



wwPDB X-ray Structure Validation Summary Report

Feb 28, 2014 – 06:25 AM GMT

PDB ID : 2RJP
Title : Crystal structure of ADAMTS4 with inhibitor bound
Authors : Mosyak, L.; Stahl, M.; Somers, W.
Deposited on : 2007-10-15
Resolution : 2.80 Å(reported)

This is a wwPDB validation summary 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/ValidationPDFNotes.html>

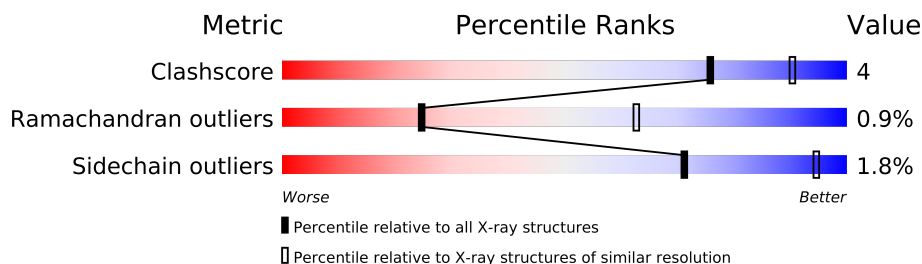
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	21963
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.80 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))
Clashscore	79885	2295 (2.80-2.80)
Ramachandran outliers	78287	2252 (2.80-2.80)
Sidechain outliers	78261	2254 (2.80-2.80)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	316	
1	B	316	
1	C	316	
1	D	316	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 8872 atoms, of which 0 are hydrogen and 0 are deuterium.

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 ADAMTS-4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	291	Total	C	N	O	S	0	0	0
			2188	1368	390	406	24			
1	B	284	Total	C	N	O	S	0	0	0
			2128	1329	379	396	24			
1	C	290	Total	C	N	O	S	0	0	0
			2183	1365	389	405	24			
1	D	278	Total	C	N	O	S	0	0	0
			2093	1307	374	388	24			

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	362	GLN	GLU	ENGINEERED	UNP O75173
A	521	ASP	-	EXPRESSION TAG	UNP O75173
A	522	TYR	-	EXPRESSION TAG	UNP O75173
A	523	LYS	-	EXPRESSION TAG	UNP O75173
A	524	ASP	-	EXPRESSION TAG	UNP O75173
A	525	ASP	-	EXPRESSION TAG	UNP O75173
A	526	ASP	-	EXPRESSION TAG	UNP O75173
A	527	ASP	-	EXPRESSION TAG	UNP O75173
A	528	LYS	-	EXPRESSION TAG	UNP O75173
B	362	GLN	GLU	ENGINEERED	UNP O75173
B	521	ASP	-	EXPRESSION TAG	UNP O75173
B	522	TYR	-	EXPRESSION TAG	UNP O75173
B	523	LYS	-	EXPRESSION TAG	UNP O75173
B	524	ASP	-	EXPRESSION TAG	UNP O75173
B	525	ASP	-	EXPRESSION TAG	UNP O75173
B	526	ASP	-	EXPRESSION TAG	UNP O75173
B	527	ASP	-	EXPRESSION TAG	UNP O75173
B	528	LYS	-	EXPRESSION TAG	UNP O75173
C	362	GLN	GLU	ENGINEERED	UNP O75173
C	521	ASP	-	EXPRESSION TAG	UNP O75173
C	522	TYR	-	EXPRESSION TAG	UNP O75173

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Chain	Residue	Modelled	Actual	Comment	Reference
C	523	LYS	-	EXPRESSION TAG	UNP O75173
C	524	ASP	-	EXPRESSION TAG	UNP O75173
C	525	ASP	-	EXPRESSION TAG	UNP O75173
C	526	ASP	-	EXPRESSION TAG	UNP O75173
C	527	ASP	-	EXPRESSION TAG	UNP O75173
C	528	LYS	-	EXPRESSION TAG	UNP O75173
D	362	GLN	GLU	ENGINEERED	UNP O75173
D	521	ASP	-	EXPRESSION TAG	UNP O75173
D	522	TYR	-	EXPRESSION TAG	UNP O75173
D	523	LYS	-	EXPRESSION TAG	UNP O75173
D	524	ASP	-	EXPRESSION TAG	UNP O75173
D	525	ASP	-	EXPRESSION TAG	UNP O75173
D	526	ASP	-	EXPRESSION TAG	UNP O75173
D	527	ASP	-	EXPRESSION TAG	UNP O75173
D	528	LYS	-	EXPRESSION TAG	UNP O75173

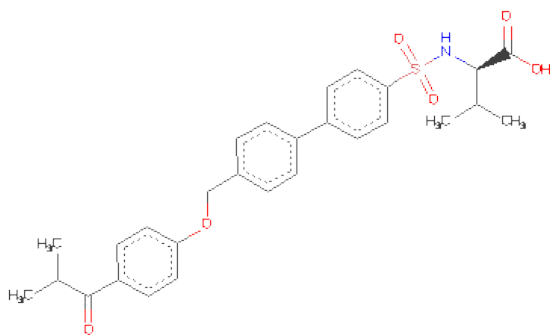
- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	3	Total Ca 3 3	0	0
3	A	3	Total Ca 3 3	0	0
3	D	3	Total Ca 3 3	0	0
3	C	3	Total Ca 3 3	0	0

