



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2024 – 05:43 PM EST

PDB ID : 3FLO
Title : Crystal structure of the carboxyl-terminal domain of yeast DNA polymerase alpha in complex with its B subunit
Authors : Klinge, S.N.; Pellegrini, L.
Deposited on : 2008-12-19
Resolution : 2.50 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
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

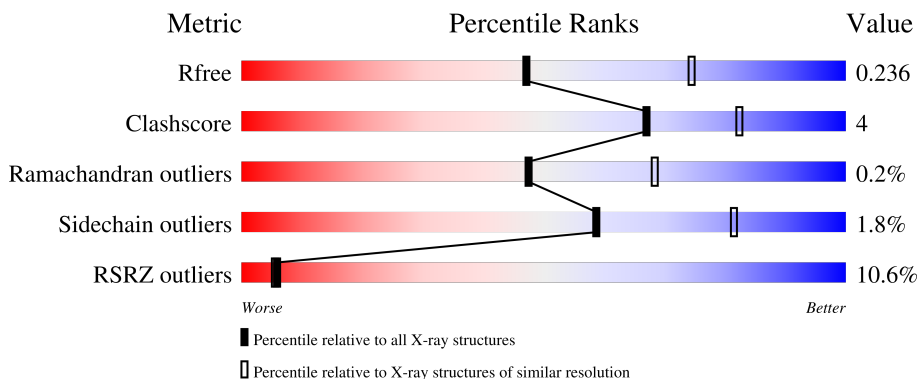
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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.



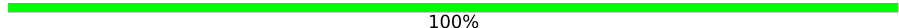
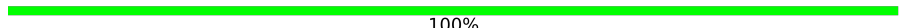

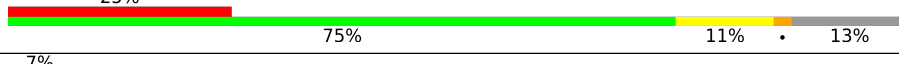
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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	460	 6% 86% 8% 6%
1	C	460	 7% 82% 12% 6%
1	E	460	 16% 82% 12% 6%
1	G	460	 4% 85% 9% 6%
2	I	3	 100%

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Mol	Chain	Length	Quality of chain
2	J	3	 100%
2	K	3	 100%
2	L	3	 100%
3	B	206	 4% 78% 9% 13%
3	D	206	 17% 79% 8% 13%
3	F	206	 25% 75% 11% 13%
3	H	206	 7% 74% 13% 13%

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
4	SO4	A	32	-	-	-	X
4	SO4	A	34	-	-	-	X
4	SO4	A	35	-	-	-	X
4	SO4	A	47	-	-	-	X
4	SO4	B	38	-	-	-	X
4	SO4	B	59	-	-	-	X
4	SO4	B	68	-	-	-	X
4	SO4	C	53	-	-	-	X
4	SO4	D	39	-	-	-	X
4	SO4	D	67	-	-	-	X
4	SO4	E	22	-	-	-	X
4	SO4	E	45	-	-	-	X
4	SO4	E	54	-	-	-	X
4	SO4	G	17	-	-	-	X
4	SO4	G	42	-	-	-	X
4	SO4	G	56	-	-	-	X
4	SO4	H	65	-	-	-	X

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 20656 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 DNA polymerase alpha subunit B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	433	Total 3458	C 2208	N 589	O 651	S 10	0	3	0
1	C	433	Total 3458	C 2208	N 589	O 651	S 10	0	3	0
1	E	433	Total 3458	C 2208	N 589	O 651	S 10	0	3	0
1	G	433	Total 3458	C 2208	N 589	O 651	S 10	0	3	0

- Molecule 2 is a protein called DNA polymerase alpha catalytic subunit A.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	I	3	Total 15	C 9	N 3	O 3	0	0	0
2	J	3	Total 15	C 9	N 3	O 3	0	0	0
2	K	3	Total 15	C 9	N 3	O 3	0	0	0
2	L	3	Total 15	C 9	N 3	O 3	0	0	0

- Molecule 3 is a protein called DNA polymerase alpha catalytic subunit A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	B	180	Total 1471	C 925	N 247	O 287	S 12	0	1	0
3	D	180	Total 1463	C 921	N 246	O 284	S 12	0	0	0
3	F	180	Total 1463	C 921	N 246	O 284	S 12	0	0	0
3	H	180	Total 1463	C 921	N 246	O 284	S 12	0	0	0

