



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 10:45 AM UTC

PDB ID : 4EJS / pdb\_00004ejs  
Title : Structure of yeast elongator subcomplex Elp456  
Authors : Lin, Z.; Zhao, W.; Long, J.; Shen, Y.  
Deposited on : 2012-04-07  
Resolution : 2.61 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>.

---

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

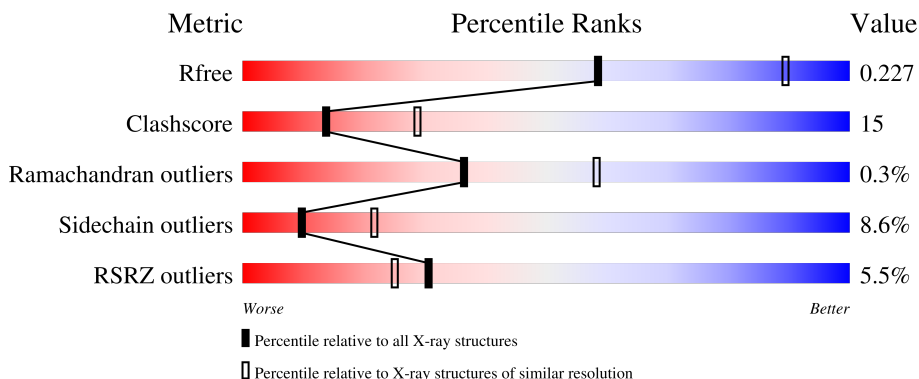
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.61 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	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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	376	<div> <div>5%</div> <div> <div></div> <div>39%</div> <div>18%</div> <div>•</div> <div>41%</div> </div> </div>
2	B	242	<div> <div>4%</div> <div> <div></div> <div>67%</div> <div>23%</div> <div>•</div> <div>9%</div> </div> </div>
3	C	277	<div> <div>4%</div> <div> <div></div> <div>71%</div> <div>23%</div> <div>• •</div> </div> </div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5502 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 Elongator complex protein 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	223	Total	C	N	O	S	0	0	0
			1654	1061	283	304	6			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	63	GLY	-	expression tag	UNP Q02884
A	64	PRO	-	expression tag	UNP Q02884
A	65	GLY	-	expression tag	UNP Q02884
A	66	SER	-	expression tag	UNP Q02884

- Molecule 2 is a protein called Elongator complex protein 5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	221	Total	C	N	O	S	0	0	0
			1731	1117	278	329	7			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-3	GLY	-	expression tag	UNP P38874
B	-2	PRO	-	expression tag	UNP P38874
B	-1	GLY	-	expression tag	UNP P38874
B	0	SER	-	expression tag	UNP P38874

- Molecule 3 is a protein called Elongator complex protein 6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	271	Total	C	N	O	S	0	0	0
			2098	1337	352	402	7			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-3	GLY	-	expression tag	UNP Q04868
C	-2	PRO	-	expression tag	UNP Q04868
C	-1	GLY	-	expression tag	UNP Q04868
C	0	SER	-	expression tag	UNP Q04868

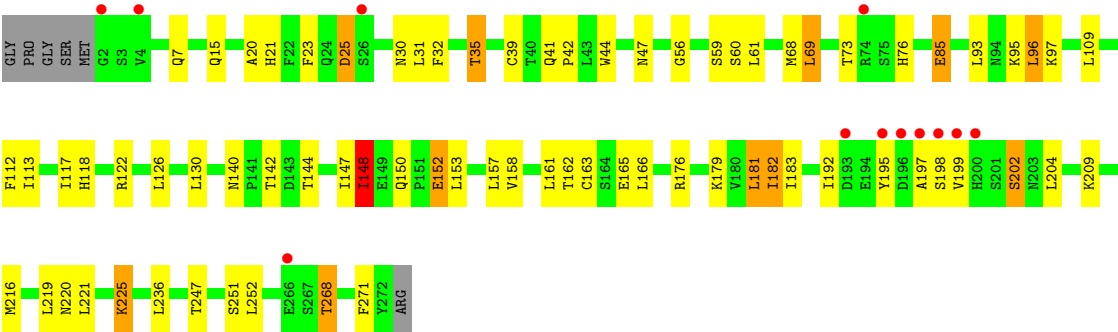
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	2	Total 2	O 2	0	0
4	B	4	Total 4	O 4	0	0
4	C	13	Total 13	O 13	0	0



