



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 1, 2026 – 01:13 PM UTC

PDB ID : 4M03 / pdb_00004m03
Title : C-terminal fragment(residues 576-751) of binding region of SraP
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Deposited on : 2013-08-01
Resolution : 2.24 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

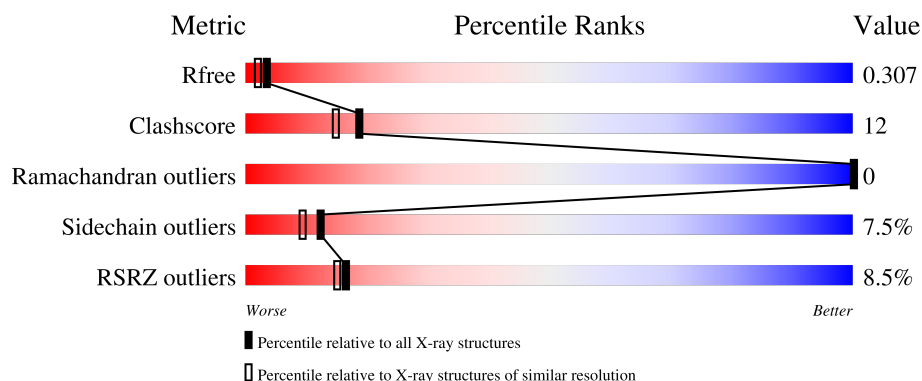
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.24 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	3416 (2.26-2.22)
Clashscore	190562	3556 (2.26-2.22)
Ramachandran outliers	187476	3500 (2.26-2.22)
Sidechain outliers	187428	3501 (2.26-2.22)
RSRZ outliers	180081	3415 (2.26-2.22)

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	210	7% 58% 17% • 21%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 1190 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 Serine-rich adhesin for platelets.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	165	Total	C	N	O	S	0	0	0
			1181	724	190	266	1			

There are 34 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	84	MET	-	expression tag	UNP Q2FUW1
A	85	GLY	-	expression tag	UNP Q2FUW1
A	86	SER	-	expression tag	UNP Q2FUW1
A	87	SER	-	expression tag	UNP Q2FUW1
A	88	HIS	-	expression tag	UNP Q2FUW1
A	89	HIS	-	expression tag	UNP Q2FUW1
A	90	HIS	-	expression tag	UNP Q2FUW1
A	91	HIS	-	expression tag	UNP Q2FUW1
A	92	HIS	-	expression tag	UNP Q2FUW1
A	93	HIS	-	expression tag	UNP Q2FUW1
A	94	SER	-	expression tag	UNP Q2FUW1
A	95	SER	-	expression tag	UNP Q2FUW1
A	96	GLY	-	expression tag	UNP Q2FUW1
A	97	LEU	-	expression tag	UNP Q2FUW1
A	98	VAL	-	expression tag	UNP Q2FUW1
A	99	PRO	-	expression tag	UNP Q2FUW1
A	100	ARG	-	expression tag	UNP Q2FUW1
A	101	GLY	-	expression tag	UNP Q2FUW1
A	102	SER	-	expression tag	UNP Q2FUW1
A	103	HIS	-	expression tag	UNP Q2FUW1
A	104	MET	-	expression tag	UNP Q2FUW1
A	105	ALA	-	expression tag	UNP Q2FUW1
A	106	SER	-	expression tag	UNP Q2FUW1
A	107	MET	-	expression tag	UNP Q2FUW1
A	108	THR	-	expression tag	UNP Q2FUW1
A	109	GLY	-	expression tag	UNP Q2FUW1
A	110	GLY	-	expression tag	UNP Q2FUW1

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Chain	Residue	Modelled	Actual	Comment	Reference
A	111	GLN	-	expression tag	UNP Q2FUW1
A	112	GLN	-	expression tag	UNP Q2FUW1
A	113	MET	-	expression tag	UNP Q2FUW1
A	114	GLY	-	expression tag	UNP Q2FUW1
A	115	ARG	-	expression tag	UNP Q2FUW1
A	116	GLY	-	expression tag	UNP Q2FUW1
A	117	SER	-	expression tag	UNP Q2FUW1

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

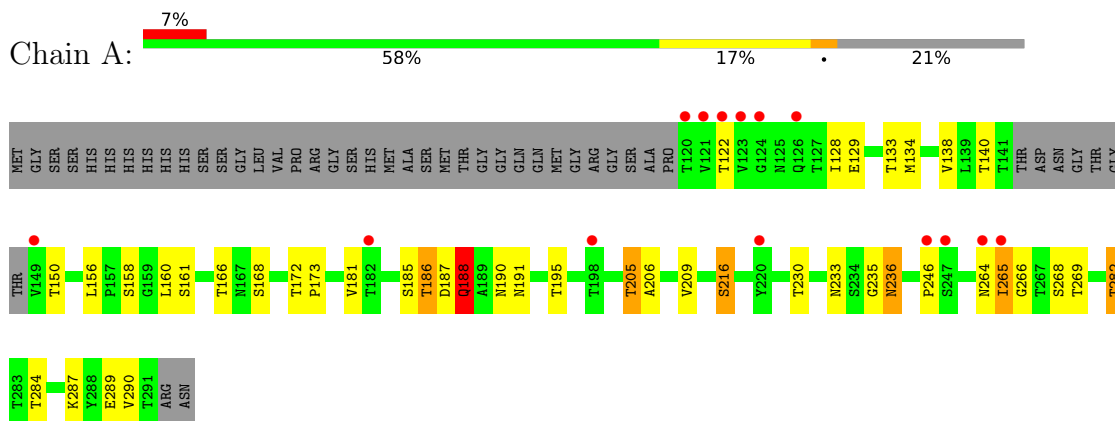
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Ca 1 1	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	8	Total O 8 8	0	0

