



wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 13, 2022 – 02:10 PM JST

PDB ID : 7WIM
Title : Crystal structure of Arabidopsis thaliana FKBP43 N-terminal domain
Authors : Singh, A.K.; Saharan, K.; Baral, S.; Vasudevan, D.
Deposited on : 2022-01-03
Resolution : 2.29 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
Xtriage (Phenix)	:	1.13
EDS	:	2.30
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)	:	2.30

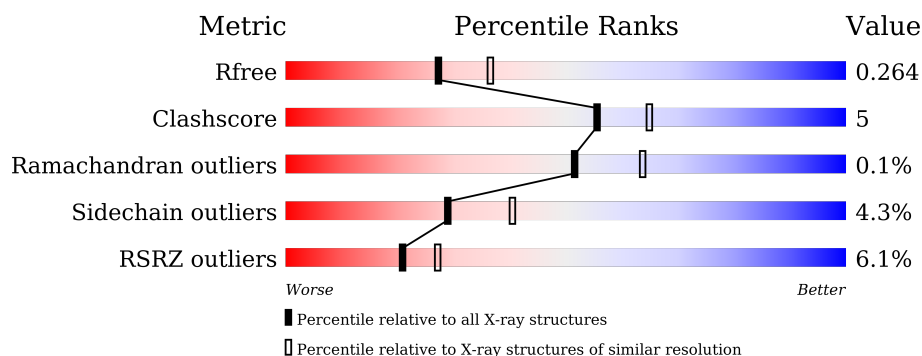
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.29 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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	118	<div> <div>5%</div> <div> <div></div> <div>53%</div> <div>15%</div> <div>5%</div> <div>26%</div> </div> </div>
1	B	118	<div> <div>4%</div> <div> <div></div> <div>68%</div> <div>11%</div> <div>21%</div> </div> </div>
1	C	118	<div> <div>3%</div> <div> <div></div> <div>59%</div> <div>14%</div> <div>•</div> <div>25%</div> </div> </div>
1	D	118	<div> <div>2%</div> <div> <div></div> <div>66%</div> <div>13%</div> <div>21%</div> </div> </div>
1	E	118	<div> <div>5%</div> <div> <div></div> <div>75%</div> <div>5%</div> <div>20%</div> </div> </div>
1	F	118	<div> <div>2%</div> <div> <div></div> <div>74%</div> <div>7%</div> <div>19%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
1	G	118	
1	H	118	
1	I	118	
1	J	118	
1	K	118	
1	L	118	
1	M	118	
1	N	118	
1	O	118	
1	P	118	
1	Q	118	
1	R	118	
1	S	118	
1	T	118	

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 13382 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 Peptidyl-prolyl cis-trans isomerase FKBP43.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	87	Total	C	N	O	S	0	0	0
			670	431	116	120	3			
1	B	93	Total	C	N	O	S	0	0	0
			702	447	120	132	3			
1	C	88	Total	C	N	O	S	0	0	0
			649	415	111	120	3			
1	D	93	Total	C	N	O	S	0	0	0
			722	460	126	133	3			
1	E	94	Total	C	N	O	S	0	0	0
			691	443	119	126	3			
1	F	95	Total	C	N	O	S	0	0	0
			690	440	120	127	3			
1	G	93	Total	C	N	O	S	0	0	0
			718	457	125	133	3			
1	H	93	Total	C	N	O	S	0	0	0
			684	438	117	126	3			
1	I	94	Total	C	N	O	S	0	1	0
			724	458	126	137	3			
1	J	95	Total	C	N	O	S	0	0	0
			709	451	123	132	3			
1	K	85	Total	C	N	O	S	0	0	0
			589	378	104	104	3			
1	L	93	Total	C	N	O	S	0	0	0
			685	438	116	128	3			
1	M	86	Total	C	N	O	S	0	0	0
			630	402	107	118	3			
1	N	93	Total	C	N	O	S	0	0	0
			701	449	119	130	3			
1	O	92	Total	C	N	O	S	0	0	0
			669	428	116	122	3			
1	P	87	Total	C	N	O	S	0	0	0
			638	410	110	115	3			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Q	91	Total	C	N	O	S	0	0	0
			665	428	111	123	3			
1	R	77	Total	C	N	O	S	0	0	0
			538	344	90	101	3			
1	S	89	Total	C	N	O	S	0	0	0
			674	434	115	122	3			
1	T	85	Total	C	N	O	S	0	0	0
			625	403	105	114	3			