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	C	1	Total	O	S	0	0
			5	4	1		
4	C	1	Total	O	S	0	0
			5	4	1		
4	C	1	Total	O	S	0	0
			5	4	1		
4	C	1	Total	O	S	0	0
			5	4	1		
4	C	1	Total	O	S	0	0
			5	4	1		
4	C	1	Total	O	S	0	0
			5	4	1		
4	C	1	Total	O	S	0	0
			5	4	1		
4	C	1	Total	O	S	0	0
			5	4	1		
4	C	1	Total	O	S	0	0
			5	4	1		
4	C	1	Total	O	S	0	0
			5	4	1		
4	D	1	Total	O	S	0	0
			5	4	1		
4	D	1	Total	O	S	0	0
			5	4	1		
4	D	1	Total	O	S	0	0
			5	4	1		
4	D	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
4	E	1	5	4	1	0	0
4	E	1	5	4	1	0	0
4	E	1	5	4	1	0	0
4	E	1	5	4	1	0	0
4	E	1	5	4	1	0	0
4	E	1	5	4	1	0	0
4	E	1	5	4	1	0	0
4	E	1	5	4	1	0	0
4	E	1	5	4	1	0	0
4	E	1	5	4	1	0	0
4	E	1	5	4	1	0	0
4	E	1	5	4	1	0	0
4	E	1	5	4	1	0	0
4	E	1	5	4	1	0	0
4	F	1	5	4	1	0	0
4	F	1	5	4	1	0	0
4	F	1	5	4	1	0	0
4	F	1	5	4	1	0	0
4	G	1	5	4	1	0	0
4	G	1	5	4	1	0	0
4	G	1	5	4	1	0	0
4	G	1	5	4	1	0	0
4	G	1	5	4	1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	G	1	Total O S 5 4 1	0	0
4	G	1	Total O S 5 4 1	0	0
4	G	1	Total O S 5 4 1	0	0
4	G	1	Total O S 5 4 1	0	0
4	G	1	Total O S 5 4 1	0	0
4	G	1	Total O S 5 4 1	0	0
4	H	1	Total O S 5 4 1	0	0
4	H	1	Total O S 5 4 1	0	0
4	H	1	Total O S 5 4 1	0	0
4	H	1	Total O S 5 4 1	0	0

- Molecule 5 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	B	2	Total Zn 2 2	0	0
5	D	2	Total Zn 2 2	0	0
5	F	2	Total Zn 2 2	0	0
5	H	2	Total Zn 2 2	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	135	Total O 135 135	0	0
6	B	79	Total O 79 79	0	0
6	C	106	Total O 106 106	0	0

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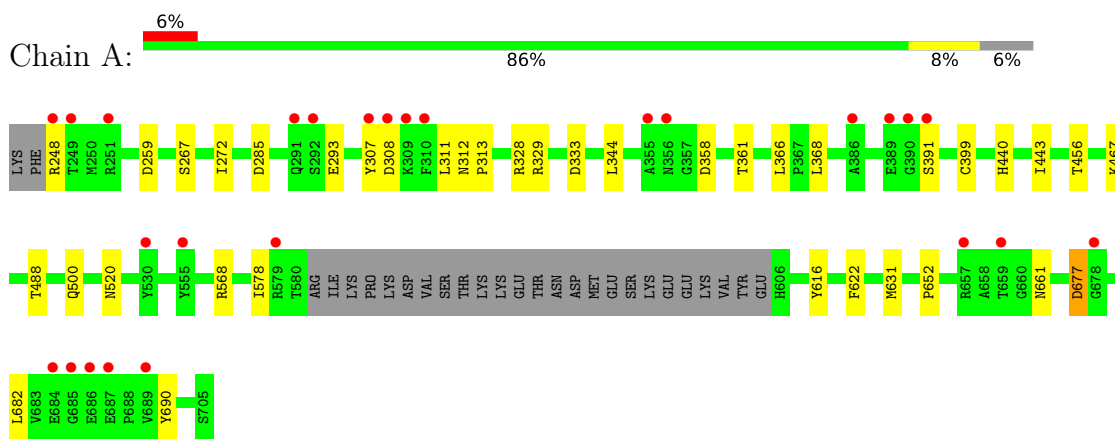
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	D	13	Total 13	O 13	0	0
6	E	65	Total 65	O 65	0	0
6	F	8	Total 8	O 8	0	0
6	G	138	Total 138	O 138	0	0
6	H	27	Total 27	O 27	0	0