i

- Molecule 1: Serine-rich adhesin for platelets



4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	34.76Å 34.76Å 237.72Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	30.10 – 2.24 30.10 – 2.24	Depositor EDS
% Data completeness (in resolution range)	99.7 (30.10-2.24) 99.9 (30.10-2.24)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	0.13	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.08 (at 2.24Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.279 , 0.326 0.273 , 0.307	Depositor DCC
R_{free} test set	420 reflections (4.75%)	wwPDB-VP
Wilson B-factor (Å ²)	44.3	Xtriage
Anisotropy	0.832	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 25.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.046 for -h,-k,l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	1190	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.45% 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	0.93	2/1194 (0.2%)	1.03	1/1645 (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 (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	264	ASN	CG-OD1	5.08	1.33	1.23
1	A	188	GLN	CD-NE2	-5.06	1.22	1.33

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	236	ASN	N-CA-C	6.28	118.99	109.95

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	235	GLY	Peptide

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	1181	0	1178	28	0
2	A	1	0	0	0	0
3	A	8	0	0	1	0
All	All	1190	0	1178	28	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 12.

All (28) 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:187:ASP:HB2	1:A:188:GLN:OE1	1.42	1.20
1:A:129:GLU:OE2	1:A:205:THR:HG22	1.82	0.80
1:A:133:THR:HA	1:A:172:THR:HG22	1.62	0.78
1:A:186:THR:HG23	1:A:190:ASN:HA	1.71	0.71
1:A:269:THR:OG1	1:A:287:LYS:HE3	1.94	0.68
1:A:134:MET:SD	1:A:160:LEU:HD22	2.35	0.67
1:A:205:THR:HG23	1:A:233:ASN:ND2	2.13	0.64
1:A:188:GLN:H	1:A:188:GLN:CD	2.04	0.63
1:A:187:ASP:CB	1:A:188:GLN:OE1	2.34	0.63
1:A:265:ILE:HD13	1:A:266:GLY:N	2.12	0.63
1:A:187:ASP:OD2	1:A:191:ASN:HB3	2.03	0.58
1:A:133:THR:CA	1:A:172:THR:HG22	2.35	0.57
1:A:265:ILE:HG12	1:A:290:VAL:O	2.05	0.56
1:A:156:LEU:HD13	1:A:161:SER:HA	1.86	0.56
1:A:129:GLU:OE2	1:A:205:THR:CG2	2.56	0.54
1:A:138:VAL:HG12	1:A:140:THR:HG23	1.91	0.52
1:A:216:SER:HA	1:A:289:GLU:O	2.08	0.52
1:A:209:VAL:HG22	1:A:230:THR:HG22	1.93	0.51
1:A:188:GLN:OE1	1:A:188:GLN:N	2.30	0.49
1:A:128:ILE:HD12	1:A:173:PRO:HG3	1.95	0.47
1:A:246:PRO:HG3	1:A:268:SER:HB2	1.97	0.47
1:A:236:ASN:HB2	3:A:405:HOH:O	2.15	0.46
1:A:166:THR:OG1	1:A:168:SER:HB2	2.17	0.44
1:A:206:ALA:HB1	1:A:282:THR:OG1	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:205:THR:HG23	1:A:233:ASN:HD21	1.82	0.43
1:A:269:THR:OG1	1:A:287:LYS:CE	2.65	0.42
1:A:150:THR:O	1:A:185:SER:HA	2.21	0.40
1:A:134:MET:SD	1:A:160:LEU:CD2	3.06	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	161/210 (77%)	157 (98%)	4 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	146/180 (81%)	135 (92%)	11 (8%)	12	9

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	122	THR
1	A	158	SER

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Mol	Chain	Res	Type
1	A	181	VAL
1	A	186	THR
1	A	188	GLN
1	A	195	THR
1	A	205	THR
1	A	216	SER
1	A	265	ILE
1	A	282	THR
1	A	284	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	125	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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 [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	165/210 (78%)	0.51	14 (8%) 16 15	26, 49, 70, 96	0

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	120	THR	8.1
1	A	121	VAL	6.9
1	A	122	THR	6.3
1	A	265	ILE	4.7
1	A	149	VAL	4.4
1	A	247	SER	2.9
1	A	123	VAL	2.5
1	A	220	TYR	2.4
1	A	182	THR	2.3
1	A	264	ASN	2.2
1	A	246	PRO	2.2
1	A	124	GLY	2.1
1	A	198	THR	2.1
1	A	126	GLN	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 oligosaccharides in this entry.

6.4 Ligands

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(Å ²)	Q<0.9
2	CA	A	301	1/1	0.98	0.04	40,40,40,40	0

6.5 Other polymers

There are no such residues in this entry.