



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 4, 2026 – 06:32 PM EDT

PDB ID : 3WEE / pdb_00003wee
Title : Structure of the full-length yeast Arp7-Arp9 Heterodimer
Authors : Lobsiger, J.; Richmond, T.J.
Deposited on : 2013-07-06
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 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
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

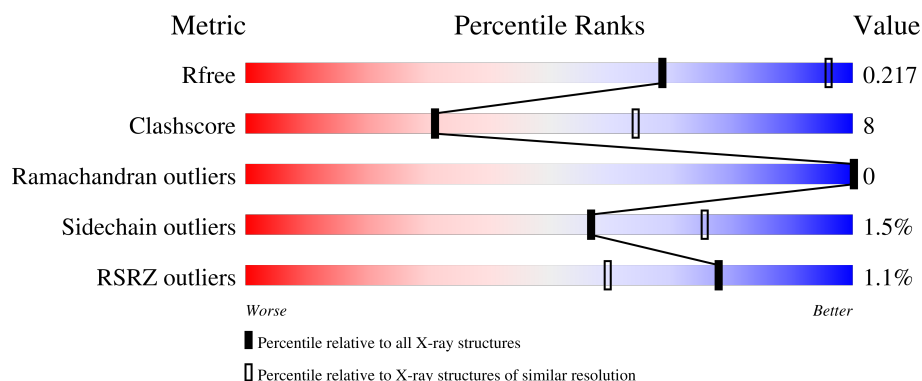
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

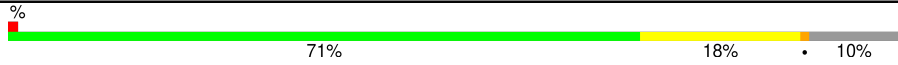
The reported resolution of this entry is 3.10 Å.

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}	180053	1456 (3.10-3.10)
Clashscore	190562	1539 (3.10-3.10)
Ramachandran outliers	187476	1467 (3.10-3.10)
Sidechain outliers	187428	1467 (3.10-3.10)
RSRZ outliers	180081	1456 (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 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	476	
2	B	485	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	SO4	B	503	-	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 6763 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 ARP9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	428	Total	C	N	O	S	0	1	0
			3424	2192	559	664	9			

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	ASP	-	expression tag	UNP Q05123
A	-6	TYR	-	expression tag	UNP Q05123
A	-5	LYS	-	expression tag	UNP Q05123
A	-4	ASP	-	expression tag	UNP Q05123
A	-3	ASP	-	expression tag	UNP Q05123
A	-2	ASP	-	expression tag	UNP Q05123
A	-1	ASP	-	expression tag	UNP Q05123
A	0	LYS	-	expression tag	UNP Q05123
A	1	GLY	MET	engineered mutation	UNP Q05123

- Molecule 2 is a protein called Actin-related protein 7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	412	Total	C	N	O	S	0	0	0
			3291	2114	542	619	16			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	478	PRO	-	expression tag	UNP Q12406
B	479	HIS	-	expression tag	UNP Q12406
B	480	HIS	-	expression tag	UNP Q12406
B	481	HIS	-	expression tag	UNP Q12406
B	482	HIS	-	expression tag	UNP Q12406
B	483	HIS	-	expression tag	UNP Q12406
B	484	HIS	-	expression tag	UNP Q12406

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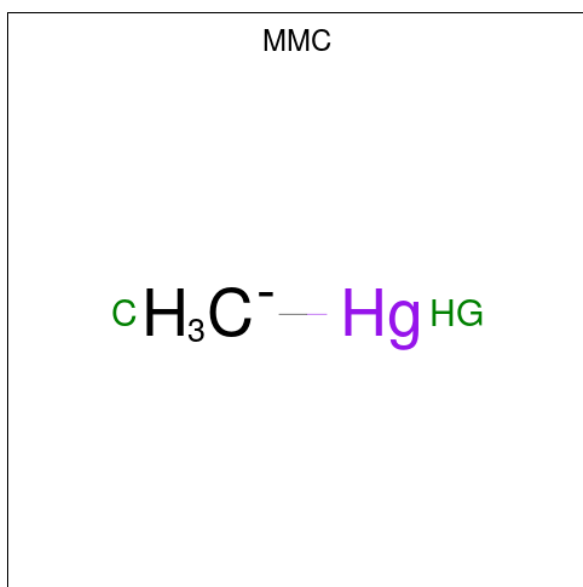
Chain	Residue	Modelled	Actual	Comment	Reference
B	485	HIS	-	expression tag	UNP Q12406

