



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 04:41 PM UTC

PDB ID : 3RPU / pdb_00003rpu
Title : Crystal structure of the MukE-MukF complex
Authors : Guarne, A.; Gloyd, M.; Ghirlando, R.
Deposited on : 2011-04-27
Resolution : 3.60 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
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

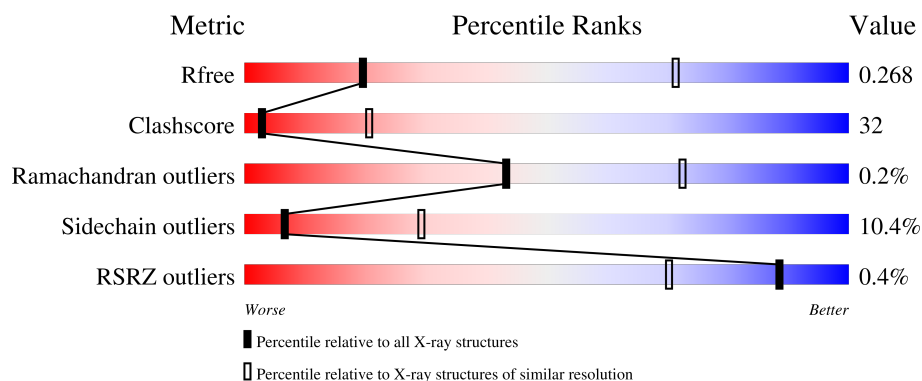
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.60 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	1747 (3.70-3.50)
Clashscore	190562	1827 (3.70-3.50)
Ramachandran outliers	187476	1773 (3.70-3.50)
Sidechain outliers	187428	1772 (3.70-3.50)
RSRZ outliers	180081	1745 (3.70-3.50)

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	% 32% 30% . 33%
1	B	460	29% 32% . 34%
1	X	460	36% 28% . 33%
2	D	245	% 35% 38% 10% 17%
2	E	245	39% 33% 6% 22%

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Mol	Chain	Length	Quality of chain
2	G	245	39%35%9%•17%
2	H	245	38%35%5%22%
2	Y	245	36%36%11%•16%
2	Z	245	39%29%9%23%

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 17083 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 Chromosome partition protein mukF.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	309	Total	C	N	O	S	0	0	0
			2503	1573	447	475	8			
1	B	302	Total	C	N	O	S	0	0	0
			2443	1536	438	462	7			
1	X	310	Total	C	N	O	S	0	0	0
			2504	1573	448	476	7			

There are 60 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	expression tag	UNP P60293
A	-18	GLY	-	expression tag	UNP P60293
A	-17	SER	-	expression tag	UNP P60293
A	-16	SER	-	expression tag	UNP P60293
A	-15	HIS	-	expression tag	UNP P60293
A	-14	HIS	-	expression tag	UNP P60293
A	-13	HIS	-	expression tag	UNP P60293
A	-12	HIS	-	expression tag	UNP P60293
A	-11	HIS	-	expression tag	UNP P60293
A	-10	HIS	-	expression tag	UNP P60293
A	-9	SER	-	expression tag	UNP P60293
A	-8	SER	-	expression tag	UNP P60293
A	-7	GLY	-	expression tag	UNP P60293
A	-6	LEU	-	expression tag	UNP P60293
A	-5	VAL	-	expression tag	UNP P60293
A	-4	PRO	-	expression tag	UNP P60293
A	-3	ARG	-	expression tag	UNP P60293
A	-2	GLY	-	expression tag	UNP P60293
A	-1	SER	-	expression tag	UNP P60293
A	0	HIS	-	expression tag	UNP P60293
B	-19	MET	-	expression tag	UNP P60293
B	-18	GLY	-	expression tag	UNP P60293
B	-17	SER	-	expression tag	UNP P60293