There are 160 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	111	LEU	-	expression tag	UNP F4J9Q6
A	112	GLU	-	expression tag	UNP F4J9Q6
A	113	HIS	-	expression tag	UNP F4J9Q6
A	114	HIS	-	expression tag	UNP F4J9Q6
A	115	HIS	-	expression tag	UNP F4J9Q6
A	116	HIS	-	expression tag	UNP F4J9Q6
A	117	HIS	-	expression tag	UNP F4J9Q6
A	118	HIS	-	expression tag	UNP F4J9Q6
B	111	LEU	-	expression tag	UNP F4J9Q6
B	112	GLU	-	expression tag	UNP F4J9Q6
B	113	HIS	-	expression tag	UNP F4J9Q6
B	114	HIS	-	expression tag	UNP F4J9Q6
B	115	HIS	-	expression tag	UNP F4J9Q6
B	116	HIS	-	expression tag	UNP F4J9Q6
B	117	HIS	-	expression tag	UNP F4J9Q6
B	118	HIS	-	expression tag	UNP F4J9Q6
C	111	LEU	-	expression tag	UNP F4J9Q6
C	112	GLU	-	expression tag	UNP F4J9Q6
C	113	HIS	-	expression tag	UNP F4J9Q6
C	114	HIS	-	expression tag	UNP F4J9Q6
C	115	HIS	-	expression tag	UNP F4J9Q6
C	116	HIS	-	expression tag	UNP F4J9Q6
C	117	HIS	-	expression tag	UNP F4J9Q6
C	118	HIS	-	expression tag	UNP F4J9Q6
D	111	LEU	-	expression tag	UNP F4J9Q6
D	112	GLU	-	expression tag	UNP F4J9Q6
D	113	HIS	-	expression tag	UNP F4J9Q6
D	114	HIS	-	expression tag	UNP F4J9Q6
D	115	HIS	-	expression tag	UNP F4J9Q6
D	116	HIS	-	expression tag	UNP F4J9Q6
D	117	HIS	-	expression tag	UNP F4J9Q6

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Chain	Residue	Modelled	Actual	Comment	Reference
D	118	HIS	-	expression tag	UNP F4J9Q6
E	111	LEU	-	expression tag	UNP F4J9Q6
E	112	GLU	-	expression tag	UNP F4J9Q6
E	113	HIS	-	expression tag	UNP F4J9Q6
E	114	HIS	-	expression tag	UNP F4J9Q6
E	115	HIS	-	expression tag	UNP F4J9Q6
E	116	HIS	-	expression tag	UNP F4J9Q6
E	117	HIS	-	expression tag	UNP F4J9Q6
E	118	HIS	-	expression tag	UNP F4J9Q6
F	111	LEU	-	expression tag	UNP F4J9Q6
F	112	GLU	-	expression tag	UNP F4J9Q6
F	113	HIS	-	expression tag	UNP F4J9Q6
F	114	HIS	-	expression tag	UNP F4J9Q6
F	115	HIS	-	expression tag	UNP F4J9Q6
F	116	HIS	-	expression tag	UNP F4J9Q6
F	117	HIS	-	expression tag	UNP F4J9Q6
F	118	HIS	-	expression tag	UNP F4J9Q6
G	111	LEU	-	expression tag	UNP F4J9Q6
G	112	GLU	-	expression tag	UNP F4J9Q6
G	113	HIS	-	expression tag	UNP F4J9Q6
G	114	HIS	-	expression tag	UNP F4J9Q6
G	115	HIS	-	expression tag	UNP F4J9Q6
G	116	HIS	-	expression tag	UNP F4J9Q6
G	117	HIS	-	expression tag	UNP F4J9Q6
G	118	HIS	-	expression tag	UNP F4J9Q6
H	111	LEU	-	expression tag	UNP F4J9Q6
H	112	GLU	-	expression tag	UNP F4J9Q6
H	113	HIS	-	expression tag	UNP F4J9Q6
H	114	HIS	-	expression tag	UNP F4J9Q6
H	115	HIS	-	expression tag	UNP F4J9Q6
H	116	HIS	-	expression tag	UNP F4J9Q6
H	117	HIS	-	expression tag	UNP F4J9Q6
H	118	HIS	-	expression tag	UNP F4J9Q6
I	111	LEU	-	expression tag	UNP F4J9Q6
I	112	GLU	-	expression tag	UNP F4J9Q6
I	113	HIS	-	expression tag	UNP F4J9Q6
I	114	HIS	-	expression tag	UNP F4J9Q6
I	115	HIS	-	expression tag	UNP F4J9Q6
I	116	HIS	-	expression tag	UNP F4J9Q6
I	117	HIS	-	expression tag	UNP F4J9Q6
I	118	HIS	-	expression tag	UNP F4J9Q6
J	111	LEU	-	expression tag	UNP F4J9Q6