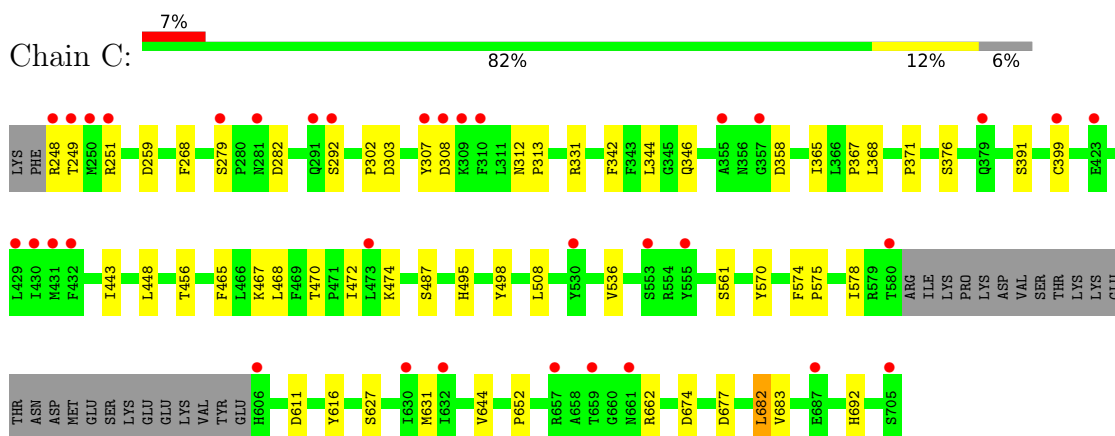
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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.

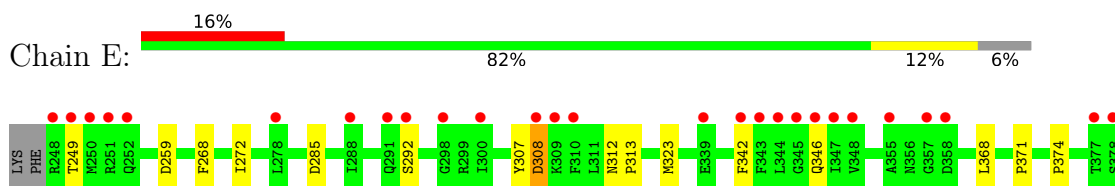
- Molecule 1: DNA polymerase alpha subunit B

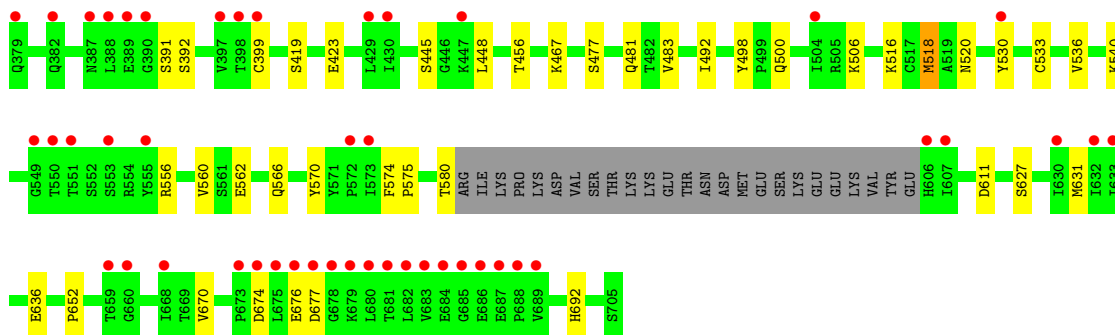


- Molecule 1: DNA polymerase alpha subunit B

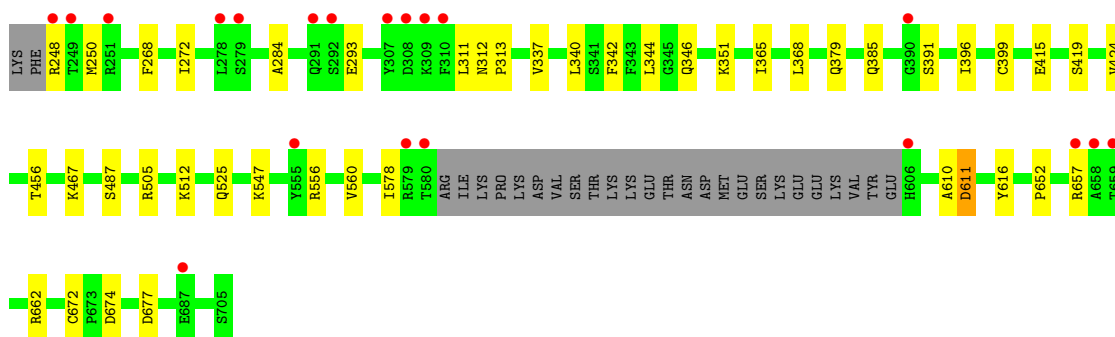
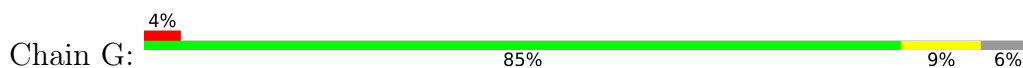


- Molecule 1: DNA polymerase alpha subunit B





- Molecule 1: DNA polymerase alpha subunit B



- Molecule 2: DNA polymerase alpha catalytic subunit A



There are no outlier residues recorded for this chain.

- Molecule 2: DNA polymerase alpha catalytic subunit A



There are no outlier residues recorded for this chain.

