



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 08:45 AM UTC

PDB ID : 2P9L / pdb_00002p9l
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

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:

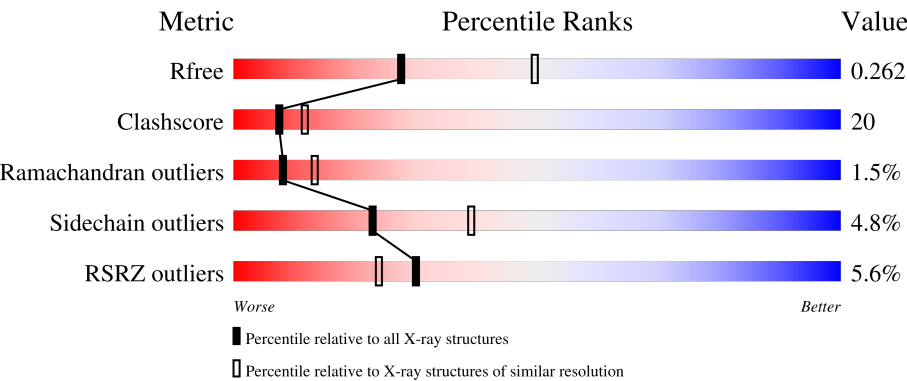
MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

1 Overall quality at a glance 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}	180053	1110 (2.66-2.66)
Clashscore	190562	1141 (2.66-2.66)
Ramachandran outliers	187476	1126 (2.66-2.66)
Sidechain outliers	187428	1126 (2.66-2.66)
RSRZ outliers	180081	1110 (2.66-2.66)

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	418	4% 61%30%5%5%
2	B	394	6% 29%17%49%
3	C	372	2% 59%30%8%
4	D	300	2% 63%26%8%
5	E	178	12% 44%45%5%

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Mol	Chain	Length	Quality of chain
6	F	168	% 66% 31% ...
7	G	151	14% 58% 28% • 9%

2 Entry composition

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
1	A	399	Total	C	N	O	S	0	0	0
			3179	2043	526	595	15			

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

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

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

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

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
4	D	277	Total	C	N	O	S	0	0	0
			2237	1422	389	418	8			

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

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

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

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

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

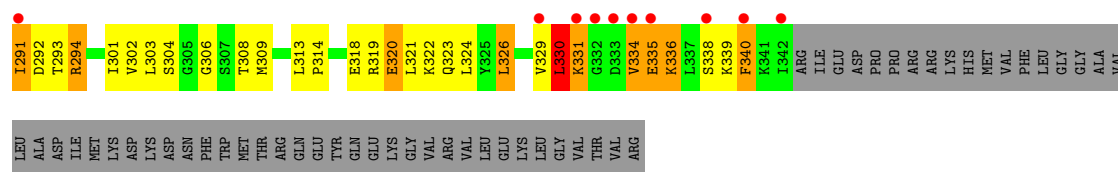
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	G	137	Total	C	N	O	S	0	0	0
			1026	644	175	204	3			

There are 2 discrepancies between the modelled and reference sequences:

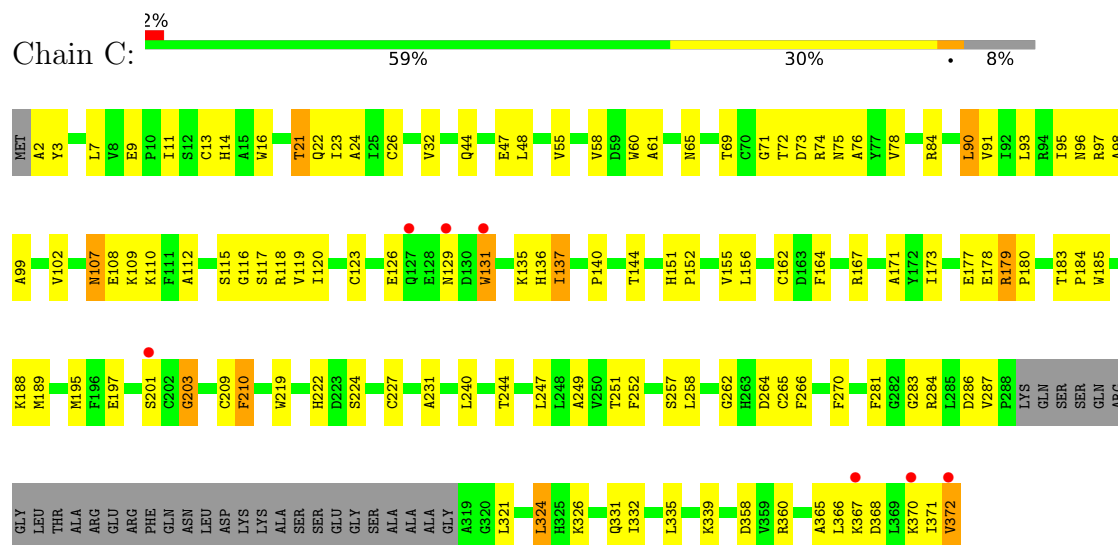
Chain	Residue	Modelled	Actual	Comment	Reference
G	17	ASP	GLY	conflict	UNP Q3SYX9
G	28	ASP	GLU	conflict	UNP Q3SYX9