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Chain	Residue	Modelled	Actual	Comment	Reference
J	112	GLU	-	expression tag	UNP F4J9Q6
J	113	HIS	-	expression tag	UNP F4J9Q6
J	114	HIS	-	expression tag	UNP F4J9Q6
J	115	HIS	-	expression tag	UNP F4J9Q6
J	116	HIS	-	expression tag	UNP F4J9Q6
J	117	HIS	-	expression tag	UNP F4J9Q6
J	118	HIS	-	expression tag	UNP F4J9Q6
K	111	LEU	-	expression tag	UNP F4J9Q6
K	112	GLU	-	expression tag	UNP F4J9Q6
K	113	HIS	-	expression tag	UNP F4J9Q6
K	114	HIS	-	expression tag	UNP F4J9Q6
K	115	HIS	-	expression tag	UNP F4J9Q6
K	116	HIS	-	expression tag	UNP F4J9Q6
K	117	HIS	-	expression tag	UNP F4J9Q6
K	118	HIS	-	expression tag	UNP F4J9Q6
L	111	LEU	-	expression tag	UNP F4J9Q6
L	112	GLU	-	expression tag	UNP F4J9Q6
L	113	HIS	-	expression tag	UNP F4J9Q6
L	114	HIS	-	expression tag	UNP F4J9Q6
L	115	HIS	-	expression tag	UNP F4J9Q6
L	116	HIS	-	expression tag	UNP F4J9Q6
L	117	HIS	-	expression tag	UNP F4J9Q6
L	118	HIS	-	expression tag	UNP F4J9Q6
M	111	LEU	-	expression tag	UNP F4J9Q6
M	112	GLU	-	expression tag	UNP F4J9Q6
M	113	HIS	-	expression tag	UNP F4J9Q6
M	114	HIS	-	expression tag	UNP F4J9Q6
M	115	HIS	-	expression tag	UNP F4J9Q6
M	116	HIS	-	expression tag	UNP F4J9Q6
M	117	HIS	-	expression tag	UNP F4J9Q6
M	118	HIS	-	expression tag	UNP F4J9Q6
N	111	LEU	-	expression tag	UNP F4J9Q6
N	112	GLU	-	expression tag	UNP F4J9Q6
N	113	HIS	-	expression tag	UNP F4J9Q6
N	114	HIS	-	expression tag	UNP F4J9Q6
N	115	HIS	-	expression tag	UNP F4J9Q6
N	116	HIS	-	expression tag	UNP F4J9Q6
N	117	HIS	-	expression tag	UNP F4J9Q6
N	118	HIS	-	expression tag	UNP F4J9Q6
O	111	LEU	-	expression tag	UNP F4J9Q6
O	112	GLU	-	expression tag	UNP F4J9Q6
O	113	HIS	-	expression tag	UNP F4J9Q6

