

Full wwPDB X-ray Structure Validation Report (i)

Dec 17, 2023 – 05:44 PM EST

PDB ID : 1C2L

Title : RECRUITING ZINC TO MEDIATE POTENT, SPECIFIC INHIBITION OF

SERINE PROTEASES

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Deposited on : 1999-07-21

Resolution : 1.50 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 (1)) were used in the production of this report:

MolProbity : 4.02b-467 Xtriage (Phenix) : 1.13

EDS : 2.36

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

Refmac : 5.8.0158

CCP4 : 7.0.044 (Gargrove)

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

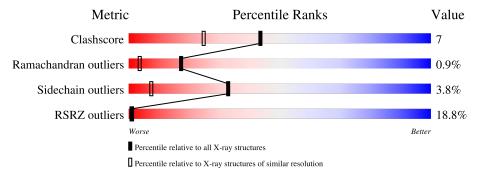
Validation Pipeline (wwPDB-VP) : 2.36

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 1.50 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 $(\# \mathrm{Entries})$	$\begin{array}{c} {\bf Similar \ resolution} \\ (\#{\bf Entries, \ resolution \ range(\AA)}) \end{array}$
Clashscore	141614	3144 (1.50-1.50)
Ramachandran outliers	138981	3066 (1.50-1.50)
Sidechain outliers	138945	3064 (1.50-1.50)
RSRZ outliers	127900	2884 (1.50-1.50)

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 <=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		
			19%		
1	A	223	79%	20%	•



2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 3975 atoms, of which 2090 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 TRYPSIN.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace		
1	A	223	Total 3320	C 1038	H 1656	N 282	O 330	S 14	0	12	0

• Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

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

• Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

\mathbf{Mol}	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Cl 1 1	0	0

• Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	2	Total Zn 2 2	0	0

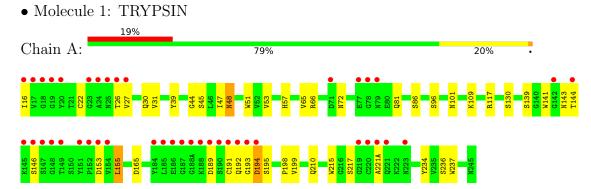
• Molecule 5 is water.

Mol	Chain	Residues	A	Atoms		ZeroOcc	AltConf
5	A	217	Total 651	H 434	O 217	0	3



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.





4 Data and refinement statistics (i)

Property	Value	Source	
Space group	P 31 2 1	Depositor	
Cell constants	55.00Å 55.00Å 109.07Å	Depositor	
a, b, c, α , β , γ	90.00° 90.00° 120.00°	Depositor	
Resolution (Å)	7.50 - 1.50	Depositor	
Resolution (A)	35.87 - 1.33	EDS	
% Data completeness	68.0 (7.50-1.50)	Depositor	
(in resolution range)	52.0 (35.87-1.33)	EDS	
R_{merge}	0.08	Depositor	
R_{sym}	(Not available)	Depositor	
$< I/\sigma(I) > 1$	2.71 (at 1.33Å)	Xtriage	
Refinement program	X-PLOR 3.1	Depositor	
D.D.	0.195 , 0.224	Depositor	
R, R_{free}	0.207 , (Not available)	DCC	
R_{free} test set	No test flags present.	wwPDB-VP	
Wilson B-factor (Å ²)	10.1	Xtriage	
Anisotropy	0.081	Xtriage	
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.28, 58.4	EDS	
L-test for twinning ²	$< L >=0.49, < L^2>=0.32$	Xtriage	
Estimated twinning fraction	0.039 for -h,-k,l	Xtriage	
F_o, F_c correlation	0.95	EDS	
Total number of atoms	3975	wwPDB-VP	
Average B, all atoms (Å ²)	25.0	wwPDB-VP	

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 8.29% 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.

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, CL, 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).

Mal	Chain	Bond	lengths	Во	ond angles
IVIOI	Chain	RMSZ	lengths $\# Z > 5$	RMSZ	# Z > 5
1	A	1.30	0/1746	1.51	$22/2367 \ (0.9\%)$

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 maintenain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

There are no bond length outliers.