- Molecule 8 is water.

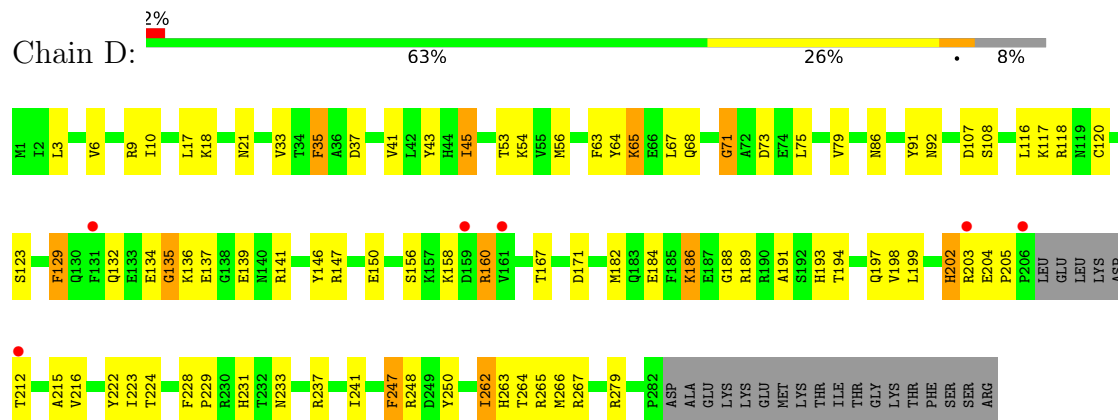
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	27	Total	O	0	0
			27	27		
8	B	6	Total	O	0	0
			6	6		
8	C	39	Total	O	0	0
			39	39		
8	D	24	Total	O	0	0
			24	24		
8	E	1	Total	O	0	0
			1	1		
8	F	25	Total	O	0	0
			25	25		
8	G	1	Total	O	0	0
			1	1		



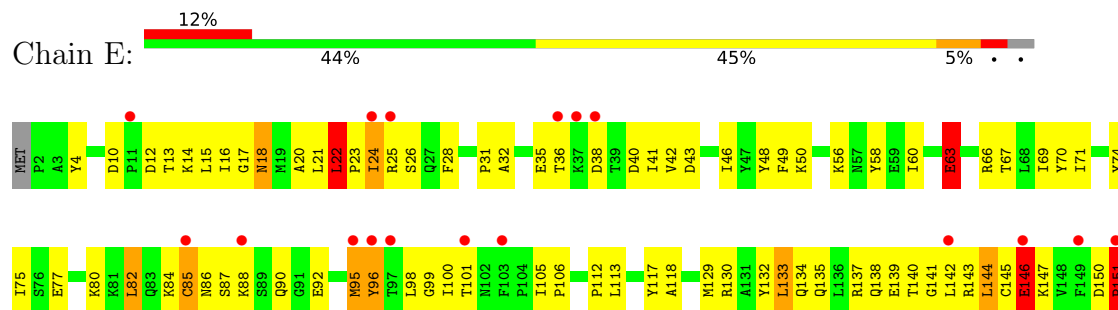
• Molecule 3: Actin-related protein 2/3 complex subunit 1B

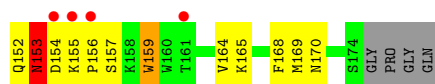


• Molecule 4: Actin-related protein 2/3 complex subunit 2



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

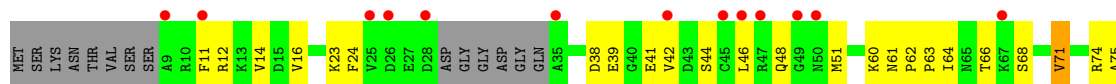




- Molecule 6: Actin-related protein 2/3 complex subunit 4



- 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, α , β , γ	111.06Å 128.06Å 204.17Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.65 30.00 – 2.65	Depositor EDS
% Data completeness (in resolution range)	89.8 (30.00-2.65) 89.7 (30.00-2.65)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.60 (at 2.65Å)	Xtriage
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 ²)	49.4	Xtriage
Anisotropy	0.430	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 61.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	13500	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtriage'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.*

