



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 1ZJK / pdb_00001zjk
Title : Crystal structure of the zymogen catalytic region of human MASP-2
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Deposited on : 2005-04-29
Resolution : 2.18 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

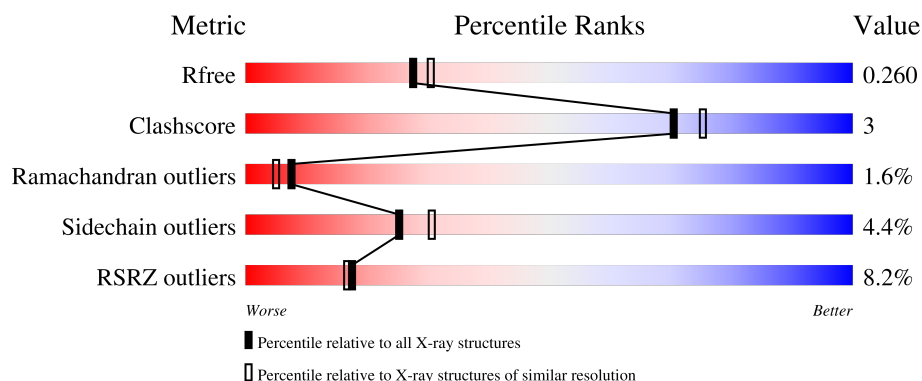
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.18 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	8975 (2.20-2.16)
Clashscore	190562	9786 (2.20-2.16)
Ramachandran outliers	187476	9664 (2.20-2.16)
Sidechain outliers	187428	9664 (2.20-2.16)
RSRZ outliers	180081	8979 (2.20-2.16)

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	403	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2994 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 Mannan-binding lectin serine protease 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	390	2910	1855	481	552	22	1	1	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	284	ALA	-	cloning artifact	UNP O00187
A	285	SER	-	cloning artifact	UNP O00187
A	286	MET	-	cloning artifact	UNP O00187
A	444	GLN	ARG	engineered mutation	UNP O00187

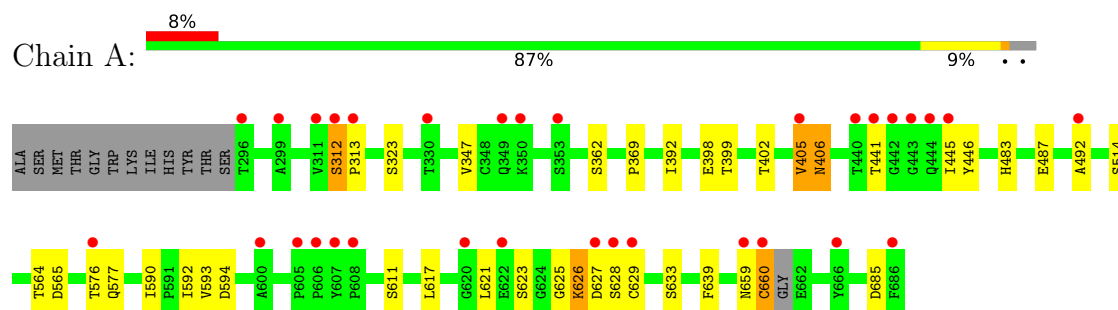
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	84	Total	O	0	0
			84	84		

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: Mannan-binding lectin serine protease 2



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	47.66Å 72.69Å 110.99Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	28.90 – 2.18 28.90 – 2.18	Depositor EDS
% Data completeness (in resolution range)	88.2 (28.90-2.18) 88.3 (28.90-2.18)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.45 (at 2.18Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.205 , 0.253 0.211 , 0.260	Depositor DCC
R_{free} test set	938 reflections (5.12%)	wwPDB-VP
Wilson B-factor (Å ²)	35.2	Xtriage
Anisotropy	0.161	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 44.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	2994	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.87% 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 [i](#)

5.1 Standard geometry [i](#)

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	0.73	1/2997 (0.0%)	0.75	3/4088 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	445	ILE	C-O	33.41	1.63	1.24

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	445	ILE	O-C-N	12.92	138.72	122.57
1	A	445	ILE	CA-C-O	-9.28	109.18	120.78
1	A	398	GLU	N-CA-C	6.68	118.56	111.28

There are no chirality outliers.

