



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 2HSI
Title : Crystal structure of putative peptidase M23 from pseudomonas aeruginosa,
New York Structural Genomics Consortium
Authors : Patskovsky, Y.; Almo, S.C.; Burley, S.K.; New York SGX Research Center for
Structural Genomics (NYSGXRC)
Deposited on : 2006-07-21
Resolution : 1.90 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
<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
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
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) : trunk26865

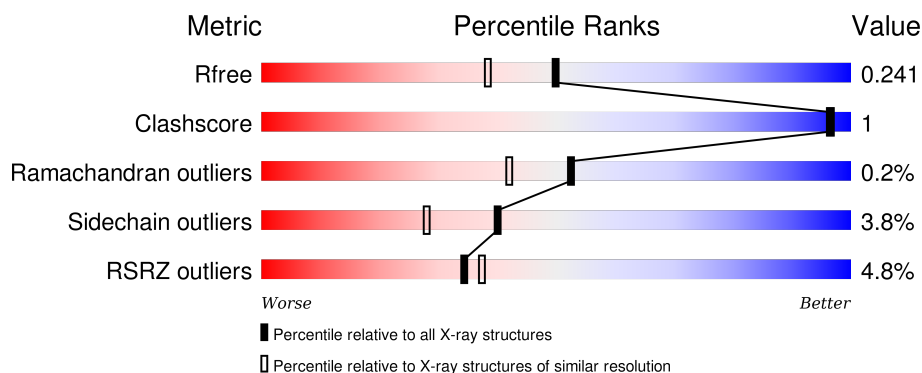
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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}	91344	4755 (1.90-1.90)
Clashscore	102246	5398 (1.90-1.90)
Ramachandran outliers	100387	5338 (1.90-1.90)
Sidechain outliers	100360	5339 (1.90-1.90)
RSRZ outliers	91569	4766 (1.90-1.90)

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	282	<div> <div>4%</div> <div>74%</div> <div>6%</div> <div>20%</div> </div>
1	B	282	<div> <div>4%</div> <div>76%</div> <div>• •</div> <div>19%</div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3971 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 Putative peptidase M23.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	227	Total	C	N	O	S	0	4	0
			1746	1122	309	310	5			
1	B	228	Total	C	N	O	S	0	2	0
			1738	1118	309	306	5			

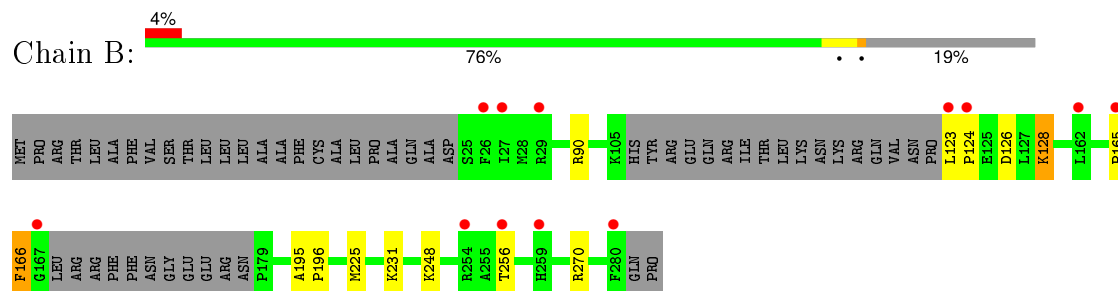
- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Zn	0	0
			1	1		
2	A	1	Total	Zn	0	0
			1	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	249	Total	O	0	0
			249	249		
3	B	236	Total	O	0	0
			236	236		