- Molecule 4 is N-({4'-[(4-ISOBUTYRYLPHENOXY)METHYL]BIPHENYL-4-YL}SULFONYL)-D-VALINE (three-letter code: 886) (formula: C₂₈H₃₁NO₆S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	B	1	Total	C	N	O	S	0	0
			36	28	1	6	1		
4	D	1	Total	C	N	O	S	0	0
			36	28	1	6	1		
4	C	1	Total	C	N	O	S	0	0
			36	28	1	6	1		
4	A	1	Total	C	N	O	S	0	0
			36	28	1	6	1		

- Molecule 5 is water.

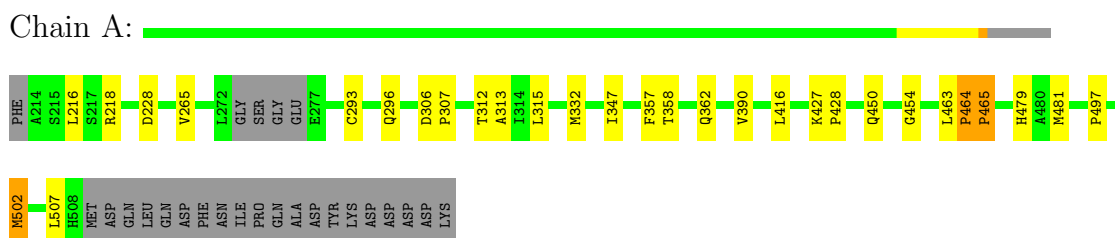
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	33	Total	O	0	0
			33	33		
5	B	45	Total	O	0	0
			45	45		
5	C	29	Total	O	0	0
			29	29		
5	D	13	Total	O	0	0
			13	13		

3 Residue-property plots

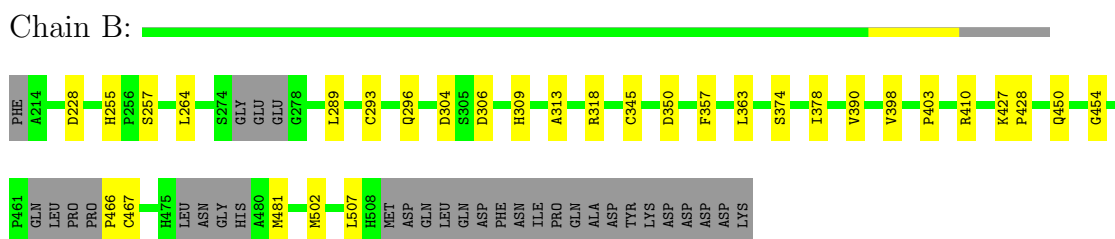
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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.

Note EDS was not executed.

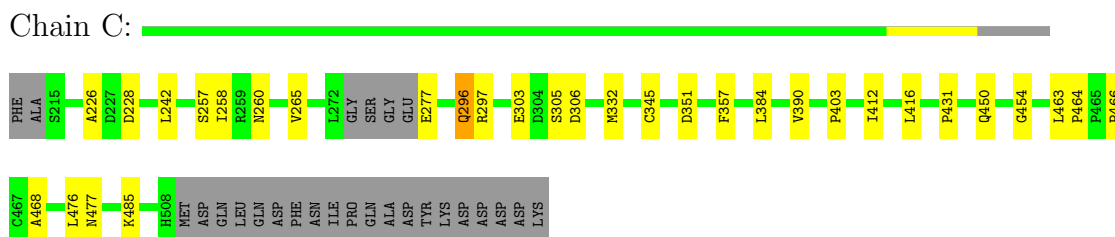
• Molecule 1: ADAMTS-4



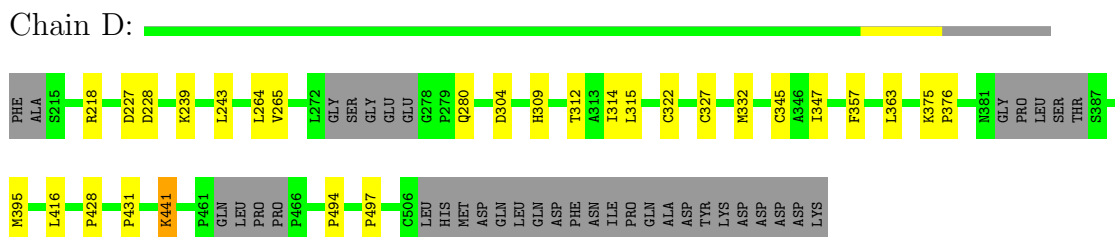
• Molecule 1: ADAMTS-4



• Molecule 1: ADAMTS-4



• Molecule 1: ADAMTS-4



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	82.57Å 82.62Å 99.33Å 90.00° 90.63° 90.00°	Depositor
Resolution (Å)	50.00 – 2.80	Depositor
% Data completeness (in resolution range)	100.0 (50.00-2.80)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.206 , 0.267	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	8872	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, CA, 886