- Molecule 2: DNA polymerase alpha catalytic subunit A



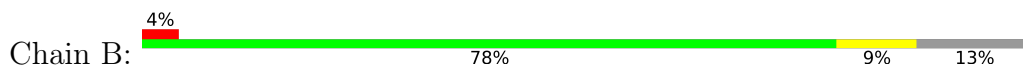
There are no outlier residues recorded for this chain.

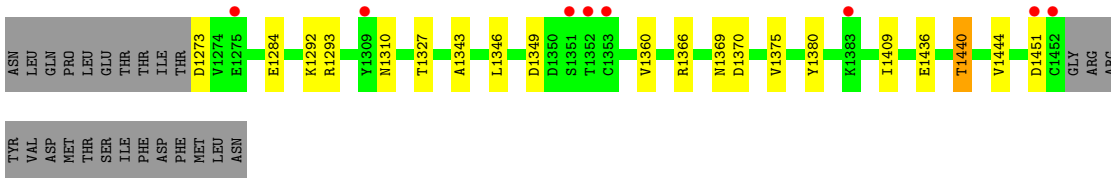
- Molecule 2: DNA polymerase alpha catalytic subunit A



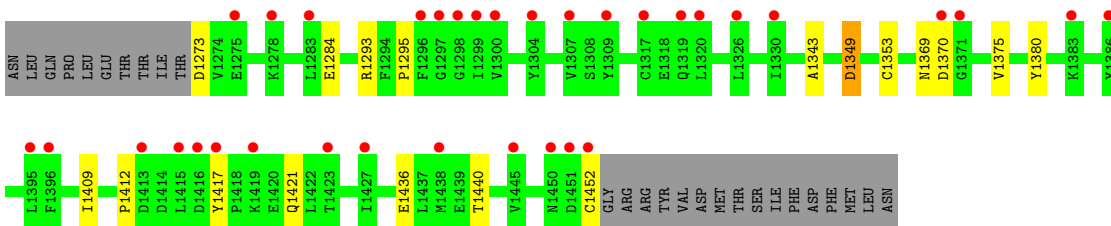
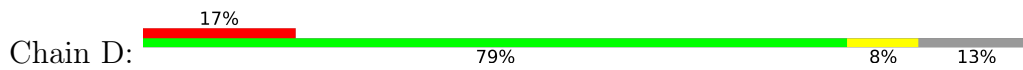
There are no outlier residues recorded for this chain.

- Molecule 3: DNA polymerase alpha catalytic subunit A

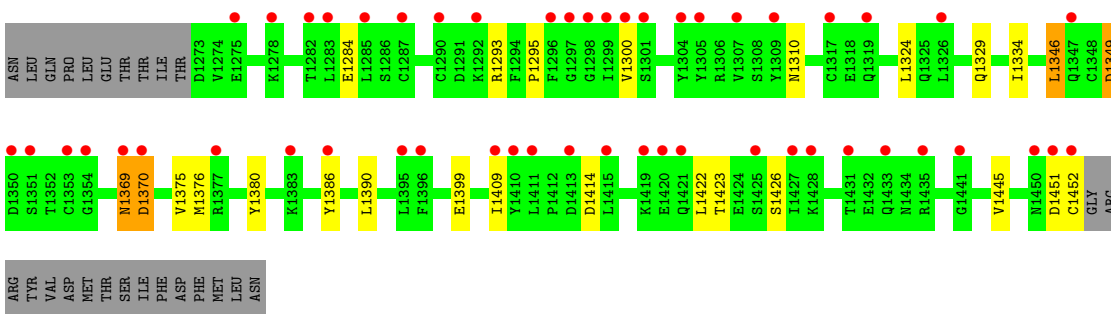
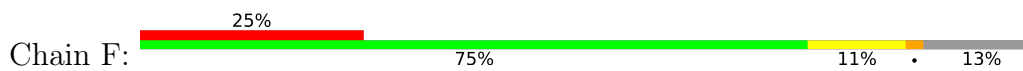




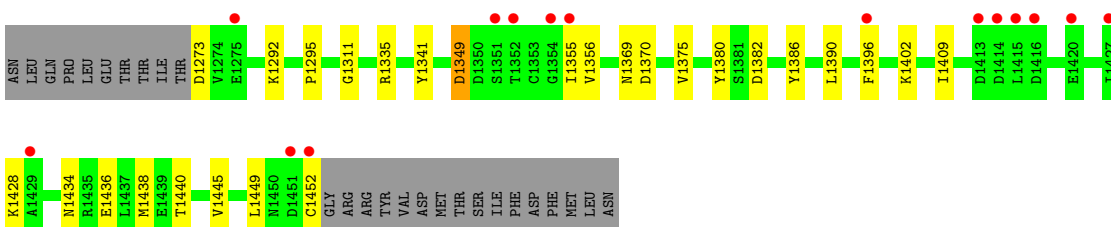
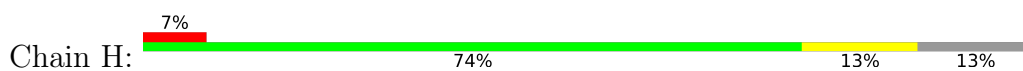
- Molecule 3: DNA polymerase alpha catalytic subunit A



