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PROTEIN DATA BANK

wwPDB X-ray Structure Validation Summary Report (i)

Dec 16, 2023 – 07:07 pm GMT

PDB ID	:	4D0K
Title	:	Complex of Chaetomium thermophilum PAN2 (WD40-CS1) with PAN3 (C-term)
Authors	:	Jonas, S.; Izaurralde, E.; Weichenrieder, O.
Deposited on	:	2014-04-28
Resolution	:	1.89 Å(reported)

The following versions of software and data (see references (i)) were used in the production of this report:

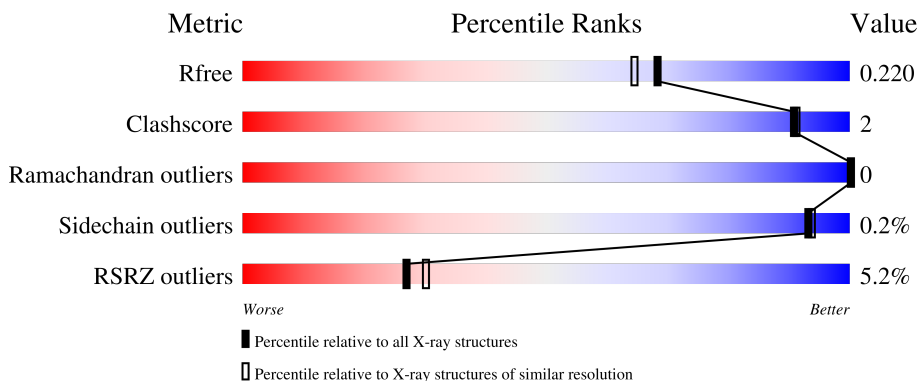|		
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.89 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	Percentile Ranks	Value
Rfree		0.220
Clashscore		2
Ramachandran outliers		0
Sidechain outliers		0.2%
RSRZ outliers		5.2%

Worse   *Better*

▮ Percentile relative to all X-ray structures
◩ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R$_{free}$	130704	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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 <=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	4% / 67% / 5% / 28%
2	B	135	4% / 78% / 22%
2	C	135	2% / 77% / · / 19%

2 Entry composition ⓘ

There are 3 unique types of molecules in this entry. The entry contains 4572 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 A-SPECIFIC RIBONUCLEASE SUBUNIT PAN2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	329	Total 2585	C 1653	N 445	O 468	S 19	0	4	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP G0SAK8
A	-1	PRO	-	expression tag	UNP G0SAK8
A	0	HIS	-	expression tag	UNP G0SAK8

- Molecule 2 is a protein called PAB-DEPENDENT POLY(A)-SPECIFIC RIBONUCLEASE SUBUNIT PAN3-LIKE PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	105	Total 861	C 541	N 153	O 162	S 5	0	1	0
2	C	109	Total 889	C 559	N 156	O 169	S 5	0	0	0

There are 54 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	421	MET	-	expression tag	UNP G0S0Y3
B	422	GLY	-	expression tag	UNP G0S0Y3
B	423	SER	-	expression tag	UNP G0S0Y3
B	424	SER	-	expression tag	UNP G0S0Y3
B	425	HIS	-	expression tag	UNP G0S0Y3
B	426	HIS	-	expression tag	UNP G0S0Y3
B	427	HIS	-	expression tag	UNP G0S0Y3
B	428	HIS	-	expression tag	UNP G0S0Y3
B	429	HIS	-	expression tag	UNP G0S0Y3
B	430	HIS	-	expression tag	UNP G0S0Y3