There are no planarity outliers.

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	2910	0	2715	19	0
2	A	84	0	0	0	0
All	All	2994	0	2715	19	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 3.

All (19) 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:492:ALA:O	1:A:514:SER:OG	2.00	0.79
1:A:312:SER:OG	1:A:313:PRO:HD3	1.90	0.71
1:A:312:SER:OG	1:A:313:PRO:CD	2.50	0.58
1:A:483:HIS:NE2	1:A:633:SER:OG	2.33	0.55
1:A:564:THR:O	1:A:565:ASP:HB2	2.08	0.54
1:A:590:ILE:HG22	1:A:621:LEU:HG	1.90	0.53
1:A:483:HIS:CE1	1:A:633:SER:HG	2.23	0.53
1:A:312:SER:CB	1:A:313:PRO:HD3	2.40	0.51
1:A:659:ASN:O	1:A:660:CYS:C	2.55	0.50
1:A:405:VAL:O	1:A:406:ASN:HB3	2.13	0.49
1:A:312:SER:CB	1:A:313:PRO:CD	2.92	0.48
1:A:369:PRO:HB3	1:A:392:ILE:HD13	1.96	0.46
1:A:483:HIS:CE1	1:A:633:SER:OG	2.70	0.44
1:A:625:GLY:O	1:A:626:LYS:C	2.62	0.43
1:A:576:THR:O	1:A:576:THR:HG22	2.19	0.42
1:A:592:ILE:HD11	1:A:639:PHE:CZ	2.54	0.42
1:A:626:LYS:O	1:A:627:ASP:C	2.63	0.42
1:A:593:VAL:O	1:A:594:ASP:C	2.63	0.41
1:A:685:ASP:O	1:A:685:ASP:CG	2.64	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	387/403 (96%)	352 (91%)	29 (8%)	6 (2%)	7 5

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	405	VAL
1	A	446	TYR
1	A	623	SER
1	A	626	LYS
1	A	577	GLN
1	A	406	ASN

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	298/330 (90%)	285 (96%)	13 (4%)	25	31

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	312	SER
1	A	323	SER
1	A	347	VAL
1	A	362	SER
1	A	399	THR
1	A	402	THR
1	A	441	THR
1	A	487	GLU
1	A	611	SER
1	A	617	LEU
1	A	628	SER
1	A	629	CYS
1	A	660	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	459	GLN
1	A	539	ASN
1	A	540	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](#)

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

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	390/403 (96%)	0.44	32 (8%) 17 17	7, 26, 46, 63	2 (0%)

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	606	PRO	6.0
1	A	442	GLY	4.9
1	A	312	SER	4.8
1	A	629	CYS	4.5
1	A	445	ILE	4.0
1	A	660	CYS	4.0
1	A	441	THR	3.9
1	A	443	GLY	3.9
1	A	440	THR	3.9
1	A	313	PRO	3.6
1	A	659	ASN	3.0
1	A	296	THR	2.8
1	A	405	VAL	2.8
1	A	350	LYS	2.8
1	A	576	THR	2.7
1	A	299	ALA	2.7
1	A	353	SER	2.6
1	A	444	GLN	2.5
1	A	605	PRO	2.5
1	A	608	PRO	2.5
1	A	686	PHE	2.5
1	A	311	VAL	2.4
1	A	627	ASP	2.4
1	A	628	SER	2.4
1	A	666	TYR	2.3
1	A	330	THR	2.3
1	A	600	ALA	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	607	TYR	2.2
1	A	622	GLU	2.1
1	A	620	GLY	2.1
1	A	492	ALA	2.0
1	A	349	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 [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.