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Chain	Residue	Modelled	Actual	Comment	Reference
O	114	HIS	-	expression tag	UNP F4J9Q6
O	115	HIS	-	expression tag	UNP F4J9Q6
O	116	HIS	-	expression tag	UNP F4J9Q6
O	117	HIS	-	expression tag	UNP F4J9Q6
O	118	HIS	-	expression tag	UNP F4J9Q6
P	111	LEU	-	expression tag	UNP F4J9Q6
P	112	GLU	-	expression tag	UNP F4J9Q6
P	113	HIS	-	expression tag	UNP F4J9Q6
P	114	HIS	-	expression tag	UNP F4J9Q6
P	115	HIS	-	expression tag	UNP F4J9Q6
P	116	HIS	-	expression tag	UNP F4J9Q6
P	117	HIS	-	expression tag	UNP F4J9Q6
P	118	HIS	-	expression tag	UNP F4J9Q6
Q	111	LEU	-	expression tag	UNP F4J9Q6
Q	112	GLU	-	expression tag	UNP F4J9Q6
Q	113	HIS	-	expression tag	UNP F4J9Q6
Q	114	HIS	-	expression tag	UNP F4J9Q6
Q	115	HIS	-	expression tag	UNP F4J9Q6
Q	116	HIS	-	expression tag	UNP F4J9Q6
Q	117	HIS	-	expression tag	UNP F4J9Q6
Q	118	HIS	-	expression tag	UNP F4J9Q6
R	111	LEU	-	expression tag	UNP F4J9Q6
R	112	GLU	-	expression tag	UNP F4J9Q6
R	113	HIS	-	expression tag	UNP F4J9Q6
R	114	HIS	-	expression tag	UNP F4J9Q6
R	115	HIS	-	expression tag	UNP F4J9Q6
R	116	HIS	-	expression tag	UNP F4J9Q6
R	117	HIS	-	expression tag	UNP F4J9Q6
R	118	HIS	-	expression tag	UNP F4J9Q6
S	111	LEU	-	expression tag	UNP F4J9Q6
S	112	GLU	-	expression tag	UNP F4J9Q6
S	113	HIS	-	expression tag	UNP F4J9Q6
S	114	HIS	-	expression tag	UNP F4J9Q6
S	115	HIS	-	expression tag	UNP F4J9Q6
S	116	HIS	-	expression tag	UNP F4J9Q6
S	117	HIS	-	expression tag	UNP F4J9Q6
S	118	HIS	-	expression tag	UNP F4J9Q6
T	111	LEU	-	expression tag	UNP F4J9Q6
T	112	GLU	-	expression tag	UNP F4J9Q6
T	113	HIS	-	expression tag	UNP F4J9Q6
T	114	HIS	-	expression tag	UNP F4J9Q6
T	115	HIS	-	expression tag	UNP F4J9Q6

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Chain	Residue	Modelled	Actual	Comment	Reference
T	116	HIS	-	expression tag	UNP F4J9Q6
T	117	HIS	-	expression tag	UNP F4J9Q6
T	118	HIS	-	expression tag	UNP F4J9Q6

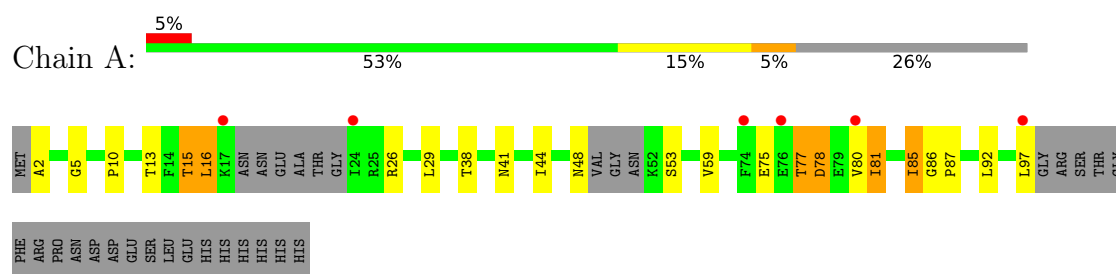
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total O 1 1	0	0
2	C	1	Total O 1 1	0	0
2	D	1	Total O 1 1	0	0
2	G	2	Total O 2 2	0	0
2	H	1	Total O 1 1	0	0
2	I	1	Total O 1 1	0	0
2	K	1	Total O 1 1	0	0
2	S	1	Total O 1 1	0	0