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Chain	Residue	Modelled	Actual	Comment	Reference
B	431	SER	-	expression tag	UNP G0S0Y3
B	432	SER	-	expression tag	UNP G0S0Y3
B	433	GLY	-	expression tag	UNP G0S0Y3
B	434	THR	-	expression tag	UNP G0S0Y3
B	435	GLY	-	expression tag	UNP G0S0Y3
B	436	SER	-	expression tag	UNP G0S0Y3
B	437	GLY	-	expression tag	UNP G0S0Y3
B	438	GLU	-	expression tag	UNP G0S0Y3
B	439	ASN	-	expression tag	UNP G0S0Y3
B	440	LEU	-	expression tag	UNP G0S0Y3
B	441	TYR	-	expression tag	UNP G0S0Y3
B	442	PHE	-	expression tag	UNP G0S0Y3
B	443	GLN	-	expression tag	UNP G0S0Y3
B	444	GLY	-	expression tag	UNP G0S0Y3
B	445	HIS	-	expression tag	UNP G0S0Y3
B	446	MET	-	expression tag	UNP G0S0Y3
B	447	LEU	-	expression tag	UNP G0S0Y3
C	421	MET	-	expression tag	UNP G0S0Y3
C	422	GLY	-	expression tag	UNP G0S0Y3
C	423	SER	-	expression tag	UNP G0S0Y3
C	424	SER	-	expression tag	UNP G0S0Y3
C	425	HIS	-	expression tag	UNP G0S0Y3
C	426	HIS	-	expression tag	UNP G0S0Y3
C	427	HIS	-	expression tag	UNP G0S0Y3
C	428	HIS	-	expression tag	UNP G0S0Y3
C	429	HIS	-	expression tag	UNP G0S0Y3
C	430	HIS	-	expression tag	UNP G0S0Y3
C	431	SER	-	expression tag	UNP G0S0Y3
C	432	SER	-	expression tag	UNP G0S0Y3
C	433	GLY	-	expression tag	UNP G0S0Y3
C	434	THR	-	expression tag	UNP G0S0Y3
C	435	GLY	-	expression tag	UNP G0S0Y3
C	436	SER	-	expression tag	UNP G0S0Y3
C	437	GLY	-	expression tag	UNP G0S0Y3
C	438	GLU	-	expression tag	UNP G0S0Y3
C	439	ASN	-	expression tag	UNP G0S0Y3
C	440	LEU	-	expression tag	UNP G0S0Y3
C	441	TYR	-	expression tag	UNP G0S0Y3
C	442	PHE	-	expression tag	UNP G0S0Y3
C	443	GLN	-	expression tag	UNP G0S0Y3
C	444	GLY	-	expression tag	UNP G0S0Y3
C	445	HIS	-	expression tag	UNP G0S0Y3

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Chain	Residue	Modelled	Actual	Comment	Reference
C	446	MET	-	expression tag	UNP G0S0Y3
C	447	LEU	-	expression tag	UNP G0S0Y3

• Molecule 3 is water.

| Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	141	Total O 141 141	0	0
3	B	70	Total O 70 70	0	0
3	C	26	Total O 26 26	0	0

3 Residue-property plots ⓘ

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.
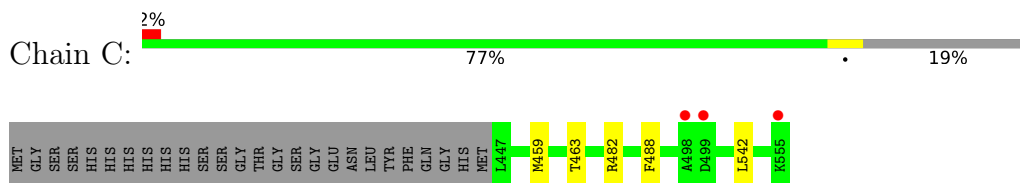
• Molecule 1: A-SPECIFIC RIBONUCLEASE SUBUNIT PAN2
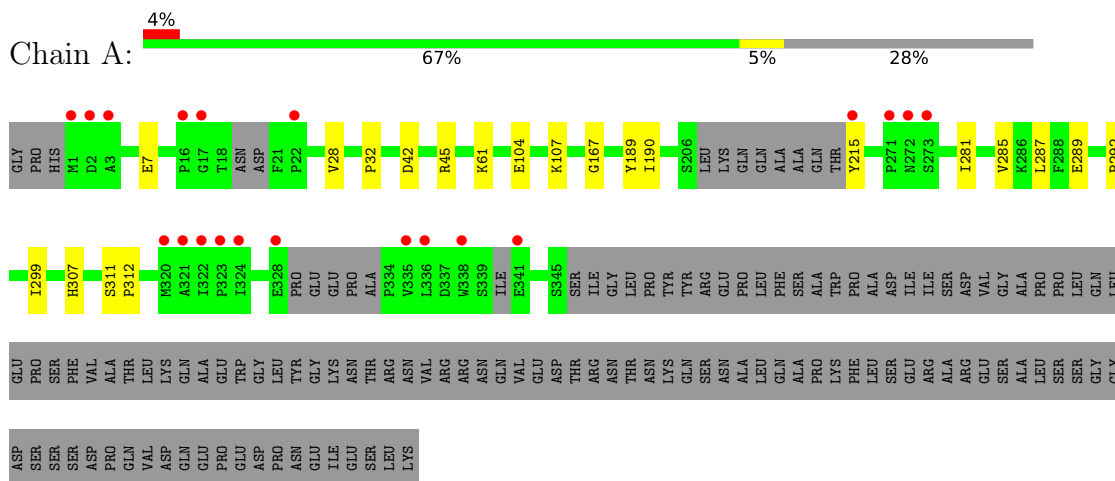
• Molecule 2: PAB-DEPENDENT POLY(A)-SPECIFIC RIBONUCLEASE SUBUNIT PAN3-LIKE PROTEIN
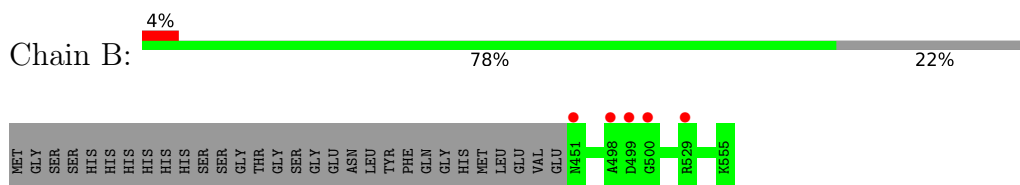
• Molecule 2: PAB-DEPENDENT POLY(A)-SPECIFIC RIBONUCLEASE SUBUNIT PAN3-LIKE PROTEIN

