tag	UNP Q9KW51
A	1250	GLU	-	expression tag	UNP Q9KW51
A	1251	HIS	-	expression tag	UNP Q9KW51
A	1252	HIS	-	expression tag	UNP Q9KW51
A	1253	HIS	-	expression tag	UNP Q9KW51
A	1254	HIS	-	expression tag	UNP Q9KW51
A	1255	HIS	-	expression tag	UNP Q9KW51
A	1256	HIS	-	expression tag	UNP Q9KW51

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Ca	0	0
			2	2		

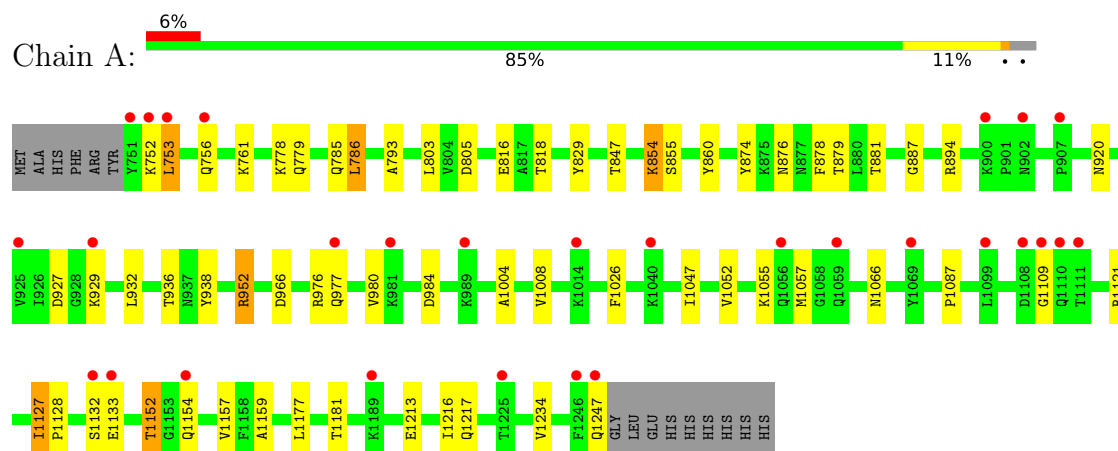
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	73	Total 73	O 73	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: Probable cell-surface antigen I/II



4 Data and refinement statistics

Property	Value	Source
Space group	I 41 2 2	Depositor
Cell constants a, b, c, α , β , γ	99.59Å 99.59Å 514.89Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.61 – 2.70 49.61 – 2.70	Depositor EDS
% Data completeness (in resolution range)	100.0 (49.61-2.70) 100.0 (49.61-2.70)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.61 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.8.0230	Depositor
R, R_{free}	0.215 , 0.244 0.218 , 0.246	Depositor DCC
R_{free} test set	1820 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	55.1	Xtriage
Anisotropy	0.501	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 47.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	3965	wwPDB-VP
Average B, all atoms (Å ²)	74.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.55% 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

Bond lengths and bond angles in the following residue types are not validated in this section: CA

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	1.00	5/3965 (0.1%)	1.17	5/5394 (0.1%)

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

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	829	TYR	C-O	-6.97	1.16	1.23
1	A	793	ALA	N-CA	5.41	1.53	1.46
1	A	818	THR	N-CA	-5.34	1.40	1.46
1	A	879	THR	N-CA	-5.32	1.40	1.46
1	A	1127	ILE	N-CA	-5.05	1.42	1.46

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	927	ASP	CA-CB-CG	6.13	118.73	112.60
1	A	816	GLU	CB-CG-CD	5.57	122.07	112.60
1	A	984	ASP	CA-CB-CG	5.32	117.92	112.60
1	A	929	LYS	CA-C-N	5.01	127.98	120.87
1	A	929	LYS	C-N-CA	5.01	127.98	120.87

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	952	ARG	Sidechain

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	3890	0	3805	33	0
2	A	2	0	0	0	0
3	A	73	0	0	1	0
All	All	3965	0	3805	33	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 4.

