



wwPDB X-ray Structure Validation Summary Report ⓘ

May 24, 2020 – 07:39 pm BST

PDB ID : 1NYU
Title : Crystal Structure of Activin A Bound to the ECD of ActRIIB
Authors : Thompson, T.B.; Woodruff, T.K.; Jardetzky, T.S.
Deposited on : 2003-02-13
Resolution : 3.10 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
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)	:	2.11

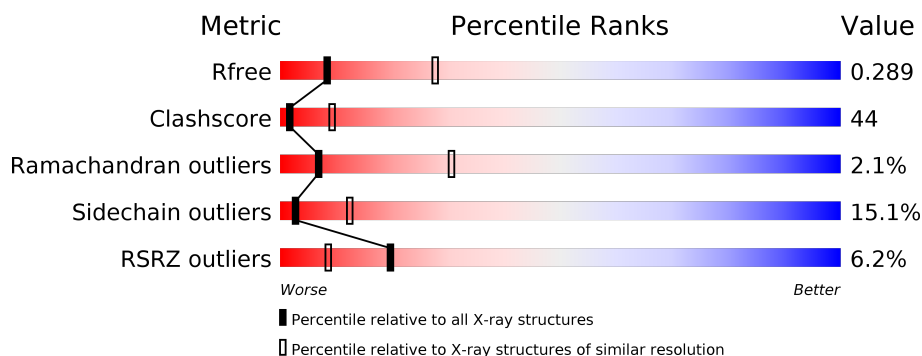
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 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}	130704	1094 (3.10-3.10)
Clashscore	141614	1184 (3.10-3.10)
Ramachandran outliers	138981	1141 (3.10-3.10)
Sidechain outliers	138945	1141 (3.10-3.10)
RSRZ outliers	127900	1067 (3.10-3.10)

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 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	105	<div> <div>43%</div> <div>40%</div> <div>5%</div> <div>12%</div> </div>
1	C	105	<div> <div>13%</div> <div>32%</div> <div>34%</div> <div>10%</div> <div>21%</div> </div>
2	B	116	<div> <div>41%</div> <div>30%</div> <div>26%</div> </div>
2	D	116	<div> <div>5%</div> <div>17%</div> <div>28%</div> <div>49%</div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2375 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 activin receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	92	Total	C	N	O	S	0	0	0
			729	453	128	138	10			
1	C	83	Total	C	N	O	S	0	0	0
			623	392	107	115	9			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	120	LEU	-	EXPRESSION TAG	UNP P38445
A	121	VAL	-	EXPRESSION TAG	UNP P38445
A	122	PRO	-	EXPRESSION TAG	UNP P38445
A	123	ARG	-	EXPRESSION TAG	UNP P38445
C	120	LEU	-	EXPRESSION TAG	UNP P38445
C	121	VAL	-	EXPRESSION TAG	UNP P38445
C	122	PRO	-	EXPRESSION TAG	UNP P38445
C	123	ARG	-	EXPRESSION TAG	UNP P38445

- Molecule 2 is a protein called Inhibin beta A chain.

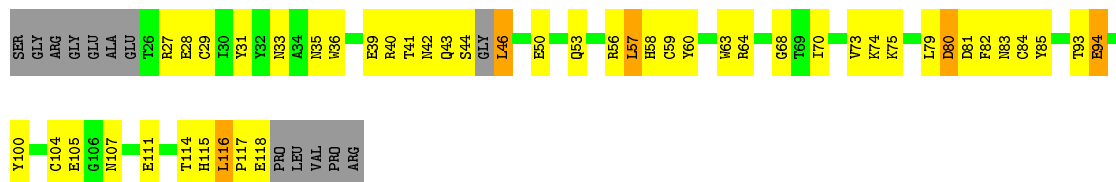
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	86	Total	C	N	O	S	0	0	0
			632	399	105	116	12			
2	D	59	Total	C	N	O	S	0	0	0
			391	248	62	71	10			

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 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.

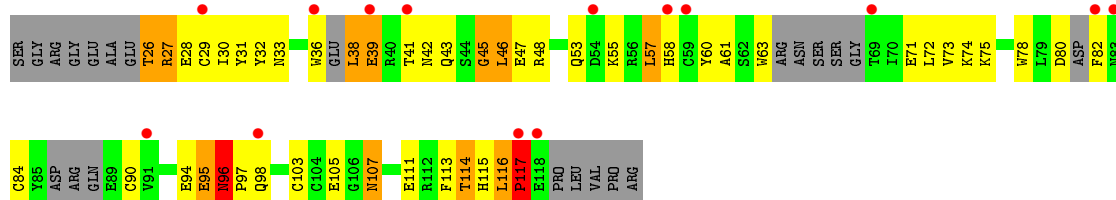
• Molecule 1: activin receptor

Chain A: 



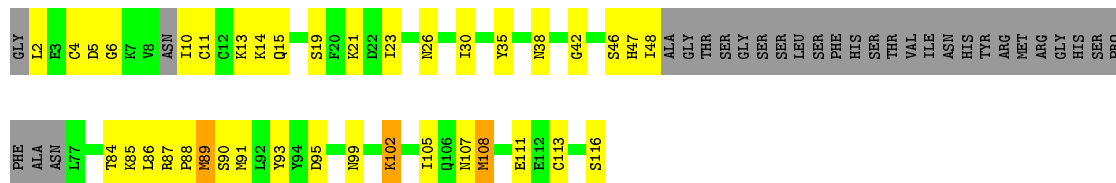
• Molecule 1: activin receptor

Chain C: 