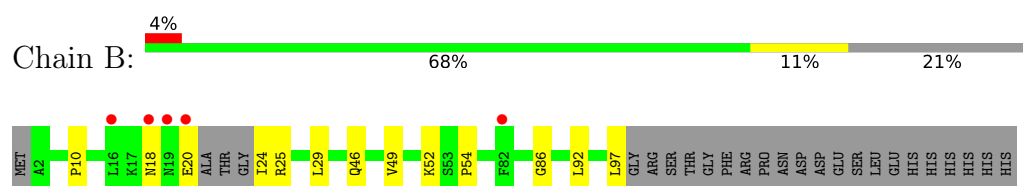
3 Residue-property plots [i](#)

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.

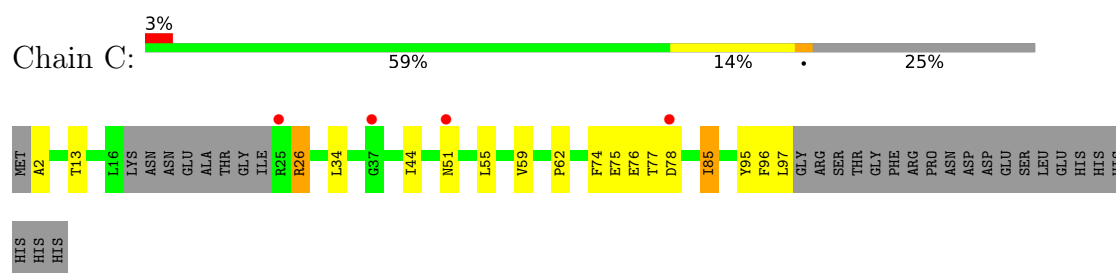
- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP43



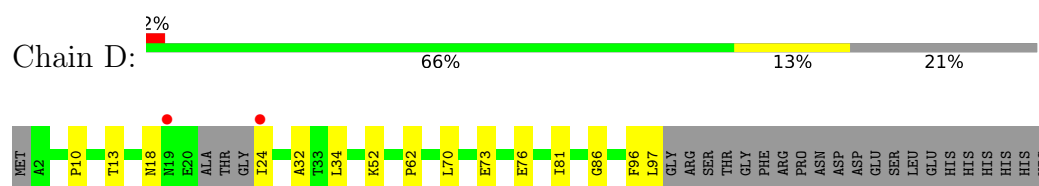
- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP43



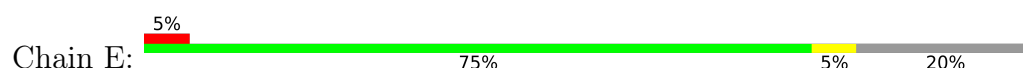
- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP43



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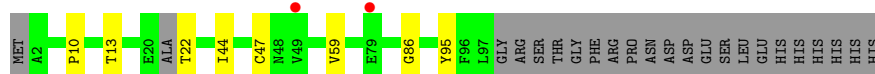
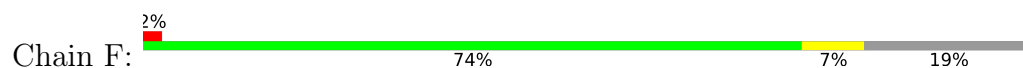


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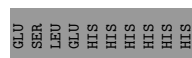
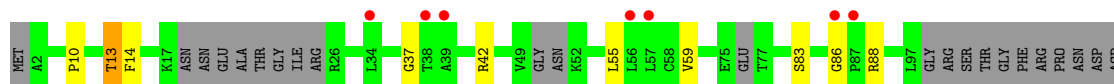
- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP43



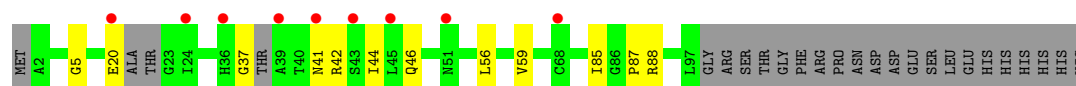
- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP43