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-16	SER	-	expression tag	UNP P60293
B	-15	HIS	-	expression tag	UNP P60293
B	-14	HIS	-	expression tag	UNP P60293
B	-13	HIS	-	expression tag	UNP P60293
B	-12	HIS	-	expression tag	UNP P60293
B	-11	HIS	-	expression tag	UNP P60293
B	-10	HIS	-	expression tag	UNP P60293
B	-9	SER	-	expression tag	UNP P60293
B	-8	SER	-	expression tag	UNP P60293
B	-7	GLY	-	expression tag	UNP P60293
B	-6	LEU	-	expression tag	UNP P60293
B	-5	VAL	-	expression tag	UNP P60293
B	-4	PRO	-	expression tag	UNP P60293
B	-3	ARG	-	expression tag	UNP P60293
B	-2	GLY	-	expression tag	UNP P60293
B	-1	SER	-	expression tag	UNP P60293
B	0	HIS	-	expression tag	UNP P60293
X	-19	MET	-	expression tag	UNP P60293
X	-18	GLY	-	expression tag	UNP P60293
X	-17	SER	-	expression tag	UNP P60293
X	-16	SER	-	expression tag	UNP P60293
X	-15	HIS	-	expression tag	UNP P60293
X	-14	HIS	-	expression tag	UNP P60293
X	-13	HIS	-	expression tag	UNP P60293
X	-12	HIS	-	expression tag	UNP P60293
X	-11	HIS	-	expression tag	UNP P60293
X	-10	HIS	-	expression tag	UNP P60293
X	-9	SER	-	expression tag	UNP P60293
X	-8	SER	-	expression tag	UNP P60293
X	-7	GLY	-	expression tag	UNP P60293
X	-6	LEU	-	expression tag	UNP P60293
X	-5	VAL	-	expression tag	UNP P60293
X	-4	PRO	-	expression tag	UNP P60293
X	-3	ARG	-	expression tag	UNP P60293
X	-2	GLY	-	expression tag	UNP P60293
X	-1	SER	-	expression tag	UNP P60293
X	0	HIS	-	expression tag	UNP P60293

- Molecule 2 is a protein called Chromosome partition protein mukE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	G	204	Total	C	N	O	S	0	0	0
			1656	1049	295	304	8			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	191	Total	C	N	O	S	0	0	0
			1561	994	277	283	7			
2	D	203	Total	C	N	O	S	0	0	0
			1649	1045	294	302	8			
2	E	191	Total	C	N	O	S	0	0	0
			1562	995	276	284	7			
2	Y	205	Total	C	N	O	S	0	0	0
			1661	1052	296	305	8			
2	Z	188	Total	C	N	O	S	0	0	0
			1542	983	272	280	7			

There are 120 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	-10	MET	-	expression tag	UNP P22524
G	-9	GLY	-	expression tag	UNP P22524
G	-8	SER	-	expression tag	UNP P22524
G	-7	SER	-	expression tag	UNP P22524
G	-6	HIS	-	expression tag	UNP P22524
G	-5	HIS	-	expression tag	UNP P22524
G	-4	HIS	-	expression tag	UNP P22524
G	-3	HIS	-	expression tag	UNP P22524
G	-2	HIS	-	expression tag	UNP P22524
G	-1	HIS	-	expression tag	UNP P22524
G	0	SER	-	expression tag	UNP P22524
G	1	SER	-	expression tag	UNP P22524
G	2	GLY	-	expression tag	UNP P22524
G	3	LEU	-	expression tag	UNP P22524
G	4	VAL	-	expression tag	UNP P22524
G	5	PRO	-	expression tag	UNP P22524
G	6	ARG	-	expression tag	UNP P22524
G	7	GLY	-	expression tag	UNP P22524
G	8	SER	-	expression tag	UNP P22524
G	9	HIS	-	expression tag	UNP P22524
H	-10	MET	-	expression tag	UNP P22524
H	-9	GLY	-	expression tag	UNP P22524
H	-8	SER	-	expression tag	UNP P22524
H	-7	SER	-	expression tag	UNP P22524
H	-6	HIS	-	expression tag	UNP P22524
H	-5	HIS	-	expression tag	UNP P22524
H	-4	HIS	-	expression tag	UNP P22524
H	-3	HIS	-	expression tag	UNP P22524
H	-2	HIS	-	expression tag	UNP P22524