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
1	A	51	TRP	CD1-NE1-CE2	9.49	117.54	109.00
1	A	141	TRP	CD1-NE1-CE2	8.88	117.00	109.00
1	A	215	TRP	CD1-NE1-CE2	8.61	116.75	109.00
1	A	237	TRP	CD1-NE1-CE2	8.49	116.64	109.00
1	A	237	TRP	NE1-CE2-CZ2	7.92	139.11	130.40
1	A	193	GLY	N-CA-C	-7.82	93.54	113.10
1	A	51	TRP	NE1-CE2-CZ2	7.73	138.90	130.40
1	A	215	TRP	NE1-CE2-CZ2	7.27	138.40	130.40
1	A	141	TRP	CG-CD1-NE1	-7.18	102.92	110.10
1	A	237	TRP	CG-CD1-NE1	-6.42	103.68	110.10
1	A	39	TYR	CB-CG-CD1	-6.37	117.18	121.00
1	A	117	ARG	NE-CZ-NH2	-6.28	117.16	120.30
1	A	51	TRP	NE1-CE2-CD2	-6.23	101.07	107.30
1	A	141	TRP	NE1-CE2-CZ2	6.18	137.20	130.40
1	A	215	TRP	NE1-CE2-CD2	-6.06	101.24	107.30
1	A	51	TRP	CG-CD1-NE1	-6.01	104.09	110.10

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Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$\mathrm{Ideal}(^{o})$
1	A	215	TRP	CG-CD1-NE1	-5.95	104.15	110.10
1	A	237	TRP	NE1-CE2-CD2	-5.70	101.60	107.30
1	A	199	VAL	N-CA-C	-5.33	96.62	111.00
1	A	189	ASP	CB-CG-OD1	-5.25	113.57	118.30
1	A	217	SER	N-CA-C	-5.09	97.26	111.00
1	A	165	ASP	CA-CB-CG	-5.04	102.31	113.40

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	66	ARG	Sidechain

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	1664	1656	1629	22	3
2	A	1	0	0	0	0
3	A	1	0	0	1	0
4	A	2	0	0	0	0
5	A	217	434	0	0	3
All	All	1885	2090	1629	22	3

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 7.

All (22) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	Clash overlap (Å)
1:A:27[B]:VAL:HG21	1:A:155:LEU:CD1	2.20	0.71
1:A:31[A]:VAL:CG1	1:A:65:VAL:HG13	2.27	0.63
1:A:27[B]:VAL:HG21	1:A:155:LEU:HD13	1.85	0.59
1:A:31[B]:VAL:HG22	1:A:44:GLY:CA	2.36	0.56
1:A:27[B]:VAL:CG2	1:A:155:LEU:CD1	2.83	0.55

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Atom-1	Atom-2	Interatomic	Clash	
	1 2 3 2 2 2 2	$\operatorname{distance}\left(\mathrm{\AA}\right)$	overlap (Å)	
1:A:30:GLN:NE2	1:A:139:SER:OG	2.42	0.52	
1:A:22:CYS:HB3	1:A:26:THR:CG2	2.40	0.52	
1:A:47:ILE:HD13	1:A:53[B]:VAL:HG13	1.95	0.48	
1:A:45:SER:OG	1:A:198:PRO:HB3	2.13	0.48	
1:A:72:ASN:HA	1:A:153:ASP:O	2.13	0.48	
1:A:143:ASN:HB3	1:A:191:CYS:SG	2.53	0.48	
1:A:194:ASP:HA	3:A:250:CL:CL	2.52	0.46	
1:A:31[A]:VAL:HG11	1:A:65:VAL:HG13	1.96	0.46	
1:A:86:SER:HB3	1:A:109:LYS:HG2	1.98	0.45	
1:A:31[B]:VAL:HG22	1:A:44:GLY:HA3	1.99	0.45	
1:A:31[B]:VAL:HG22	1:A:44:GLY:C	2.41	0.41	
1:A:31[A]:VAL:CG1	1:A:65:VAL:CG1	2.97	0.41	
1:A:57:HIS:NE2	1:A:195[B]:SER:HB2	2.35	0.41	
1:A:16:ILE:O	1:A:144:THR:HA	2.20	0.40	
1:A:101:ASN:HA	1:A:234:TYR:OH	2.22	0.40	
1:A:48:ASN:HD22	1:A:48:ASN:C	2.25	0.40	