- Molecule 3: DNA polymerase alpha catalytic subunit A



- Molecule 3: DNA polymerase alpha catalytic subunit A



4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	85.41Å 142.63Å 175.25Å 90.00° 102.33° 90.00°	Depositor
Resolution (Å)	31.90 – 2.50 31.90 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.8 (31.90-2.50) 99.8 (31.90-2.50)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.59 (at 2.51Å)	Xtrriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.191 , 0.218 0.214 , 0.236	Depositor DCC
R_{free} test set	7082 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	49.6	Xtrriage
Anisotropy	0.187	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 51.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.015 for h,-k,-h-l	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	20656	wwPDB-VP
Average B, all atoms (Å ²)	63.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.12% 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

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

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	0.83	0/3537	0.81	3/4801 (0.1%)
1	C	0.77	0/3537	0.79	3/4801 (0.1%)
1	E	0.70	3/3537 (0.1%)	0.76	3/4801 (0.1%)
1	G	0.83	1/3537 (0.0%)	0.82	2/4801 (0.0%)
3	B	0.88	0/1500	0.81	0/2024
3	D	0.67	0/1492	0.75	1/2013 (0.0%)
3	F	0.63	0/1492	0.71	0/2013
3	H	0.69	0/1492	0.77	2/2013 (0.1%)
All	All	0.77	4/20124 (0.0%)	0.79	14/27267 (0.1%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	415	GLU	CG-CD	6.25	1.61	1.51
1	E	533	CYS	CB-SG	-5.52	1.72	1.81
1	E	676	GLU	CD-OE2	5.49	1.31	1.25
1	E	676	GLU	CD-OE1	5.28	1.31	1.25

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	518	MET	CG-SD-CE	6.32	110.31	100.20
1	C	662	ARG	NE-CZ-NH1	5.91	123.25	120.30
1	E	611	ASP	CB-CG-OD2	-5.74	113.14	118.30
3	D	1349	ASP	CB-CA-C	-5.71	98.99	110.40
1	C	259	ASP	CB-CG-OD1	5.68	123.41	118.30

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	3458	0	3444	21	0
1	C	3458	0	3444	31	0
1	E	3458	0	3444	40	0
1	G	3458	0	3444	26	0
2	I	15	0	5	0	0
2	J	15	0	5	0	0
2	K	15	0	5	0	0
2	L	15	0	5	0	0
3	B	1471	0	1422	9	0
3	D	1463	0	1419	9	0
3	F	1463	0	1419	13	0
3	H	1463	0	1419	14	0
4	A	65	0	0	1	0
4	B	30	0	0	0	0
4	C	55	0	0	1	0
4	D	20	0	0	0	0
4	E	60	0	0	1	0
4	F	20	0	0	0	0
4	G	55	0	0	0	0
4	H	20	0	0	0	0
5	B	2	0	0	0	0
5	D	2	0	0	0	0
5	F	2	0	0	0	0
5	H	2	0	0	0	0
6	A	135	0	0	1	0
6	B	79	0	0	0	0
6	C	106	0	0	1	0
6	D	13	0	0	0	0
6	E	65	0	0	0	0
6	F	8	0	0	0	0
6	G	138	0	0	1	0
6	H	27	0	0	0	0
All	All	20656	0	19475	153	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 4.

The worst 5 of 153 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:E:374:PRO:HB2	1:E:530:TYR:CE2	1.48	1.49
1:E:374:PRO:CB	1:E:530:TYR:CE2	2.01	1.42
1:C:474:LYS:NZ	6:C:807:HOH:O	1.67	1.28
1:A:399[B]:CYS:SG	1:A:652:PRO:HG2	1.87	1.13
1:E:374:PRO:CG	1:E:530:TYR:CD2	2.37	1.08

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	432/460 (94%)	421 (98%)	10 (2%)	1 (0%)	47	68
1	C	432/460 (94%)	419 (97%)	12 (3%)	1 (0%)	47	68
1	E	432/460 (94%)	421 (98%)	10 (2%)	1 (0%)	47	68
1	G	432/460 (94%)	421 (98%)	10 (2%)	1 (0%)	47	68
3	B	179/206 (87%)	173 (97%)	6 (3%)	0	100	100
3	D	178/206 (86%)	171 (96%)	7 (4%)	0	100	100
3	F	178/206 (86%)	173 (97%)	5 (3%)	0	100	100
3	H	178/206 (86%)	172 (97%)	6 (3%)	0	100	100
All	All	2441/2664 (92%)	2371 (97%)	66 (3%)	4 (0%)	47	68