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Chain	Residue	Modelled	Actual	Comment	Reference
H	-1	HIS	-	expression tag	UNP P22524
H	0	SER	-	expression tag	UNP P22524
H	1	SER	-	expression tag	UNP P22524
H	2	GLY	-	expression tag	UNP P22524
H	3	LEU	-	expression tag	UNP P22524
H	4	VAL	-	expression tag	UNP P22524
H	5	PRO	-	expression tag	UNP P22524
H	6	ARG	-	expression tag	UNP P22524
H	7	GLY	-	expression tag	UNP P22524
H	8	SER	-	expression tag	UNP P22524
H	9	HIS	-	expression tag	UNP P22524
D	-10	MET	-	expression tag	UNP P22524
D	-9	GLY	-	expression tag	UNP P22524
D	-8	SER	-	expression tag	UNP P22524
D	-7	SER	-	expression tag	UNP P22524
D	-6	HIS	-	expression tag	UNP P22524
D	-5	HIS	-	expression tag	UNP P22524
D	-4	HIS	-	expression tag	UNP P22524
D	-3	HIS	-	expression tag	UNP P22524
D	-2	HIS	-	expression tag	UNP P22524
D	-1	HIS	-	expression tag	UNP P22524
D	0	SER	-	expression tag	UNP P22524
D	1	SER	-	expression tag	UNP P22524
D	2	GLY	-	expression tag	UNP P22524
D	3	LEU	-	expression tag	UNP P22524
D	4	VAL	-	expression tag	UNP P22524
D	5	PRO	-	expression tag	UNP P22524
D	6	ARG	-	expression tag	UNP P22524
D	7	GLY	-	expression tag	UNP P22524
D	8	SER	-	expression tag	UNP P22524
D	9	HIS	-	expression tag	UNP P22524
E	-10	MET	-	expression tag	UNP P22524
E	-9	GLY	-	expression tag	UNP P22524
E	-8	SER	-	expression tag	UNP P22524
E	-7	SER	-	expression tag	UNP P22524
E	-6	HIS	-	expression tag	UNP P22524
E	-5	HIS	-	expression tag	UNP P22524
E	-4	HIS	-	expression tag	UNP P22524
E	-3	HIS	-	expression tag	UNP P22524
E	-2	HIS	-	expression tag	UNP P22524
E	-1	HIS	-	expression tag	UNP P22524
E	0	SER	-	expression tag	UNP P22524

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Chain	Residue	Modelled	Actual	Comment	Reference
E	1	SER	-	expression tag	UNP P22524
E	2	GLY	-	expression tag	UNP P22524
E	3	LEU	-	expression tag	UNP P22524
E	4	VAL	-	expression tag	UNP P22524
E	5	PRO	-	expression tag	UNP P22524
E	6	ARG	-	expression tag	UNP P22524
E	7	GLY	-	expression tag	UNP P22524
E	8	SER	-	expression tag	UNP P22524
E	9	HIS	-	expression tag	UNP P22524
Y	-10	MET	-	expression tag	UNP P22524
Y	-9	GLY	-	expression tag	UNP P22524
Y	-8	SER	-	expression tag	UNP P22524
Y	-7	SER	-	expression tag	UNP P22524
Y	-6	HIS	-	expression tag	UNP P22524
Y	-5	HIS	-	expression tag	UNP P22524
Y	-4	HIS	-	expression tag	UNP P22524
Y	-3	HIS	-	expression tag	UNP P22524
Y	-2	HIS	-	expression tag	UNP P22524
Y	-1	HIS	-	expression tag	UNP P22524
Y	0	SER	-	expression tag	UNP P22524
Y	1	SER	-	expression tag	UNP P22524
Y	2	GLY	-	expression tag	UNP P22524
Y	3	LEU	-	expression tag	UNP P22524
Y	4	VAL	-	expression tag	UNP P22524
Y	5	PRO	-	expression tag	UNP P22524
Y	6	ARG	-	expression tag	UNP P22524
Y	7	GLY	-	expression tag	UNP P22524
Y	8	SER	-	expression tag	UNP P22524
Y	9	HIS	-	expression tag	UNP P22524
Z	-10	MET	-	expression tag	UNP P22524
Z	-9	GLY	-	expression tag	UNP P22524
Z	-8	SER	-	expression tag	UNP P22524
Z	-7	SER	-	expression tag	UNP P22524
Z	-6	HIS	-	expression tag	UNP P22524
Z	-5	HIS	-	expression tag	UNP P22524
Z	-4	HIS	-	expression tag	UNP P22524
Z	-3	HIS	-	expression tag	UNP P22524
Z	-2	HIS	-	expression tag	UNP P22524
Z	-1	HIS	-	expression tag	UNP P22524
Z	0	SER	-	expression tag	UNP P22524
Z	1	SER	-	expression tag	UNP P22524
Z	2	GLY	-	expression tag	UNP P22524