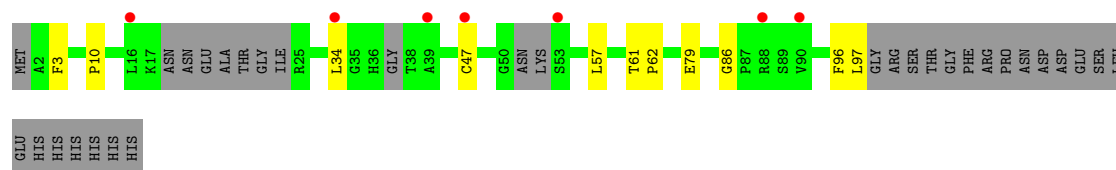
- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP43



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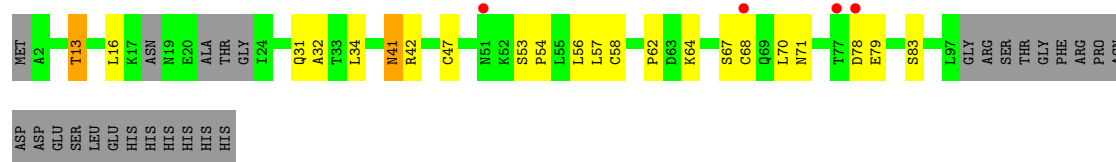
- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP43



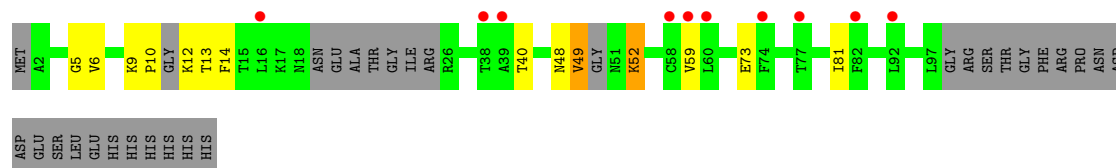
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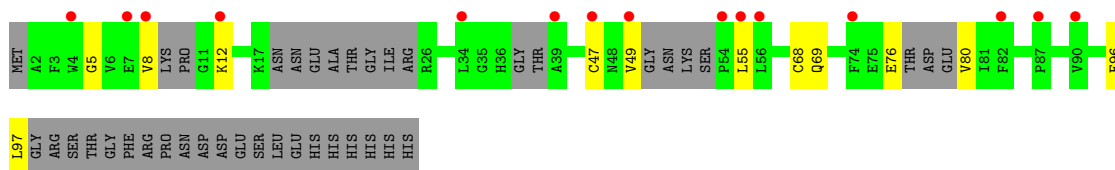


- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP43





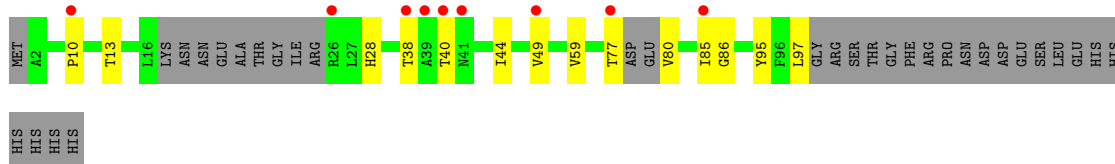
- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP43



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- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP43