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	G	391	SER
1	A	391	SER
1	C	391	SER
1	E	391	SER

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	392/416 (94%)	388 (99%)	4 (1%)	76	90
1	C	392/416 (94%)	389 (99%)	3 (1%)	81	93
1	E	392/416 (94%)	386 (98%)	6 (2%)	65	85
1	G	392/416 (94%)	388 (99%)	4 (1%)	76	90
3	B	169/193 (88%)	162 (96%)	7 (4%)	30	55
3	D	168/193 (87%)	164 (98%)	4 (2%)	49	74
3	F	168/193 (87%)	160 (95%)	8 (5%)	25	48
3	H	168/193 (87%)	164 (98%)	4 (2%)	49	74
All	All	2241/2436 (92%)	2201 (98%)	40 (2%)	59	81

5 of 40 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	F	1380	TYR
1	G	525	GLN
3	F	1399	GLU
1	G	379	GLN
3	H	1292	LYS

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

Mol	Chain	Res	Type
1	E	363	ASN
1	G	372	ASN
3	H	1434	ASN
1	G	525	GLN
3	D	1421	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 73 ligands modelled in this entry, 8 are monoatomic - leaving 65 for Mogul analysis.

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	$\# Z > 2$
4	SO4	A	32	-	4,4,4	0.18	0	6,6,6	0.12	0
4	SO4	D	67	-	4,4,4	0.19	0	6,6,6	0.41	0
4	SO4	E	20	-	4,4,4	0.12	0	6,6,6	0.22	0
4	SO4	A	3	-	4,4,4	0.19	0	6,6,6	0.57	0
4	SO4	A	12	-	4,4,4	0.17	0	6,6,6	0.26	0
4	SO4	B	62	-	4,4,4	0.25	0	6,6,6	0.56	0
4	SO4	C	6	-	4,4,4	0.11	0	6,6,6	0.21	0
4	SO4	F	28	-	4,4,4	0.18	0	6,6,6	0.16	0
4	SO4	B	57	-	4,4,4	0.20	0	6,6,6	0.22	0
4	SO4	E	26	-	4,4,4	0.23	0	6,6,6	0.45	0
4	SO4	E	33	-	4,4,4	0.12	0	6,6,6	0.38	0
4	SO4	G	18	-	4,4,4	0.14	0	6,6,6	0.54	0
4	SO4	A	31	-	4,4,4	0.23	0	6,6,6	0.40	0
4	SO4	E	22	-	4,4,4	0.16	0	6,6,6	0.29	0
4	SO4	C	53	-	4,4,4	0.17	0	6,6,6	0.34	0
4	SO4	F	41	-	4,4,4	0.15	0	6,6,6	0.14	0
4	SO4	A	5	-	4,4,4	0.21	0	6,6,6	0.18	0
4	SO4	F	64	-	4,4,4	0.22	0	6,6,6	0.14	0
4	SO4	A	34	-	4,4,4	0.14	0	6,6,6	0.17	0
4	SO4	G	2	-	4,4,4	0.15	0	6,6,6	0.29	0
4	SO4	H	60	-	4,4,4	0.17	0	6,6,6	0.36	0
4	SO4	H	65	-	4,4,4	0.20	0	6,6,6	0.47	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	SO4	D	40	-	4,4,4	0.15	0	6,6,6	0.18	0
4	SO4	E	23	-	4,4,4	0.20	0	6,6,6	0.26	0
4	SO4	G	55	-	4,4,4	0.26	0	6,6,6	0.43	0
4	SO4	B	38	-	4,4,4	0.13	0	6,6,6	0.20	0
4	SO4	A	49	-	4,4,4	0.13	0	6,6,6	0.51	0
4	SO4	C	9	-	4,4,4	0.17	0	6,6,6	0.16	0