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Chain	Residue	Modelled	Actual	Comment	Reference
Z	3	LEU	-	expression tag	UNP P22524
Z	4	VAL	-	expression tag	UNP P22524
Z	5	PRO	-	expression tag	UNP P22524
Z	6	ARG	-	expression tag	UNP P22524
Z	7	GLY	-	expression tag	UNP P22524
Z	8	SER	-	expression tag	UNP P22524
Z	9	HIS	-	expression tag	UNP P22524

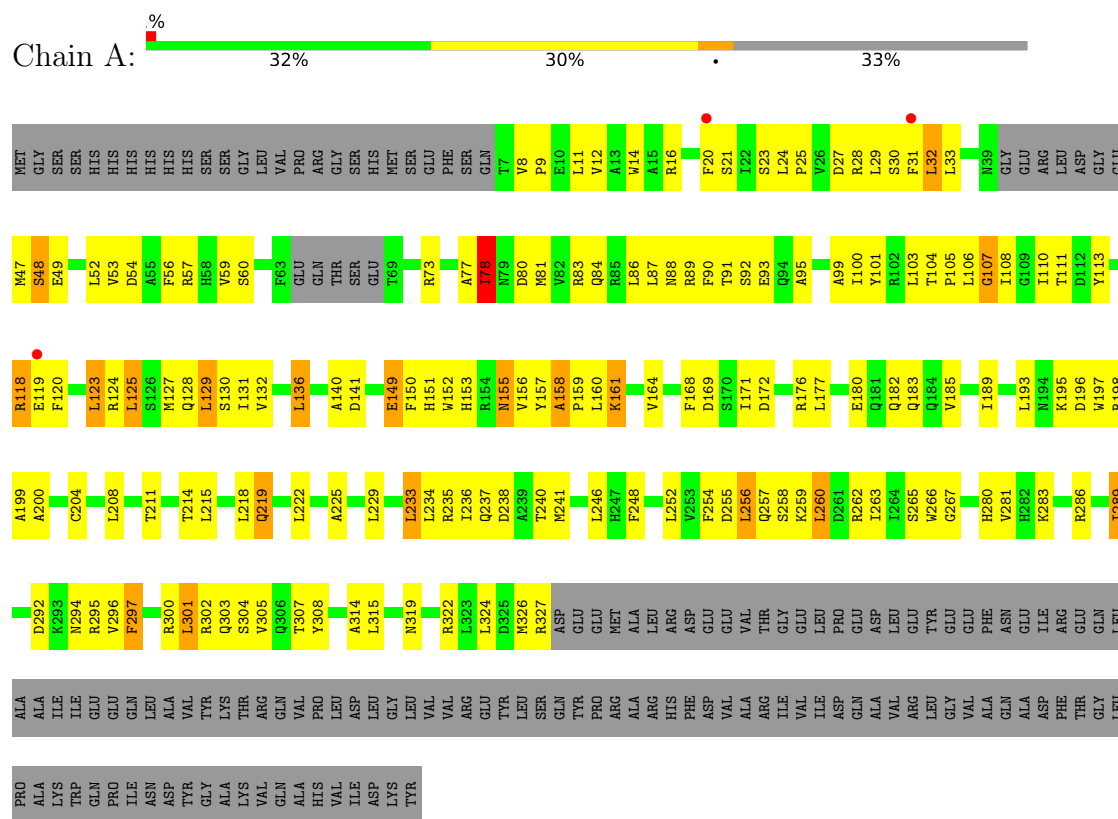
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	G	1	Total O 1 1	0	0
3	Y	1	Total O 1 1	0	0