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



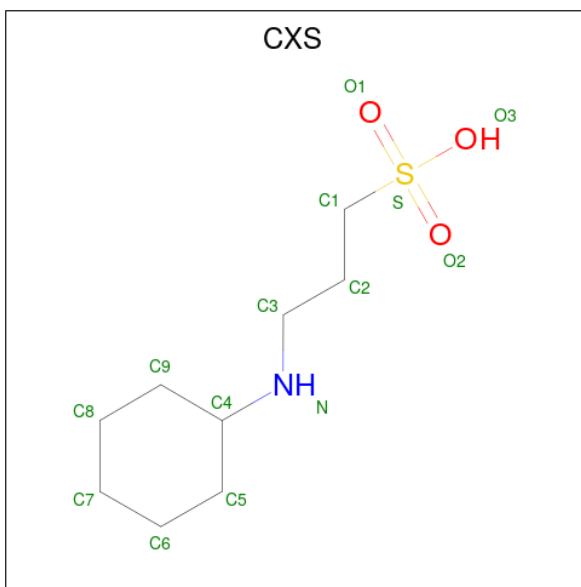
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is METHYL MERCURY ION (CCD ID: MMC) (formula: CH₃Hg).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	Hg	0	0
			2	1	1		
4	A	1	Total	C	Hg	0	0
			2	1	1		
4	A	1	Total	C	Hg	0	1
			4	2	2		
4	B	1	Total	C	Hg	0	0
			2	1	1		
4	B	1	Total	C	Hg	0	0
			2	1	1		
4	B	1	Total	C	Hg	0	0
			2	1	1		

- Molecule 5 is 3-CYCLOHEXYL-1-PROPYLSULFONIC ACID (CCD ID: CXS) (formula: $\text{C}_9\text{H}_{19}\text{NO}_3\text{S}$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
5	B	1	14	9	1	3	1	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	103.77Å 103.77Å 184.45Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	29.73 – 3.10 29.73 – 3.10	Depositor EDS
% Data completeness (in resolution range)	100.0 (29.73-3.10) 99.8 (29.73-3.10)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.54 (at 3.11Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, R_{free}	0.199 , 0.220 0.198 , 0.217	Depositor DCC
R_{free} test set	2004 reflections (9.33%)	wwPDB-VP
Wilson B-factor (Å ²)	63.8	Xtriage
Anisotropy	0.054	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 51.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.034 for -h,-k,l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	6763	wwPDB-VP
Average B, all atoms (Å ²)	70.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.33% 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

Bond lengths and bond angles in the following residue types are not validated in this section: MMC, SO4, CXS

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	0.47	0/3491	0.80	6/4730 (0.1%)
2	B	0.47	0/3360	0.82	3/4542 (0.1%)
All	All	0.47	0/6851	0.81	9/9272 (0.1%)

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	3
2	B	0	2
All	All	0	5

There are no bond length outliers.

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	322	LYS	N-CA-C	-11.30	99.63	113.41
2	B	52	TYR	N-CA-C	-8.55	99.50	110.53
1	A	231	SER	N-CA-C	-7.12	91.07	111.00
1	A	392	THR	N-CA-C	-5.88	104.72	112.24
1	A	230	SER	CA-C-N	5.79	132.12	121.70

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	230	SER	Peptide

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Mol	Chain	Res	Type	Group
1	A	273	ASN	Peptide
1	A	393	ALA	Peptide
2	B	321	ASP	Peptide
2	B	322	LYS	Peptide

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	3424	0	3422	60	0
2	B	3291	0	3302	55	0
3	A	5	0	0	1	0
3	B	15	0	0	2	0
4	A	8	0	0	1	0
4	B	6	0	0	0	0
5	B	14	0	19	4	0
All	All	6763	0	6743	111	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 8.