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	$\begin{array}{c} \text{Clash} \\ \text{overlap } (\text{\AA}) \end{array}$	
1:A:22:CYS:O	5:A:355:HOH:H1[5_555]	1.51	0.09	
1:A:96:SER:OG	5:A:373:HOH:H1[4_656]	1.57	0.03	
1:A:81:GLN:OE1	5:A:401:HOH:H1[3_664]	1.58	0.02	

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	233/223 (104%)	223 (96%)	8 (3%)	2 (1%)	17 3

All (2) Ramachandran outliers are listed below:



Mol	Chain	Res	Type
1	A	221(A)	ALA
1	A	194	ASP

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	Analysed Rotameric Outliers		Percentiles	
1	A	196/184 (106%)	188 (96%)	8 (4%)	30 6	

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

Mol	Chain	Res	Type
1	A	48	ASN
1	A	130	SER
1	A	146	SER
1	A	155	LEU
1	A	192	GLN
1	A	210	GLN
1	A	236[A]	SER
1	A	236[B]	SER

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	30	GLN
1	A	48	ASN
1	A	210	GLN

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 4 ligands modelled in this entry, 4 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 (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, 95^{th} 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	$\langle { m RSRZ} \rangle$	$\#\mathrm{RSRZ}{>}2$		$OWAB(A^2)$	Q<0.9	
1	A	223/223 (100%)	1.11	42 (18%)	1	1	6, 17, 48, 56	29 (13%)

All (42) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ	
1	A	146	SER	15.9	
1	A	24	ALA	12.1	
1	A	187	GLY	10.6	
1	A	147	SER	10.3	
1	A	149	THR	9.8	
1	A	221(A)	ALA	9.1	
1	A	188(A)	GLY	8.6	
1	A	219	GLY	8.4	
1	A	185	LEU	7.8	
1	A	18	GLY	7.4	
1	A	191	CYS	6.6	
1	A	19	GLY	6.2	
1	A	17	VAL	6.1	
1	A	223	ASN	6.1	
1	A	145	LYS	6.0	
1	A	25	ASN	5.8	
1	A	220	CYS	5.5	
1	A	71	ASP	5.2	
1	A	23	GLY	5.1	
1	A	20	TYR	5.0	
1	A	144	THR	4.8	
1	A	192	GLN	4.8	
1	A	190[A]	SER	4.7	
1	A	188	LYS	4.2	
1	A	189	ASP	4.0	
1	A	184	TYR	3.9	
1	A	16	ILE	3.9	

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Mol	Chain	Res	Type	RSRZ
1	A	78	GLY	3.8
1	A	221	GLN	3.5
1	A	193	GLY	3.4
1	A	26	THR	3.4
1	A	151	TYR	3.3
1	A	148	GLY	3.2
1	A	152	PRO	3.2
1	A	186	GLU	2.9
1	A	79	ASN	2.9
1	A	154	VAL	2.7
1	A	27[A]	VAL	2.4
1	A	194	ASP	2.4
1	A	77	GLU	2.2
1	A	153	ASP	2.2
1	A	142	GLY	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 monosaccharides 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, 95^{th} 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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
4	ZN	A	409	1/1	0.71	0.26	62,62,62,62	1
3	CL	A	250	1/1	0.98	0.04	25,25,25,25	0
4	ZN	A	410	1/1	0.98	0.05	33,33,33,33	0
2	CA	A	247	1/1	0.99	0.05	12,12,12,12	0

6.5 Other polymers (i)

There are no such residues in this entry.