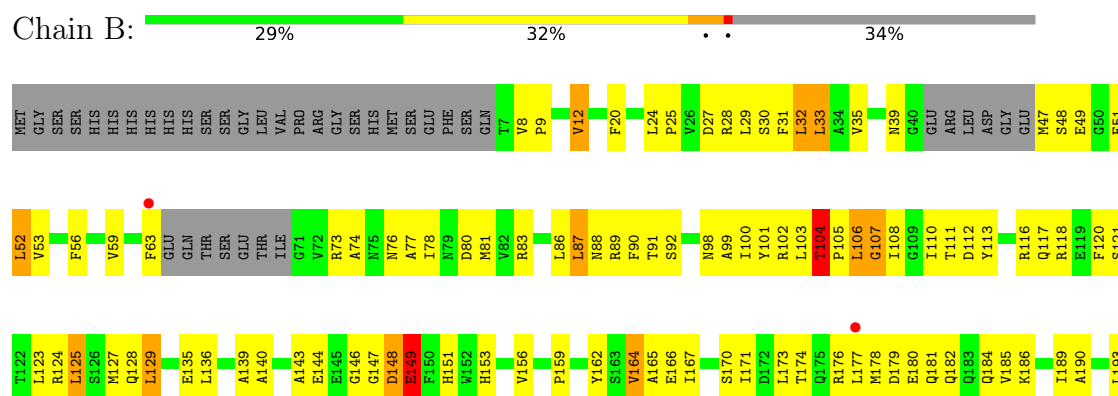
3 Residue-property plots

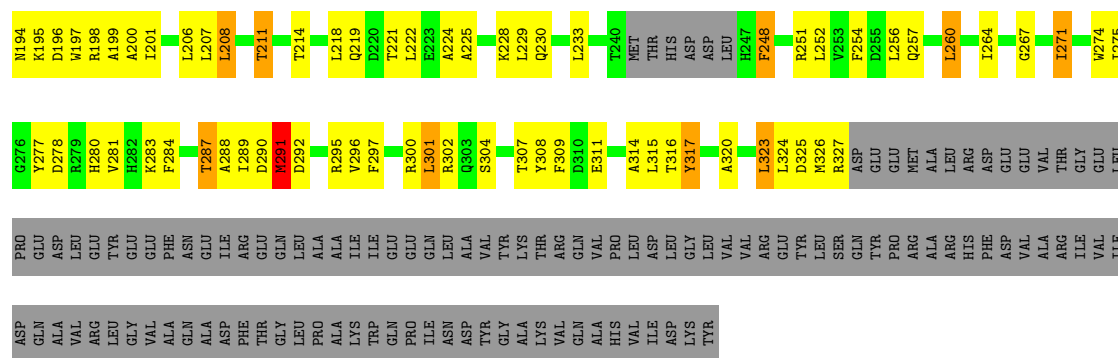
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Chromosome partition protein mukF

