



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 10, 2024 – 05:18 PM EST

PDB ID : 2P9L  
Title : Crystal Structure of bovine Arp2/3 complex  
Authors : Nolen, B.J.; Pollard, T.D.  
Deposited on : 2007-03-26  
Resolution : 2.65 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](mailto: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>.

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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 : 2.36  
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

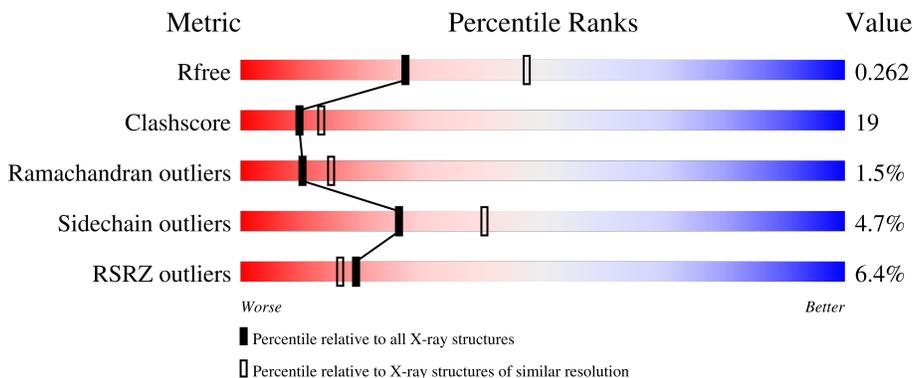
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.65 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	1332 (2.68-2.64)
Clashscore	141614	1374 (2.68-2.64)
Ramachandran outliers	138981	1349 (2.68-2.64)
Sidechain outliers	138945	1349 (2.68-2.64)
RSRZ outliers	127900	1318 (2.68-2.64)

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  $\geq 3$ , 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	418	 6% 64% 28% • 5%
2	B	394	 7% 30% 16% • 49%
3	C	372	 2% 63% 27% • 8%
4	D	300	 2% 66% 24% • 8%
5	E	178	 13% 48% 43% 5% • •

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Mol	Chain	Length	Quality of chain
6	F	168	 <p>% 68% 29% ...</p>
7	G	151	 <p>13% 59% 29% 9%</p>

## 2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 13500 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 Actin-like protein 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	399	3179	2043	526	595	15	0	0	0

- Molecule 2 is a protein called Actin-like protein 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	201	1523	972	263	284	4	0	0	0

- Molecule 3 is a protein called Actin-related protein 2/3 complex subunit 1B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	C	341	2648	1680	464	485	19	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	58	VAL	ILE	conflict	UNP Q58CQ2

- Molecule 4 is a protein called Actin-related protein 2/3 complex subunit 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	D	277	2237	1422	389	418	8	0	0	0

- Molecule 5 is a protein called Actin-related protein 2/3 complex subunit 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
5	E	173	1404	900	235	260	9	0	0	0

- Molecule 6 is a protein called Actin-related protein 2/3 complex subunit 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
6	F	166	1360	869	238	244	9	0	0	0

- Molecule 7 is a protein called Actin-related protein 2/3 complex subunit 5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
7	G	137	1026	644	175	204	3	0	0	0

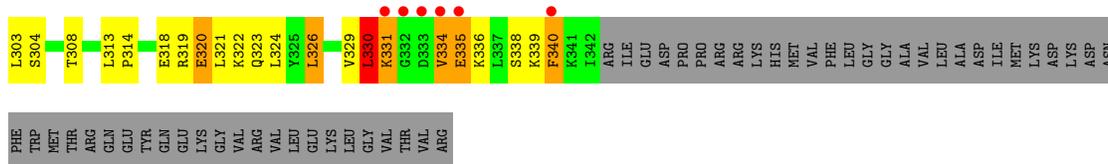
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	17	ASP	GLY	conflict	UNP Q3SYX9
G	28	ASP	GLU	conflict	UNP Q3SYX9