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	0.48	0/2249	0.56	0/3068
1	B	0.41	0/2184	0.53	0/2973
1	C	0.42	0/2244	0.54	0/3061
1	D	0.60	4/2148 (0.2%)	0.59	2/2923 (0.1%)
All	All	0.48	4/8825 (0.0%)	0.55	2/12025 (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	A	0	1
1	C	0	1
All	All	0	2

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	441	LYS	CD-CE	16.46	1.92	1.51
1	D	280	GLN	CD-OE1	8.17	1.42	1.24
1	D	441	LYS	CE-NZ	6.34	1.65	1.49
1	D	441	LYS	CG-CD	5.10	1.69	1.52

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	441	LYS	CD-CE-NZ	-7.90	93.52	111.70
1	D	441	LYS	CG-CD-CE	-7.57	89.18	111.90

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	464	PRO	Peptide
1	C	463	LEU	Peptide

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2188	0	2090	16	0
1	B	2128	0	2035	16	0
1	C	2183	0	2087	18	0
1	D	2093	0	1996	14	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	3	0	0	0	0
3	B	3	0	0	0	0
3	C	3	0	0	0	0
3	D	3	0	0	0	0
4	A	36	0	30	4	0
4	B	36	0	30	3	0
4	C	36	0	30	3	0
4	D	36	0	30	2	0
5	A	33	0	0	0	0
5	B	45	0	0	1	0
5	C	29	0	0	0	0
5	D	13	0	0	0	0
All	All	8872	0	8328	66	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 4.

The worst 5 of 66 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:441:LYS:CD	1:D:441:LYS:CE	1.92	1.47
1:D:441:LYS:CG	1:D:441:LYS:CE	2.54	0.85
1:C:296:GLN:HG3	1:C:297:ARG:N	1.99	0.77
1:C:464:PRO:O	1:C:466:PRO:HD3	1.95	0.67
1:A:463:LEU:O	1:A:465:PRO:HD2	1.95	0.67

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

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	287/316 (91%)	276 (96%)	8 (3%)	3 (1%)	22	60
1	B	276/316 (87%)	265 (96%)	10 (4%)	1 (0%)	43	80
1	C	286/316 (90%)	270 (94%)	14 (5%)	2 (1%)	30	69
1	D	270/316 (85%)	259 (96%)	7 (3%)	4 (2%)	15	46
All	All	1119/1264 (88%)	1070 (96%)	39 (4%)	10 (1%)	25	63

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	465	PRO
1	D	395	MET
1	B	228	ASP
1	C	228	ASP
1	A	228	ASP

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	239/261 (92%)	233 (98%)	6 (2%)	60	90
1	B	232/261 (89%)	229 (99%)	3 (1%)	80	97
1	C	239/261 (92%)	235 (98%)	4 (2%)	73	95
1	D	228/261 (87%)	224 (98%)	4 (2%)	71	94
All	All	938/1044 (90%)	921 (98%)	17 (2%)	71	94

5 of 17 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	306	ASP
1	B	481	MET
1	D	227	ASP
1	B	289	LEU
1	D	264	LEU

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

Mol	Chain	Res	Type
1	C	234	HIS

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 20 ligands modelled in this entry, 16 are monoatomic - leaving 4 for Mogul analysis.

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	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	886	A	510	2	38,38,38	1.63	4 (10%)	54,54,54	1.45	8 (14%)
4	886	B	510	2	38,38,38	1.56	3 (7%)	54,54,54	1.57	8 (14%)
4	886	C	510	2	38,38,38	1.53	4 (10%)	54,54,54	1.65	8 (14%)
4	886	D	510	2	38,38,38	1.71	3 (7%)	54,54,54	1.14	5 (9%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	886	A	510	2	-	0/36/36/36	0/3/3/3
4	886	B	510	2	-	0/36/36/36	0/3/3/3
4	886	C	510	2	-	0/36/36/36	0/3/3/3
4	886	D	510	2	-	0/36/36/36	0/3/3/3

The worst 5 of 14 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	510	886	C4-N1	6.08	1.53	1.46
4	A	510	886	C4-N1	5.30	1.52	1.46
4	B	510	886	C4-N1	5.09	1.52	1.46
4	C	510	886	C4-N1	4.72	1.51	1.46
4	D	510	886	S1-N1	4.72	1.69	1.61

The worst 5 of 29 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	510	886	C5-C4-N1	-5.93	103.96	111.38
4	B	510	886	C5-C4-N1	-5.71	104.23	111.38
4	C	510	886	C2-C4-C5	5.03	117.51	110.90
4	C	510	886	C5-C4-N1	-4.76	105.42	111.38
4	C	510	886	C2-C4-N1	-4.48	103.97	110.30

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section will therefore be empty.

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.