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	0.45	0/3259	0.97	16/4425 (0.4%)
2	B	0.43	0/1548	0.94	7/2099 (0.3%)
3	C	0.45	0/2717	0.99	13/3688 (0.4%)
4	D	0.46	0/2285	0.91	9/3084 (0.3%)
5	E	0.38	0/1437	1.00	9/1938 (0.5%)
6	F	0.49	0/1382	0.95	4/1853 (0.2%)
7	G	0.39	0/1038	0.87	1/1400 (0.1%)
All	All	0.44	0/13666	0.96	59/18487 (0.3%)

There are no bond length outliers.

The worst 5 of 59 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	336	LYS	N-CA-C	-12.72	97.69	113.97
3	C	11	ILE	N-CA-C	-9.38	93.54	107.51
5	E	63	GLU	N-CA-C	-9.29	101.37	112.89
1	A	178	ILE	N-CA-C	8.82	117.78	107.73
1	A	373	GLN	N-CA-C	7.97	119.97	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	3179	0	3107	118	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	1523	0	1487	81	0
3	C	2648	0	2602	93	0
4	D	2237	0	2202	73	0
5	E	1404	0	1406	108	0
6	F	1360	0	1399	47	0
7	G	1026	0	1019	59	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	541	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 20.

The worst 5 of 541 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)
4:D:262:ILE:HG22	4:D:266:MET:HE2	1.35	1.06
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

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	391/418 (94%)	356 (91%)	29 (7%)	6 (2%)	8	13
2	B	197/394 (50%)	159 (81%)	29 (15%)	9 (5%)	2	2
3	C	337/372 (91%)	319 (95%)	16 (5%)	2 (1%)	21	34
4	D	273/300 (91%)	253 (93%)	18 (7%)	2 (1%)	18	30
5	E	171/178 (96%)	149 (87%)	19 (11%)	3 (2%)	6	11
6	F	164/168 (98%)	156 (95%)	7 (4%)	1 (1%)	21	34
7	G	133/151 (88%)	120 (90%)	11 (8%)	2 (2%)	8	13
All	All	1666/1981 (84%)	1512 (91%)	129 (8%)	25 (2%)	8	13

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 ⓘ

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%)	332 (96%)	14 (4%)	28	47
2	B	154/345 (45%)	140 (91%)	14 (9%)	9	14
3	C	290/313 (93%)	280 (97%)	10 (3%)	32	53
4	D	243/264 (92%)	231 (95%)	12 (5%)	22	38
5	E	155/159 (98%)	144 (93%)	11 (7%)	13	23
6	F	152/155 (98%)	149 (98%)	3 (2%)	48	69
7	G	108/124 (87%)	102 (94%)	6 (6%)	19	32
All	All	1448/1723 (84%)	1378 (95%)	70 (5%)	23	39

5 of 70 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	E	146	GLU
5	E	153	ASN
7	G	71	VAL
2	B	303	LEU
2	B	294	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 42 such sidechains are listed below:

Mol	Chain	Res	Type
4	D	231	HIS
6	F	100	ASN
5	E	62	ASN
5	E	134	GLN
6	F	137	HIS

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 [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	399/418 (95%)	0.12	17 (4%) 40 32	25, 50, 88, 106	0
2	B	201/394 (51%)	0.62	22 (10%) 10 9	33, 59, 95, 102	0
3	C	341/372 (91%)	-0.20	7 (2%) 63 57	28, 41, 70, 97	0
4	D	277/300 (92%)	-0.00	6 (2%) 62 56	26, 45, 74, 97	0
5	E	173/178 (97%)	0.93	21 (12%) 8 7	44, 69, 101, 111	0
6	F	166/168 (98%)	-0.35	1 (0%) 85 83	27, 41, 54, 77	0
7	G	137/151 (90%)	0.96	21 (15%) 5 4	35, 79, 99, 103	0
All	All	1694/1981 (85%)	0.20	95 (5%) 30 24	25, 49, 93, 111	0

The worst 5 of 95 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
7	G	35	ALA	5.2
7	G	46	LEU	4.4
2	B	334	VAL	4.3
7	G	45	CYS	4.2
7	G	9	ALA	4.0

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.