4	SO4	C	43	-	4,4,4	0.14	0	6,6,6	0.16	0
4	SO4	C	10	-	4,4,4	0.12	0	6,6,6	0.25	0
4	SO4	E	45	-	4,4,4	0.20	0	6,6,6	0.17	0
4	SO4	B	37	-	4,4,4	0.15	0	6,6,6	0.24	0
4	SO4	G	27	-	4,4,4	0.16	0	6,6,6	0.42	0
4	SO4	H	61	-	4,4,4	0.13	0	6,6,6	0.26	0
4	SO4	A	13	-	4,4,4	0.13	0	6,6,6	0.53	0
4	SO4	A	30	-	4,4,4	0.06	0	6,6,6	0.65	0
4	SO4	E	4	-	4,4,4	0.11	0	6,6,6	0.19	0
4	SO4	D	39	-	4,4,4	0.13	0	6,6,6	0.26	0
4	SO4	E	24	-	4,4,4	0.13	0	6,6,6	0.33	0
4	SO4	C	8	-	4,4,4	0.28	0	6,6,6	0.22	0
4	SO4	E	58	-	4,4,4	0.17	0	6,6,6	0.15	0
4	SO4	C	15	-	4,4,4	0.22	0	6,6,6	0.59	0
4	SO4	C	11	-	4,4,4	0.15	0	6,6,6	0.58	0
4	SO4	C	46	-	4,4,4	0.19	0	6,6,6	0.20	0
4	SO4	G	51	-	4,4,4	0.16	0	6,6,6	0.28	0
4	SO4	D	63	-	4,4,4	0.21	0	6,6,6	0.25	0
4	SO4	A	35	-	4,4,4	0.15	0	6,6,6	0.24	0
4	SO4	A	47	-	4,4,4	0.22	0	6,6,6	0.25	0
4	SO4	H	19	-	4,4,4	0.07	0	6,6,6	0.23	0
4	SO4	G	56	-	4,4,4	0.16	0	6,6,6	0.22	0
4	SO4	A	48	-	4,4,4	0.08	0	6,6,6	0.56	0
4	SO4	E	44	-	4,4,4	0.16	0	6,6,6	0.16	0
4	SO4	C	52	-	4,4,4	0.17	0	6,6,6	0.30	0
4	SO4	G	16	-	4,4,4	0.13	0	6,6,6	0.30	0
4	SO4	E	54	-	4,4,4	0.15	0	6,6,6	0.21	0
4	SO4	F	66	-	4,4,4	0.19	0	6,6,6	0.32	0
4	SO4	C	69	-	4,4,4	0.66	0	6,6,6	0.35	0
4	SO4	G	7	-	4,4,4	0.18	0	6,6,6	0.33	0
4	SO4	B	59	-	4,4,4	0.19	0	6,6,6	0.42	0
4	SO4	A	50	-	4,4,4	0.10	0	6,6,6	0.24	0
4	SO4	B	68	-	4,4,4	0.28	0	6,6,6	0.35	0
4	SO4	G	1	-	4,4,4	0.14	0	6,6,6	0.28	0
4	SO4	G	17	-	4,4,4	0.17	0	6,6,6	0.32	0
4	SO4	E	25	-	4,4,4	0.10	0	6,6,6	0.23	0
4	SO4	G	42	-	4,4,4	0.18	0	6,6,6	0.22	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	E	26	SO4	1	0
4	C	69	SO4	1	0
4	A	50	SO4	1	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	433/460 (94%)	0.01	26 (6%) 21 22	10, 37, 95, 141	0
1	C	433/460 (94%)	0.39	34 (7%) 12 12	20, 49, 109, 165	0
1	E	433/460 (94%)	0.90	73 (16%) 1 1	28, 67, 153, 211	0
1	G	433/460 (94%)	0.03	20 (4%) 32 34	14, 38, 94, 143	0
2	I	0/3	-	-	-	-
2	J	0/3	-	-	-	-
2	K	0/3	-	-	-	-
2	L	0/3	-	-	-	-
3	B	180/206 (87%)	0.17	8 (4%) 34 37	19, 46, 77, 87	0
3	D	180/206 (87%)	1.03	34 (18%) 1 1	35, 82, 176, 213	0
3	F	180/206 (87%)	1.45	51 (28%) 0 0	50, 103, 210, 256	0
3	H	180/206 (87%)	0.57	15 (8%) 11 11	30, 68, 151, 189	0
All	All	2452/2676 (91%)	0.47	261 (10%) 6 5	10, 52, 139, 256	0