The worst 5 of 111 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:230:SER:HB2	1:A:231:SER:HB2	1.63	0.78
2:B:341:GLY:HA2	2:B:384:VAL:HG21	1.67	0.76
1:A:280:GLU:HG2	1:A:281:PHE:CD1	2.25	0.71
2:B:344:ILE:HG21	2:B:384:VAL:HG11	1.74	0.69
2:B:51:THR:HB	5:B:501:CXS:H31	1.80	0.64

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	421/476 (88%)	403 (96%)	18 (4%)	0	100	100
2	B	404/485 (83%)	390 (96%)	14 (4%)	0	100	100
All	All	825/961 (86%)	793 (96%)	32 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	390/431 (90%)	383 (98%)	7 (2%)	51	73
2	B	363/428 (85%)	358 (99%)	5 (1%)	59	76
All	All	753/859 (88%)	741 (98%)	12 (2%)	57	75

5 of 12 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	51	THR
2	B	107	THR
2	B	347	MET
2	B	119	ILE
1	A	403[B]	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	229	GLN
2	B	237	GLN
2	B	296	ASN
2	B	289	ASN
1	A	352	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

12 ligands are modelled in this entry.

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	$\# Z > 2$
3	SO4	A	501	-	4,4,4	0.24	0	6,6,6	0.20	0
4	MMC	A	503	1	0,1,1	-	-	-		
3	SO4	B	504	-	4,4,4	0.30	0	6,6,6	0.13	0
4	MMC	A	502	1	0,1,1	-	-	-		
3	SO4	B	503	-	4,4,4	0.30	0	6,6,6	0.09	0
4	MMC	A	504[A]	1	0,1,1	-	-	-		
4	MMC	B	505	2	0,1,1	-	-	-		
3	SO4	B	502	-	4,4,4	0.30	0	6,6,6	0.41	0
4	MMC	A	504[B]	1	0,1,1	-	-	-		
5	CXS	B	501	-	14,14,14	2.40	2 (14%)	18,18,18	5.43	6 (33%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	MMC	B	506	2	0,1,1	-	-	-		
4	MMC	B	507	2	0,1,1	-	-	-		

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
5	CXS	B	501	-	-	4/8/16/16	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	501	CXS	C1-S	-7.67	1.66	1.77
5	B	501	CXS	O3-S	4.34	1.63	1.47

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	501	CXS	O1-S-C1	-15.66	83.07	106.73
5	B	501	CXS	O3-S-C1	-11.22	84.05	106.00
5	B	501	CXS	O2-S-C1	-10.95	90.19	106.73
5	B	501	CXS	O3-S-O2	3.65	120.52	111.40
5	B	501	CXS	O3-S-O1	3.61	120.43	111.40

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	501	CXS	C2-C1-S-O1
5	B	501	CXS	C2-C1-S-O2
5	B	501	CXS	C2-C1-S-O3
5	B	501	CXS	C1-C2-C3-N

There are no ring outliers.

4 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	501	SO4	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	503	SO4	2	0
4	A	504[B]	MMC	1	0
5	B	501	CXS	4	0

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	428/476 (89%)	-0.07	6 (1%)	73 53	34, 60, 138, 193	1 (0%)
2	B	412/485 (84%)	-0.13	3 (0%)	84 68	39, 61, 128, 170	0
All	All	840/961 (87%)	-0.10	9 (1%)	78 59	34, 60, 136, 193	1 (0%)

The worst 5 of 9 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	260	GLN	3.4
1	A	394	PHE	3.3
1	A	393	ALA	2.9
1	A	87	PHE	2.3
1	A	32	VAL	2.3

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](#)

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, 95th 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	B-factors($\text{\AA}^2$)	Q<0.9
3	SO4	B	504	5/5	0.88	0.15	113,113,113,113	0
3	SO4	B	502	5/5	0.89	0.11	76,76,76,76	0
3	SO4	B	503	5/5	0.90	0.13	97,97,97,97	0
3	SO4	A	501	5/5	0.95	0.08	62,62,62,62	0
4	MMC	A	504[A]	2/2	0.96	0.23	85,85,85,87	2
4	MMC	A	504[B]	2/2	0.96	0.23	78,78,78,80	2
5	CXS	B	501	14/14	0.97	0.09	35,35,35,35	0
4	MMC	A	503	2/2	1.00	0.09	68,68,68,70	1
4	MMC	B	505	2/2	1.00	0.10	62,62,62,63	1
4	MMC	B	506	2/2	1.00	0.12	51,51,51,51	1
4	MMC	B	507	2/2	1.00	0.08	59,59,59,60	2
4	MMC	A	502	2/2	1.00	0.08	63,63,63,63	2

6.5 Other polymers [i](#)

There are no such residues in this entry.