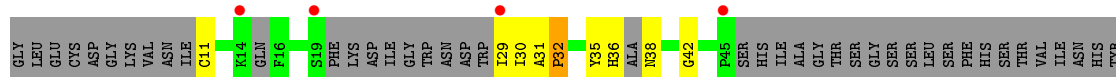
• Molecule 2: Inhibin beta A chain

Chain B: 



• Molecule 2: Inhibin beta A chain

Chain D: 



ARG	MET	ARG	GLY	HIS	SER	PRO	PHE	ASN	ASN	LEU	LYS	SER	C80	C81	V82	T84	K85	L86	R87	R88	M89	S90	M91	L92	Y93	Y94	D95	D96	G97	GLN	ASN	I100	I101	K102	K103	D104	I105	I106	M107	M108	I109	V110	E111	E112	C113	G114	C115	S116
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4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	141.33Å 141.33Å 46.02Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	14.99 – 3.10 14.99 – 3.00	Depositor EDS
% Data completeness (in resolution range)	99.5 (14.99-3.10) 99.6 (14.99-3.00)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.48 (at 3.01Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.268 , 0.291 0.267 , 0.289	Depositor DCC
R_{free} test set	704 reflections (7.27%)	wwPDB-VP
Wilson B-factor (Å ²)	75.6	Xtriage
Anisotropy	0.219	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 88.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	2375	wwPDB-VP
Average B, all atoms (Å ²)	95.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 11.83% 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

5.1 Standard geometry

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	0.56	0/746	0.90	3/1011 (0.3%)
1	C	0.44	0/634	0.88	3/856 (0.4%)
2	B	0.47	0/646	0.83	1/872 (0.1%)
2	D	0.54	0/394	1.19	5/530 (0.9%)
All	All	0.50	0/2420	0.93	12/3269 (0.4%)

There are no bond length outliers.

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	104	ASP	N-CA-C	-7.36	91.13	111.00
2	B	46	SER	N-CA-C	6.60	128.82	111.00
2	D	116	SER	N-CA-C	6.49	128.52	111.00
1	A	29	CYS	CA-CB-SG	-6.30	102.66	114.00
1	A	59	CYS	CA-CB-SG	-6.16	102.91	114.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-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 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	729	0	621	42	2
1	C	623	0	515	61	1
2	B	632	0	546	35	0
2	D	391	0	313	60	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	2375	0	1995	192	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 44.

The worst 5 of 192 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:33:ASN:HD22	1:A:41:THR:HG21	1.01	1.12
1:C:27:ARG:HD2	1:C:107:ASN:HD21	1.10	1.06
2:D:29:ILE:HA	2:D:93:TYR:HB3	1.34	1.05
1:C:46:LEU:H	1:C:46:LEU:HD13	1.18	1.03
1:A:114:THR:HG22	1:A:115:HIS:H	1.27	0.99

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	Interatomic distance (Å)	Clash overlap (Å)
1:C:111:GLU:OE2	1:C:111:GLU:OE2[7_555]	1.55	0.65
1:A:111:GLU:OE2	1:A:111:GLU:OE2[7_556]	1.92	0.28
1:A:75:LYS:NZ	1:A:111:GLU:OE1[7_556]	2.12	0.08

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	88/105 (84%)	78 (89%)	8 (9%)	2 (2%)	6	28
1	C	73/105 (70%)	66 (90%)	4 (6%)	3 (4%)	3	16
2	B	80/116 (69%)	77 (96%)	3 (4%)	0	100	100
2	D	47/116 (40%)	43 (92%)	3 (6%)	1 (2%)	7	30

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	288/442 (65%)	264 (92%)	18 (6%)	6 (2%)	7	30

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	53	GLN
1	C	96	ASN
1	C	117	PRO
1	A	68	GLY
1	A	80	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	74/94 (79%)	67 (90%)	7 (10%)	8	31
1	C	59/94 (63%)	45 (76%)	14 (24%)	1	2
2	B	64/102 (63%)	56 (88%)	8 (12%)	4	18
2	D	35/102 (34%)	29 (83%)	6 (17%)	2	9
All	All	232/392 (59%)	197 (85%)	35 (15%)	3	12

5 of 35 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	26	THR
1	C	42	ASN
2	D	108	MET
1	C	27	ARG
1	C	38	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	36	HIS
2	D	107	ASN
1	C	107	ASN
1	A	107	ASN
2	B	106	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 carbohydrates 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 [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, 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	92/105 (87%)	-0.26	0 100 100	25, 52, 134, 201	0
1	C	83/105 (79%)	0.70	14 (16%) 1 0	84, 130, 186, 199	0
2	B	86/116 (74%)	-0.44	0 100 100	28, 68, 118, 148	0
2	D	59/116 (50%)	0.50	6 (10%) 6 2	79, 134, 176, 186	0
All	All	320/442 (72%)	0.08	20 (6%) 20 8	25, 99, 170, 201	0

The worst 5 of 20 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	41	THR	4.6
1	C	59	CYS	4.5
1	C	39	GLU	3.7
1	C	83	ASN	3.6
1	C	91	VAL	3.2

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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.