- Molecule 1: Elongator complex protein 4





## 4 Data and refinement statistics

Property	Value	Source
Space group	I 2 3	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	186.51Å 186.51Å 186.51Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.77 – 2.61 39.77 – 2.61	Depositor EDS
% Data completeness (in resolution range)	99.1 (39.77-2.61) 99.9 (39.77-2.61)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	8.60 (at 2.61Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6.4_486)	Depositor
R, $R_{free}$	0.174 , 0.224 0.176 , 0.227	Depositor DCC
$R_{free}$ test set	1674 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	51.8	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 74.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.027 for -l,-k,-h	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	5502	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.24% 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	0.51	0/1686	0.94	5/2300 (0.2%)
2	B	0.53	0/1766	0.85	1/2407 (0.0%)
3	C	0.58	0/2142	0.92	4/2917 (0.1%)
All	All	0.54	0/5594	0.90	10/7624 (0.1%)

There are no bond length outliers.

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	288	ILE	CA-C-N	7.99	127.92	119.05
1	A	288	ILE	C-N-CA	7.99	127.92	119.05
3	C	118	HIS	N-CA-C	7.84	119.46	111.07
3	C	199	VAL	N-CA-C	6.50	116.64	110.53
1	A	146	ASN	N-CA-C	6.38	117.92	108.60

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	1654	0	1635	78	0
2	B	1731	0	1695	40	0
3	C	2098	0	2059	53	0
4	A	2	0	0	0	0
4	B	4	0	0	0	0

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	C	13	0	0	1	0
All	All	5502	0	5389	158	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 15.

The worst 5 of 158 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:339:PRO:HG3	3:C:195:TYR:OH	1.34	1.24
1:A:339:PRO:HG3	3:C:195:TYR:CZ	1.85	1.09
1:A:72:HIS:HD2	1:A:74:GLY:H	1.15	0.93
1:A:339:PRO:CG	3:C:195:TYR:OH	2.18	0.91
2:B:55:ILE:HG12	2:B:103:MET:HE2	1.53	0.89

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	215/376 (57%)	199 (93%)	15 (7%)	1 (0%)	24	46
2	B	217/242 (90%)	204 (94%)	13 (6%)	0	100	100
3	C	269/277 (97%)	249 (93%)	19 (7%)	1 (0%)	30	51
All	All	701/895 (78%)	652 (93%)	47 (7%)	2 (0%)	36	58

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	25	ASP
1	A	115	THR

### 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	178/337 (53%)	167 (94%)	11 (6%)	16	36
2	B	193/226 (85%)	179 (93%)	14 (7%)	13	29
3	C	243/257 (95%)	215 (88%)	28 (12%)	5	11
All	All	614/820 (75%)	561 (91%)	53 (9%)	10	22

5 of 53 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	59	SER
3	C	97	LYS
3	C	236	LEU
3	C	69	LEU
3	C	93	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
3	C	115	ASN
3	C	222	ASN
3	C	205	GLN
2	B	162	GLN
3	C	53	HIS

### 5.3.3 RNA ⓘ

There are no RNA molecules 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 [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, 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	223/376 (59%)	0.16	18 (8%)	18 14	35, 71, 115, 156	0
2	B	221/242 (91%)	-0.18	9 (4%)	41 36	34, 58, 115, 139	0
3	C	271/277 (97%)	-0.25	12 (4%)	39 33	30, 48, 106, 132	0
All	All	715/895 (79%)	-0.10	39 (5%)	30 25	30, 56, 113, 156	0

The worst 5 of 39 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	C	195	TYR	8.3
3	C	197	ALA	7.1
1	A	136	ILE	5.3
1	A	248	MET	4.1
1	A	116	THR	4.1

### 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.