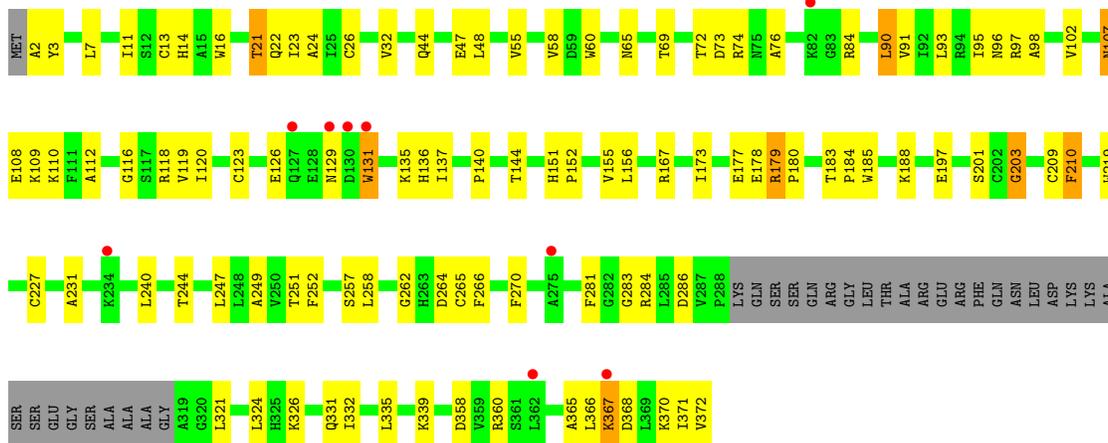
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	27	Total 27	O 27	0	0
8	B	6	Total 6	O 6	0	0
8	C	39	Total 39	O 39	0	0
8	D	24	Total 24	O 24	0	0
8	E	1	Total 1	O 1	0	0
8	F	25	Total 25	O 25	0	0
8	G	1	Total 1	O 1	0	0

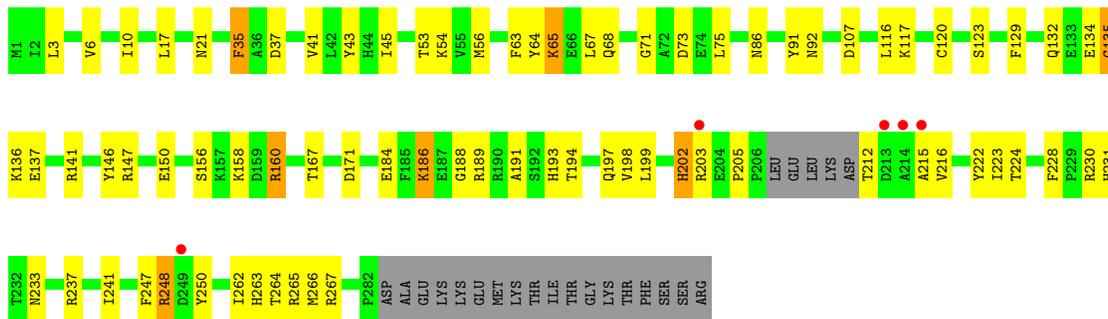




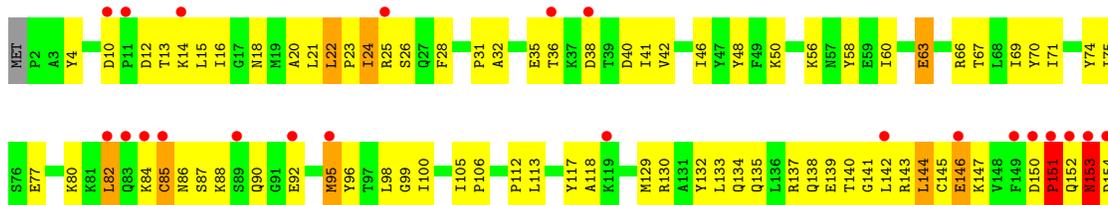
• Molecule 3: Actin-related protein 2/3 complex subunit 1B



• Molecule 4: Actin-related protein 2/3 complex subunit 2



• Molecule 5: Actin-related protein 2/3 complex subunit 3





• Molecule 6: Actin-related protein 2/3 complex subunit 4



• Molecule 7: Actin-related protein 2/3 complex subunit 5



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	111.06Å 128.06Å 204.17Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.65 45.58 – 2.65	Depositor EDS
% Data completeness (in resolution range)	89.8 (30.00-2.65) 89.6 (45.58-2.65)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.60 (at 2.65Å)	Xtrriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.223 , 0.266 0.220 , 0.262	Depositor DCC
$R_{free}$ test set	4094 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	49.4	Xtrriage
Anisotropy	0.430	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 64.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	13500	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	54.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.43% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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	0.38	0/3259	0.61	0/4425
2	B	0.35	0/1548	0.62	0/2099
3	C	0.38	0/2717	0.67	1/3688 (0.0%)
4	D	0.38	0/2285	0.61	0/3084
5	E	0.34	0/1437	0.62	0/1938
6	F	0.40	0/1382	0.63	0/1853
7	G	0.32	0/1038	0.53	0/1400
All	All	0.37	0/13666	0.62	1/18487 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	11	ILE	N-CA-C	-6.47	93.54	111.00