The worst 5 of 261 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	309	LYS	8.7
3	D	1452	CYS	7.4
1	C	309	LYS	7.3
1	E	688	PRO	7.2
3	F	1451	ASP	6.8

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 [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(Å ²)	Q<0.9
4	SO4	F	28	5/5	0.43	0.35	136,136,137,137	0
4	SO4	A	34	5/5	0.48	0.55	144,144,145,145	0
4	SO4	H	60	5/5	0.51	0.38	129,129,130,130	0
4	SO4	F	41	5/5	0.53	0.38	144,144,144,144	0
4	SO4	B	38	5/5	0.65	0.60	139,139,139,139	0
4	SO4	G	55	5/5	0.66	0.32	101,103,104,105	0
4	SO4	D	67	5/5	0.68	0.44	117,118,120,120	0
4	SO4	E	54	5/5	0.68	0.41	129,129,129,130	0
4	SO4	E	22	5/5	0.69	0.41	121,122,122,123	0
4	SO4	G	42	5/5	0.69	0.47	105,106,107,107	0
4	SO4	B	68	5/5	0.69	0.40	111,112,112,113	0
4	SO4	A	47	5/5	0.69	0.42	136,137,137,138	0
4	SO4	E	45	5/5	0.70	0.64	140,140,140,141	0
4	SO4	C	46	5/5	0.72	0.38	127,127,128,128	0
4	SO4	B	59	5/5	0.72	0.40	120,120,121,122	0
4	SO4	G	17	5/5	0.74	0.45	122,122,123,123	0
4	SO4	C	52	5/5	0.75	0.35	125,125,126,126	0
4	SO4	C	53	5/5	0.75	0.44	119,119,120,120	0
4	SO4	A	35	5/5	0.76	0.41	137,137,137,138	0
4	SO4	G	56	5/5	0.76	0.60	135,135,135,136	0
4	SO4	A	31	5/5	0.76	0.36	102,102,103,104	0
4	SO4	G	16	5/5	0.77	0.31	114,114,115,115	0
4	SO4	B	57	5/5	0.77	0.24	123,123,123,124	0
4	SO4	D	39	5/5	0.77	0.47	133,133,134,134	0
4	SO4	H	65	5/5	0.78	0.43	105,106,106,107	0
4	SO4	A	30	5/5	0.79	0.30	96,97,97,98	0
4	SO4	A	32	5/5	0.79	0.44	138,139,139,140	0
4	SO4	C	43	5/5	0.80	0.33	120,120,120,121	0
4	SO4	A	50	5/5	0.80	0.65	136,136,136,137	0
4	SO4	C	10	5/5	0.81	0.19	128,128,128,129	0
4	SO4	H	19	5/5	0.81	0.28	123,124,124,124	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	SO4	G	51	5/5	0.81	0.38	125,126,127,127	0
4	SO4	E	44	5/5	0.81	0.39	148,148,148,148	0
4	SO4	E	33	5/5	0.82	0.35	116,117,117,117	0
4	SO4	D	40	5/5	0.82	0.30	119,120,120,121	0
4	SO4	E	26	5/5	0.82	0.42	112,112,113,114	0
4	SO4	D	63	5/5	0.83	0.33	121,122,122,123	0
4	SO4	B	37	5/5	0.84	0.29	118,119,120,120	0
4	SO4	E	25	5/5	0.84	0.32	110,111,111,111	0
4	SO4	A	48	5/5	0.84	0.28	98,100,101,102	0
4	SO4	C	11	5/5	0.85	0.39	97,97,98,99	0
4	SO4	A	49	5/5	0.85	0.49	112,112,112,113	0
4	SO4	F	66	5/5	0.85	0.32	121,121,122,122	0
4	SO4	E	20	5/5	0.86	0.54	117,117,118,118	0
4	SO4	A	3	5/5	0.86	0.18	93,94,95,95	0
4	SO4	A	12	5/5	0.86	0.35	117,117,118,118	0
4	SO4	E	4	5/5	0.86	0.20	123,123,124,124	0
4	SO4	C	8	5/5	0.87	0.38	93,93,94,94	0
4	SO4	E	24	5/5	0.87	0.43	105,106,107,107	0
4	SO4	G	2	5/5	0.87	0.52	106,106,107,107	0
4	SO4	C	69	5/5	0.87	0.42	81,82,82,83	0
4	SO4	H	61	5/5	0.88	0.33	111,111,112,112	0
4	SO4	G	18	5/5	0.88	0.42	101,102,102,103	0
4	SO4	A	13	5/5	0.89	0.51	99,100,101,101	0
4	SO4	B	62	5/5	0.89	0.27	97,97,98,99	0
4	SO4	C	9	5/5	0.89	0.39	114,114,115,115	0
5	ZN	D	1	1/1	0.89	0.09	70,70,70,70	0
4	SO4	C	15	5/5	0.90	0.26	89,89,90,91	0
4	SO4	A	5	5/5	0.91	0.21	96,97,97,98	0
4	SO4	C	6	5/5	0.91	0.19	120,121,121,121	0
5	ZN	F	1	1/1	0.91	0.22	72,72,72,72	0
5	ZN	H	1	1/1	0.91	0.07	67,67,67,67	0
4	SO4	G	27	5/5	0.92	0.40	91,91,92,93	0
4	SO4	E	23	5/5	0.92	0.32	91,92,92,93	0
5	ZN	D	2	1/1	0.92	0.05	66,66,66,66	0
4	SO4	E	58	5/5	0.92	0.55	123,123,124,124	0
4	SO4	G	7	5/5	0.92	0.30	87,87,88,88	0
5	ZN	B	2	1/1	0.93	0.06	63,63,63,63	0
4	SO4	G	1	5/5	0.94	0.14	89,90,91,92	0
5	ZN	F	2	1/1	0.94	0.08	68,68,68,68	0
4	SO4	F	64	5/5	0.94	0.29	115,115,115,116	0
5	ZN	B	1	1/1	0.96	0.05	59,59,59,59	0
5	ZN	H	2	1/1	0.97	0.05	61,61,61,61	0

6.5 Other polymers [i](#)

There are no such residues in this entry.