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	53.06Å 203.91Å 94.55Å 90.00° 96.14° 90.00°	Depositor
Resolution (Å)	47.00 – 2.29 47.00 – 2.29	Depositor EDS
% Data completeness (in resolution range)	99.0 (47.00-2.29) 99.3 (47.00-2.29)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.11 (at 2.29Å)	Xtriage
Refinement program	PHENIX (1.14_3260: ???)	Depositor
R, R_{free}	0.223 , 0.258 0.234 , 0.264	Depositor DCC
R_{free} test set	4454 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	47.0	Xtriage
Anisotropy	0.753	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 54.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	13382	wwPDB-VP
Average B, all atoms (Å ²)	67.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 37.60 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 4.1839e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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	0.28	0/682	0.53	0/924
1	B	0.35	0/715	0.53	0/974
1	C	0.57	0/662	0.58	0/901
1	D	0.58	0/735	0.56	0/996
1	E	0.39	0/704	0.60	0/958
1	F	0.34	0/703	0.53	0/959
1	G	0.54	0/731	0.53	0/992
1	H	0.41	0/697	0.51	0/951
1	I	0.52	0/737	0.52	0/1003
1	J	0.48	0/722	0.53	0/983
1	K	0.26	0/600	0.50	0/817
1	L	0.56	0/696	0.56	0/946
1	M	0.26	0/641	0.48	0/872
1	N	0.37	0/714	0.51	0/972
1	O	0.43	0/681	0.63	0/928
1	P	0.44	0/649	0.59	0/883
1	Q	0.48	0/678	0.53	0/926
1	R	0.30	0/546	0.63	0/740
1	S	0.28	0/686	0.55	0/932
1	T	0.29	0/637	0.49	0/868
All	All	0.42	0/13616	0.54	0/18525

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 [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	670	0	676	18	0
1	B	702	0	675	6	0
1	C	649	0	612	15	0
1	D	722	0	728	8	0
1	E	691	0	669	5	0
1	F	690	0	649	8	0
1	G	718	0	717	6	0
1	H	684	0	655	11	0
1	I	724	0	708	10	0
1	J	709	0	689	5	0
1	K	589	0	516	5	0
1	L	685	0	657	6	0
1	M	630	0	582	5	0
1	N	701	0	684	8	0
1	O	669	0	626	15	0
1	P	638	0	592	7	0
1	Q	665	0	636	6	0
1	R	538	0	453	5	0
1	S	674	0	666	5	0
1	T	625	0	597	6	0
2	A	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	G	2	0	0	0	0
2	H	1	0	0	0	0
2	I	1	0	0	0	0
2	K	1	0	0	0	0
2	S	1	0	0	0	0
All	All	13382	0	12787	132	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 5.

The worst 5 of 132 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:R:8:VAL:C	1:R:12:LYS:CB	2.45	0.84
1:H:95:TYR:CE2	1:I:73:GLU:HG3	2.15	0.81
1:L:44:ILE:HD12	1:L:85:ILE:HD11	1.73	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2:ALA:N	1:C:76:GLU:OE2	2.25	0.69
1:A:16:LEU:HB2	1:A:80:VAL:HG11	1.74	0.69

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	81/118 (69%)	76 (94%)	5 (6%)	0	100	100
1	B	89/118 (75%)	85 (96%)	4 (4%)	0	100	100
1	C	84/118 (71%)	78 (93%)	6 (7%)	0	100	100
1	D	89/118 (75%)	82 (92%)	7 (8%)	0	100	100
1	E	90/118 (76%)	85 (94%)	5 (6%)	0	100	100
1	F	91/118 (77%)	87 (96%)	4 (4%)	0	100	100
1	G	89/118 (75%)	82 (92%)	7 (8%)	0	100	100
1	H	89/118 (75%)	86 (97%)	3 (3%)	0	100	100
1	I	91/118 (77%)	85 (93%)	6 (7%)	0	100	100
1	J	91/118 (77%)	85 (93%)	6 (7%)	0	100	100
1	K	77/118 (65%)	72 (94%)	5 (6%)	0	100	100
1	L	87/118 (74%)	83 (95%)	4 (5%)	0	100	100
1	M	78/118 (66%)	73 (94%)	5 (6%)	0	100	100
1	N	89/118 (75%)	83 (93%)	6 (7%)	0	100	100
1	O	86/118 (73%)	80 (93%)	5 (6%)	1 (1%)	13	14
1	P	79/118 (67%)	72 (91%)	7 (9%)	0	100	100
1	Q	87/118 (74%)	82 (94%)	5 (6%)	0	100	100
1	R	65/118 (55%)	60 (92%)	5 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	S	83/118 (70%)	78 (94%)	5 (6%)	0	100	100
1	T	79/118 (67%)	76 (96%)	3 (4%)	0	100	100
All	All	1694/2360 (72%)	1590 (94%)	103 (6%)	1 (0%)	51	64

