

Full wwPDB X-ray Structure Validation Report (i)

Oct 3, 2023 – 08:17 AM EDT

PDB ID : 6OG4

Title : plasminogen binding group A streptococcal M protein

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Deposited on : 2019-04-01

Resolution : 1.70 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 (i) 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 (i)) were used in the production of this report:

MolProbity : FAILED

Mogul : 1.8.5 (274361), CSD as541be (2020)

Xtriage (Phenix) : 1.13 EDS : FAILED

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

Validation Pipeline (wwPDB-VP) : 2.35.1

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 1.70 Å.

There are no overall percentile quality scores available for this entry.

MolProbity and EDS failed to run properly - the sequence quality summary graphics cannot be shown.



2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 1739 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 Plasminogen.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	A	83	Total 666			O 126	S 8	0	0	0
1	В	80	Total 647	C 401		O 122	S 8	0	1	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	159	ALA	-	expression tag	UNP P00747
A	160	ALA	-	expression tag	UNP P00747
A	161	GLN	-	expression tag	UNP P00747
A	162	PRO	-	expression tag	UNP P00747
A	163	ALA	-	expression tag	UNP P00747
A	169	ALA	CYS	engineered mutation	UNP P00747
В	159	ALA	_	expression tag	UNP P00747
В	160	ALA	-	expression tag	UNP P00747
В	161	GLN	-	expression tag	UNP P00747
В	162	PRO	-	expression tag	UNP P00747
В	163	ALA	-	expression tag	UNP P00747
В	169	ALA	CYS	engineered mutation	UNP P00747

• Molecule 2 is a protein called Plasminogen-binding group A streptococcal M-like protein PAM.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	С	34	Total 288	C 170	N 58	O 60	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
С	74	GLY	-	expression tag	UNP P49054

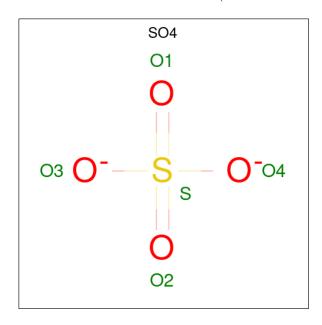
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Chain	Residue	Modelled	Actual	Comment	Reference
С	75	SER	-	expression tag	UNP P49054

 \bullet Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total O S 5 4 1	0	0
3	В	1	Total O S 5 4 1	0	0

• Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	50	Total O 50 50	0	0
4	В	51	Total O 51 51	0	0
4	С	27	Total O 27 27	0	0

MolProbity and EDS failed to run properly - this section is therefore empty.



3 Data and refinement statistics (i)

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants	52.60Å 52.60Å 198.25Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.46 - 1.70	Depositor
% Data completeness	99.7 (46.46-1.70)	Depositor
(in resolution range)	, ,	
R_{merge}	0.03	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	1.97 (at 1.70Å)	Xtriage
Refinement program	PHENIX 1.14_3260, BUSTER 2.10.2	Depositor
R, R_{free}	0.203 , 0.220	Depositor
Wilson B-factor (\mathring{A}^2)	26.8	Xtriage
Anisotropy	0.015	Xtriage
L-test for twinning ²	$< L > = 0.47, < L^2> = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	1739	wwPDB-VP
Average B, all atoms $(Å^2)$	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 6.05% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical values of <|L|>, $<L^2>$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



¹Intensities estimated from amplitudes.

4 Model quality (i)

4.1 Standard geometry (i)

MolProbity failed to run properly - this section is therefore empty.

4.2 Too-close contacts (i)

MolProbity failed to run properly - this section is therefore empty.

4.3 Torsion angles (i)

4.3.1 Protein backbone (i)

MolProbity failed to run properly - this section is therefore empty.

4.3.2 Protein sidechains (i)

MolProbity failed to run properly - this section is therefore empty.

4.3.3 RNA (i)

MolProbity failed to run properly - this section is therefore empty.

4.4 Non-standard residues in protein, DNA, RNA chains (i)

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

4.5 Carbohydrates (i)

There are no monosaccharides in this entry.

4.6 Ligand geometry (i)

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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| > 2 is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Tiple	В	ond leng	${ m gths}$	В	ond ang	gles
MIOI	туре	Chain	nes	Link	Counts	RMSZ	# Z > 2	Counts	s RMSZ $\# Z > 2$	# Z > 2
3	SO4	В	301	-	4,4,4	0.17	0	6,6,6	0.23	0
3	SO4	A	301	-	4,4,4	0.17	0	6,6,6	0.29	0

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.

4.7 Other polymers (i)

There are no such residues in this entry.

4.8 Polymer linkage issues (i)

There are no chain breaks in this entry.



5 Fit of model and data (i)

5.1 Protein, DNA and RNA chains (i)

EDS failed to run properly - this section is therefore empty.

5.2 Non-standard residues in protein, DNA, RNA chains (i)

EDS failed to run properly - this section is therefore empty.

5.3 Carbohydrates (i)

EDS failed to run properly - this section is therefore empty.

5.4 Ligands (i)

EDS failed to run properly - this section is therefore empty.

5.5 Other polymers (i)

EDS failed to run properly - this section is therefore empty.