All (33) 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:854:LYS:HD2	1:A:855:SER:H	1.00	1.17
1:A:854:LYS:HD2	1:A:855:SER:N	1.69	1.07
1:A:785:GLN:HG2	1:A:860:TYR:CE2	2.19	0.78
1:A:881:THR:HG22	1:A:887:GLY:HA3	1.71	0.73
1:A:920:ASN:HB2	1:A:1133:GLU:OE2	1.94	0.67
1:A:936:THR:HG21	1:A:976:ARG:HH11	1.62	0.63
1:A:854:LYS:CD	1:A:855:SER:H	1.93	0.62
1:A:752:LYS:O	1:A:753:LEU:HB2	2.00	0.60
1:A:756:GLN:NE2	3:A:1401:HOH:O	2.30	0.59
1:A:785:GLN:HG2	1:A:860:TYR:HE2	1.68	0.54
1:A:977:GLN:O	1:A:980:VAL:HG13	2.10	0.52
1:A:1004:ALA:HB1	1:A:1008:VAL:HG11	1.92	0.51
1:A:778:LYS:O	1:A:779:GLN:HB2	2.12	0.50
1:A:1127:ILE:HD11	1:A:1234:VAL:HG11	1.94	0.50
1:A:1159:ALA:HB2	1:A:1177:LEU:HD11	1.94	0.49
1:A:932:LEU:HD23	1:A:1087:PRO:HG3	1.95	0.49
1:A:1026:PHE:CZ	1:A:1047:ILE:HG21	2.49	0.47
1:A:936:THR:OG1	1:A:938:TYR:CE1	2.68	0.47
1:A:1055:LYS:C	1:A:1057:MET:H	2.23	0.46
1:A:785:GLN:C	1:A:786:LEU:HD23	2.40	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:936:THR:HG22	1:A:1052:VAL:HB	1.98	0.45
1:A:805:ASP:OD1	1:A:805:ASP:C	2.60	0.44
1:A:1152:THR:HG22	1:A:1154:GLN:HB2	2.00	0.44
1:A:1127:ILE:HA	1:A:1128:PRO:HD3	1.88	0.44
1:A:874:TYR:O	1:A:894:ARG:HA	2.18	0.43
1:A:803:LEU:HD23	1:A:878:PHE:CE2	2.54	0.43
1:A:966:ASP:OD1	1:A:1066:ASN:OD1	2.37	0.42
1:A:786:LEU:HD23	1:A:786:LEU:N	2.35	0.42
1:A:1152:THR:HG21	1:A:1217:GLN:OE1	2.19	0.42
1:A:1121:ARG:NH1	1:A:1213:GLU:OE1	2.53	0.42
1:A:761:LYS:HE2	1:A:876:ASN:HB3	1.91	0.41
1:A:1157:VAL:HG21	1:A:1181:THR:HG21	2.02	0.41
1:A:854:LYS:HD3	1:A:854:LYS:HA	1.69	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	496/512 (97%)	470 (95%)	24 (5%)	2 (0%)	30	54

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1109	GLY
1	A	1132	SER

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	428/440 (97%)	420 (98%)	8 (2%)	50 77

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	753	LEU
1	A	786	LEU
1	A	847	THR
1	A	854	LYS
1	A	952	ARG
1	A	1152	THR
1	A	1216	ILE
1	A	1247	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	902	ASN
1	A	906	ASN
1	A	950	ASN
1	A	977	GLN
1	A	988	ASN
1	A	997	HIS
1	A	1024	GLN
1	A	1030	ASN
1	A	1119	ASN
1	A	1228	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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 are 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 [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 ⓘ

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	497/512 (97%)	0.35	29 (5%)	29 25	37, 73, 105, 146	1 (0%)

All (29) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1246	PHE	11.3
1	A	1109	GLY	6.4
1	A	1108	ASP	5.5
1	A	751	TYR	5.4
1	A	1110	GLN	4.9
1	A	1111	THR	3.9
1	A	752	LYS	3.7
1	A	1247	GLN	3.4
1	A	753	LEU	3.4
1	A	1189	LYS	3.2
1	A	900	LYS	3.1
1	A	989	LYS	2.9
1	A	1132	SER	2.9
1	A	1014	LYS	2.7
1	A	902	ASN	2.7
1	A	756	GLN	2.7
1	A	1059	GLN	2.6
1	A	1133	GLU	2.5
1	A	907	PRO	2.5
1	A	1099	LEU	2.4
1	A	981	LYS	2.3
1	A	1056	GLN	2.3
1	A	925	VAL	2.2
1	A	977	GLN	2.2
1	A	1069	TYR	2.1
1	A	1154	GLN	2.1
1	A	929	LYS	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	1040	LYS	2.1
1	A	1225	THR	2.1

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](#)

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. 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	B-factors($\text{\AA}^2$)	Q<0.9
2	CA	A	1302	1/1	0.95	0.08	102,102,102,102	0
2	CA	A	1301	1/1	0.96	0.08	84,84,84,84	0

6.5 Other polymers [i](#)

There are no such residues in this entry.