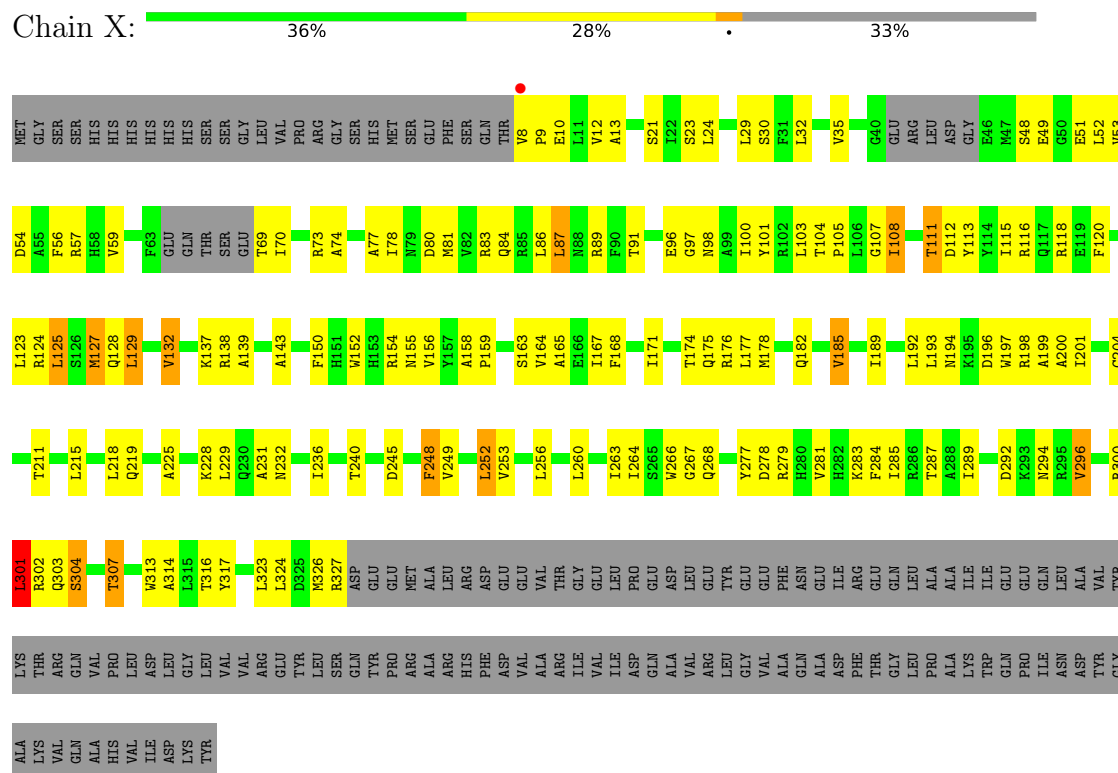


• Molecule 1: Chromosome partition protein mukF

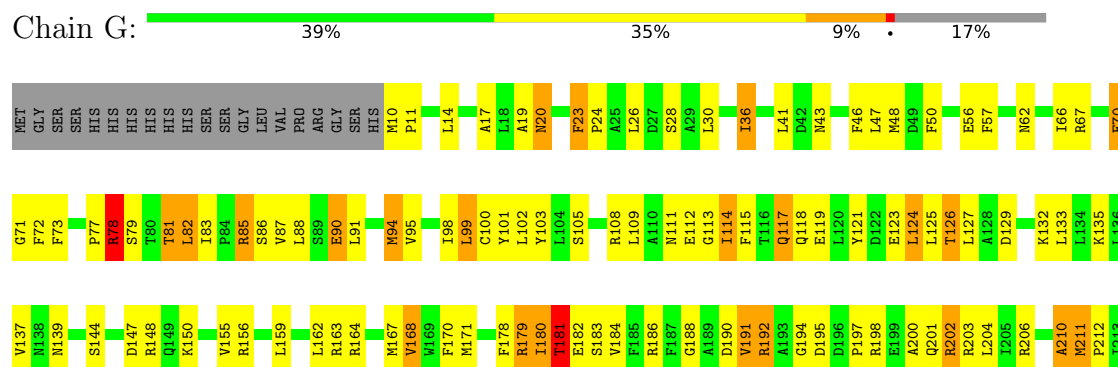




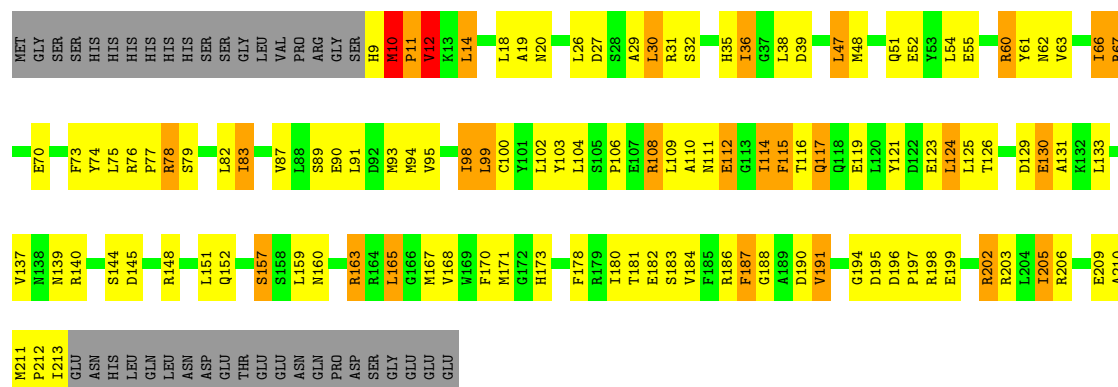
• Molecule 1: Chromosome partition protein mukF



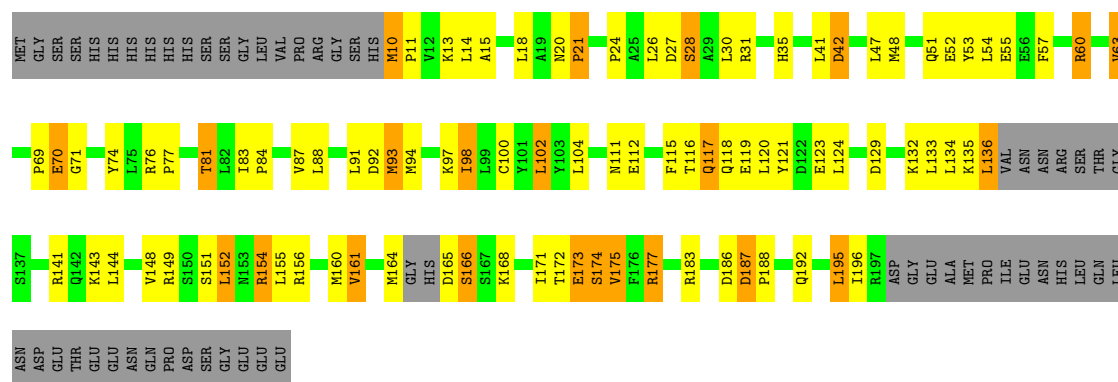
• Molecule 2: Chromosome partition protein mukE



Chain Y: 36% 36% 11% 16%



Chain Z: 39% 29% 9% 23%



4 Data and refinement statistics

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, α , β , γ	149.89Å 149.89Å 738.55Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	19.98 – 3.60 19.98 – 3.60	Depositor EDS
% Data completeness (in resolution range)	98.4 (19.98-3.60) 97.7 (19.98-3.60)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.09 (at 3.62Å)	Xtrriage
Refinement program	PHENIX (phenix.refine: 1.7_650)	Depositor
R, R_{free}	0.217 , 0.274 0.209 , 0.268	Depositor DCC
R_{free} test set	2896 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å ²)	105.8	Xtrriage