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	72.41Å 93.57Å 110.68Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.97 – 1.89 43.97 – 1.89	Depositor EDS
% Data completeness (in resolution range)	99.2 (43.97-1.89) 99.2 (43.97-1.89)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.04	Depositor
$< I/\sigma(I) >$ [1]	1.41 (at 1.89Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE 1.8.4_1496)	Depositor
R, R_{free}	0.187 , 0.216 0.194 , 0.220	Depositor DCC
R_{free} test set	3036 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å^2)	36.2	Xtriage
Anisotropy	0.405	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 42.6	EDS
L-test for twinning[2]	$< |L| > = 0.48, < L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	4572	wwPDB-VP
Average B, all atoms (Å^2)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.23% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.
[2]Theoretical values of $< |L| >$, $< L^2 >$ 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 ⓘ

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	0.27	0/2662	0.47	0/3619
2	B	0.26	0/878	0.43	0/1181
2	C	0.25	0/903	0.45	0/1215
All	All	0.27	0/4443	0.46	0/6015

There are no bond length outliers.

There are no bond angle outliers.

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	2585	0	2553	13	0
2	B	861	0	856	0	0
2	C	889	0	882	2	0
3	A	141	0	0	1	0
3	B	70	0	0	0	0
3	C	26	0	0	0	0
All	All	4572	0	4291	15	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 2.

The worst 5 of 15 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:61:LYS:NZ	3:A:2033:HOH:O	2.31	0.57
1:A:104:GLU:O	1:A:107:LYS:NZ	2.38	0.56
1:A:299:ILE:HG23	1:A:307:HIS:HB2	1.96	0.47
2:C:488:PHE:CD1	2:C:542:LEU:HD21	2.49	0.47
1:A:281:ILE:HG22	1:A:307:HIS:CD2	2.51	0.46

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	323/460 (70%)	310 (96%)	13 (4%)	0	100	100
2	B	104/135 (77%)	103 (99%)	1 (1%)	0	100	100
2	C	107/135 (79%)	105 (98%)	2 (2%)	0	100	100
All	All	534/730 (73%)	518 (97%)	16 (3%)	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	281/395 (71%)	281 (100%)	0	100	100
2	B	95/119 (80%)	95 (100%)	0	100	100
2	C	98/119 (82%)	97 (99%)	1 (1%)	76	76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	474/633 (75%)	473 (100%)	1 (0%)	93 94

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	C	482	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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(Å²)	Q<0.9
1	A	329/460 (71%)	0.19	20 (6%)	21	24	24, 40, 90, 120	0
2	B	105/135 (77%)	0.01	5 (4%)	30	33	28, 37, 66, 94	0
2	C	109/135 (80%)	0.21	3 (2%)	53	56	29, 43, 74, 111	0
All	All	543/730 (74%)	0.16	28 (5%)	27	30	24, 41, 84, 120	0

The worst 5 of 28 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	499	ASP	5.3
1	A	336	LEU	5.3
1	A	322	ILE	5.2
1	A	3	ALA	5.0
1	A	320	MET	5.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no monosaccharides in this entry.

6.4 Ligands ⓘ

There are no ligands in this entry.

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6.5 Other polymers ⓘ

There are no such residues in this entry.