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	3179	0	3107	113	0
2	B	1523	0	1487	76	0
3	C	2648	0	2602	90	0
4	D	2237	0	2202	68	0
5	E	1404	0	1406	100	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	F	1360	0	1399	47	0
7	G	1026	0	1019	56	0
8	A	27	0	0	0	0
8	B	6	0	0	0	0
8	C	39	0	0	2	0
8	D	24	0	0	2	0
8	E	1	0	0	0	0
8	F	25	0	0	0	0
8	G	1	0	0	0	0
All	All	13500	0	13222	512	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 19.

The worst 5 of 512 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)
6:F:4:THR:HG23	6:F:55:ARG:HE	1.28	0.96
5:E:25:ARG:HG3	5:E:35:GLU:HB3	1.48	0.94
3:C:284:ARG:HD3	3:C:286:ASP:O	1.67	0.94
7:G:87:LYS:HE3	7:G:87:LYS:H	1.33	0.94
2:B:291:ILE:HG22	2:B:292:ASP:H	1.34	0.93

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	391/418 (94%)	356 (91%)	29 (7%)	6 (2%)	10 15
2	B	197/394 (50%)	159 (81%)	29 (15%)	9 (5%)	2 2

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	C	337/372 (91%)	319 (95%)	16 (5%)	2 (1%)	25	37
4	D	273/300 (91%)	253 (93%)	18 (7%)	2 (1%)	22	33
5	E	171/178 (96%)	149 (87%)	19 (11%)	3 (2%)	8	12
6	F	164/168 (98%)	156 (95%)	7 (4%)	1 (1%)	25	37
7	G	133/151 (88%)	120 (90%)	11 (8%)	2 (2%)	10	15
All	All	1666/1981 (84%)	1512 (91%)	129 (8%)	25 (2%)	10	15

5 of 25 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	273	TYR
2	B	174	SER
2	B	278	VAL
2	B	291	ILE
2	B	331	LYS

### 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	Rotameric	Outliers	Percentiles	
1	A	346/363 (95%)	331 (96%)	15 (4%)	29	44
2	B	154/345 (45%)	139 (90%)	15 (10%)	8	11
3	C	290/313 (93%)	281 (97%)	9 (3%)	40	57
4	D	243/264 (92%)	233 (96%)	10 (4%)	30	46
5	E	155/159 (98%)	145 (94%)	10 (6%)	17	26
6	F	152/155 (98%)	149 (98%)	3 (2%)	55	73
7	G	108/124 (87%)	102 (94%)	6 (6%)	21	33
All	All	1448/1723 (84%)	1380 (95%)	68 (5%)	26	40

5 of 68 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	E	153	ASN
6	F	102	PHE
7	G	87	LYS
2	B	294	ARG
2	B	274	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 40 such sidechains are listed below:

Mol	Chain	Res	Type
4	D	231	HIS
6	F	137	HIS
5	E	83	GLN
5	E	153	ASN
7	G	61	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 monosaccharides 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q < 0.9
1	A	399/418 (95%)	0.26	23 (5%) 23 19	25, 50, 88, 106	0
2	B	201/394 (51%)	0.48	27 (13%) 3 2	33, 59, 95, 102	0
3	C	341/372 (91%)	0.04	9 (2%) 56 52	28, 41, 70, 97	0
4	D	277/300 (92%)	0.13	5 (1%) 68 65	26, 45, 74, 97	0
5	E	173/178 (97%)	0.61	24 (13%) 2 2	44, 69, 101, 111	0
6	F	166/168 (98%)	-0.16	1 (0%) 89 89	27, 41, 54, 77	0
7	G	137/151 (90%)	0.63	19 (13%) 2 2	35, 79, 99, 103	0
All	All	1694/1981 (85%)	0.25	108 (6%) 19 16	25, 49, 93, 111	0

The worst 5 of 108 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	178	LEU	6.2
3	C	127	GLN	6.0
7	G	50	ASN	5.5
5	E	154	ASP	5.5
2	B	289	ALA	5.0

### 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 monosaccharides in this entry.

## 6.4 Ligands

There are no ligands in this entry.

## 6.5 Other polymers

There are no such residues in this entry.