- Molecule 1: Putative peptidase M23



4 Data and refinement statistics

Property	Value	Source
Space group	P 61	Depositor
Cell constants a, b, c, α , β , γ	108.31 Å 108.31 Å 83.18 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 1.90 27.08 – 1.90	Depositor EDS
% Data completeness (in resolution range)	100.0 (20.00-1.90) 99.9 (27.08-1.90)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.54 (at 1.91 Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.204 , 0.245 0.203 , 0.241	Depositor DCC
R_{free} test set	1360 reflections (3.21%)	DCC
Wilson B-factor (Å ²)	25.2	Xtriage
Anisotropy	0.181	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 33.9	EDS
Estimated twinning fraction	0.254 for h,-h-k,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.41$, $\langle L^2 \rangle = 0.24$	Xtriage
Outliers	0 of 43675 reflections	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	3971	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.01% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.46	0/1803	0.64	0/2442
1	B	0.44	0/1789	0.63	1/2424 (0.0%)
All	All	0.45	0/3592	0.64	1/4866 (0.0%)

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	B	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	B	126	ASP	CB-CG-OD2	5.85	123.56	118.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	165	PRO	Peptide

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	1746	0	1771	7	0
1	B	1738	0	1766	3	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	249	0	0	1	0
3	B	236	0	0	0	0
All	All	3971	0	3537	10	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 1.

All (10) 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:150:SER:OG	1:A:151:ASN:OD1	2.31	0.48
1:B:123:LEU:HB3	1:B:124:PRO:HD2	1.97	0.47
1:A:165:PRO:O	1:A:180:HIS:ND1	2.48	0.47
1:A:225:MET:HB3	1:A:263:ASN:HB2	1.97	0.46
1:B:128:LYS:HE2	1:B:128:LYS:HB2	1.42	0.44
1:A:124:PRO:HA	1:A:125:GLU:HA	1.66	0.43
1:B:195:ALA:HA	1:B:196:PRO:HD3	1.90	0.43
1:A:85:GLN:HG3	1:A:102:VAL:HG23	2.01	0.41
1:A:128:LYS:HE2	1:A:128:LYS:HB2	1.92	0.41
1:A:90:ARG:NH2	3:A:518:HOH:O	2.52	0.41

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	225/282 (80%)	220 (98%)	5 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	224/282 (79%)	217 (97%)	6 (3%)	1 (0%)	39	27
All	All	449/564 (80%)	437 (97%)	11 (2%)	1 (0%)	52	42

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	166	PHE

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	186/229 (81%)	180 (97%)	6 (3%)	46	35
1	B	184/229 (80%)	176 (96%)	8 (4%)	35	23
All	All	370/458 (81%)	356 (96%)	14 (4%)	40	28

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	166	PHE
1	A	225	MET
1	A	231	LYS
1	A	248	LYS
1	A	256	THR
1	A	270	ARG
1	B	90	ARG
1	B	128	LYS
1	B	166	PHE
1	B	225	MET
1	B	231	LYS
1	B	248	LYS
1	B	256	THR
1	B	270	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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](#)

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	227/282 (80%)	0.03	10 (4%) 38 41	15, 23, 56, 94	0
1	B	228/282 (80%)	-0.11	12 (5%) 30 33	15, 24, 56, 70	0
All	All	455/564 (80%)	-0.04	22 (4%) 34 37	15, 24, 56, 94	0

All (22) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	179	PRO	5.7
1	A	256	THR	5.4
1	A	281	GLN	5.4
1	A	125	GLU	4.8
1	B	26	PHE	4.5
1	B	167	GLY	3.9
1	B	256	THR	3.9
1	A	26	PHE	3.8
1	B	29	ARG	3.8
1	B	254	ARG	3.8
1	B	280	PHE	3.7
1	A	127	LEU	3.6
1	A	29	ARG	3.6
1	A	124	PRO	3.6
1	A	280	PHE	3.4
1	A	165	PRO	3.2
1	B	124	PRO	2.6
1	B	165	PRO	2.6
1	B	27	ILE	2.4
1	B	123	LEU	2.3
1	B	259	HIS	2.2
1	B	162	LEU	2.2

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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
2	ZN	B	283	1/1	0.98	0.04	-2.15	46,46,46,46	0
2	ZN	A	283	1/1	0.98	0.03	-2.24	50,50,50,50	0

6.5 Other polymers [i](#)

There are no such residues in this entry.