Anisotropy	0.481	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 78.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	17083	wwPDB-VP
Average B, all atoms (Å ²)	129.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.82% 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

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	0.85	1/2545 (0.0%)	1.22	10/3442 (0.3%)
1	B	0.74	0/2483	1.09	11/3355 (0.3%)
1	X	0.78	0/2546	1.21	15/3443 (0.4%)
2	D	0.90	2/1679 (0.1%)	1.35	18/2260 (0.8%)
2	E	0.82	0/1589	1.19	13/2138 (0.6%)
2	G	0.85	0/1687	1.28	19/2273 (0.8%)
2	H	0.78	0/1590	1.16	8/2140 (0.4%)
2	Y	1.00	3/1692 (0.2%)	1.44	19/2280 (0.8%)
2	Z	0.91	0/1569	1.27	15/2110 (0.7%)
All	All	0.84	6/17380 (0.0%)	1.24	128/23441 (0.5%)

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
2	Y	0	1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	78	ILE	CA-CB	6.27	1.61	1.54
2	Y	191	VAL	CA-CB	-5.71	1.48	1.54
2	D	209	ALA	CA-CB	-5.29	1.46	1.53
2	D	36	ILE	CA-CB	-5.06	1.48	1.53
2	Y	104	LEU	CA-C	5.05	1.59	1.52