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	O	64	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	75/104 (72%)	66 (88%)	9 (12%)	5	5
1	B	76/104 (73%)	74 (97%)	2 (3%)	46	63
1	C	67/104 (64%)	64 (96%)	3 (4%)	27	39
1	D	82/104 (79%)	80 (98%)	2 (2%)	49	66
1	E	72/104 (69%)	70 (97%)	2 (3%)	43	60
1	F	70/104 (67%)	68 (97%)	2 (3%)	42	58
1	G	81/104 (78%)	80 (99%)	1 (1%)	71	84
1	H	72/104 (69%)	71 (99%)	1 (1%)	67	81
1	I	81/104 (78%)	79 (98%)	2 (2%)	47	65
1	J	76/104 (73%)	72 (95%)	4 (5%)	22	31
1	K	52/104 (50%)	49 (94%)	3 (6%)	20	27
1	L	72/104 (69%)	69 (96%)	3 (4%)	30	42
1	M	65/104 (62%)	63 (97%)	2 (3%)	40	55
1	N	76/104 (73%)	72 (95%)	4 (5%)	22	31
1	O	68/104 (65%)	64 (94%)	4 (6%)	19	27
1	P	64/104 (62%)	60 (94%)	4 (6%)	18	24

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	Q	70/104 (67%)	69 (99%)	1 (1%)	67	81
1	R	49/104 (47%)	45 (92%)	4 (8%)	11	14
1	S	74/104 (71%)	71 (96%)	3 (4%)	30	43
1	T	66/104 (64%)	62 (94%)	4 (6%)	18	25
All	All	1408/2080 (68%)	1348 (96%)	60 (4%)	29	40

5 of 60 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	K	13	THR
1	S	76	GLU
1	M	79	GLU
1	S	13	THR
1	T	59	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	I	36	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 monosaccharides 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

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(Å ²)	Q<0.9
1	A	87/118 (73%)	0.91	6 (6%) 16 22	52, 80, 112, 132	0
1	B	93/118 (78%)	0.50	5 (5%) 25 32	30, 64, 93, 124	0
1	C	88/118 (74%)	0.53	4 (4%) 33 40	30, 61, 96, 111	0
1	D	93/118 (78%)	0.22	2 (2%) 62 69	30, 48, 73, 120	0
1	E	94/118 (79%)	0.41	6 (6%) 19 25	28, 56, 89, 125	0
1	F	95/118 (80%)	0.57	2 (2%) 63 70	38, 62, 100, 128	0
1	G	93/118 (78%)	0.27	4 (4%) 35 42	34, 51, 99, 124	0
1	H	93/118 (78%)	0.46	1 (1%) 80 85	37, 57, 83, 131	0
1	I	94/118 (79%)	0.50	5 (5%) 26 33	32, 53, 98, 123	0
1	J	95/118 (80%)	0.31	2 (2%) 63 70	36, 59, 90, 130	0
1	K	85/118 (72%)	0.81	7 (8%) 11 15	50, 87, 117, 134	0
1	L	93/118 (78%)	0.73	9 (9%) 7 10	30, 69, 101, 126	0
1	M	86/118 (72%)	0.66	7 (8%) 12 16	46, 76, 105, 130	0
1	N	93/118 (78%)	0.47	4 (4%) 35 42	37, 55, 88, 102	0
1	O	92/118 (77%)	0.53	4 (4%) 35 42	30, 63, 98, 127	0
1	P	87/118 (73%)	0.95	10 (11%) 4 7	61, 88, 120, 148	0
1	Q	91/118 (77%)	0.48	3 (3%) 46 53	30, 65, 97, 122	0
1	R	77/118 (65%)	1.21	15 (19%) 1 1	28, 93, 136, 178	0
1	S	89/118 (75%)	0.47	5 (5%) 24 30	37, 60, 98, 126	0
1	T	85/118 (72%)	0.88	9 (10%) 6 8	30, 73, 115, 138	0
All	All	1803/2360 (76%)	0.58	110 (6%) 21 27	28, 66, 110, 178	0

The worst 5 of 110 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	O	77	THR	5.4
1	K	39	ALA	4.4
1	M	90	VAL	4.3
1	C	78	ASP	4.2
1	P	38	THR	4.2

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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.