The worst 5 of 128 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	Y	76	ARG	CA-C-N	15.44	136.46	119.93
2	Y	76	ARG	C-N-CA	15.44	136.46	119.93

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	Y	10	MET	CA-C-N	11.92	132.05	119.89
2	Y	10	MET	C-N-CA	11.92	132.05	119.89
1	A	158	ALA	CA-C-N	-9.69	109.67	119.56

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	Y	194	GLY	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	2503	0	2463	202	0
1	B	2443	0	2405	234	0
1	X	2504	0	2453	131	0
2	D	1649	0	1652	152	0
2	E	1562	0	1571	97	0
2	G	1656	0	1660	108	0
2	H	1561	0	1567	87	0
2	Y	1661	0	1662	124	0
2	Z	1542	0	1554	81	0
3	G	1	0	0	0	0
3	Y	1	0	0	0	0
All	All	17083	0	16987	1102	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 32.

The worst 5 of 1102 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:281:VAL:HG22	2:G:109:LEU:HD22	1.28	1.15
2:Y:10:MET:HE2	2:Y:14:LEU:HD13	1.24	1.13

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:118:ARG:HB3	1:X:177:LEU:HD21	1.12	1.11
1:B:300:ARG:HH22	2:D:193:GLY:HA2	1.06	1.10
2:Y:167:MET:HE2	2:Y:187:PHE:CE2	1.86	1.09

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	303/460 (66%)	284 (94%)	19 (6%)	0	100	100
1	B	294/460 (64%)	277 (94%)	17 (6%)	0	100	100
1	X	304/460 (66%)	286 (94%)	18 (6%)	0	100	100
2	D	199/245 (81%)	190 (96%)	8 (4%)	1 (0%)	24	57
2	E	185/245 (76%)	167 (90%)	17 (9%)	1 (0%)	24	57
2	G	202/245 (82%)	189 (94%)	11 (5%)	2 (1%)	12	45
2	H	187/245 (76%)	181 (97%)	6 (3%)	0	100	100
2	Y	203/245 (83%)	191 (94%)	12 (6%)	0	100	100
2	Z	182/245 (74%)	171 (94%)	11 (6%)	0	100	100
All	All	2059/2850 (72%)	1936 (94%)	119 (6%)	4 (0%)	43	72

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	126	THR
2	E	131	ALA
2	G	126	THR
2	G	137	VAL

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	268/397 (68%)	252 (94%)	16 (6%)	17	45
1	B	260/397 (66%)	235 (90%)	25 (10%)	8	32
1	X	266/397 (67%)	247 (93%)	19 (7%)	13	40
2	D	177/215 (82%)	152 (86%)	25 (14%)	3	19
2	E	168/215 (78%)	155 (92%)	13 (8%)	12	38
2	G	178/215 (83%)	156 (88%)	22 (12%)	4	23
2	H	167/215 (78%)	156 (93%)	11 (7%)	15	43
2	Y	178/215 (83%)	143 (80%)	35 (20%)	1	8
2	Z	166/215 (77%)	141 (85%)	25 (15%)	3	17
All	All	1828/2481 (74%)	1637 (90%)	191 (10%)	7	29

5 of 191 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	X	69	THR
2	Y	79	SER
1	X	125	LEU
1	X	307	THR
2	Y	112	GLU

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

Mol	Chain	Res	Type
2	E	117	GLN
2	Y	117	GLN
1	X	219	GLN
1	B	128	GLN
2	E	35	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 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, 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	309/460 (67%)	-0.22	3 (0%) 79 54	75, 131, 215, 275	0
1	B	302/460 (65%)	-0.23	2 (0%) 84 61	81, 149, 217, 294	0
1	X	310/460 (67%)	-0.23	1 (0%) 90 75	61, 141, 209, 280	0
2	D	203/245 (82%)	-0.40	3 (1%) 72 44	73, 113, 175, 222	0
2	E	191/245 (77%)	-0.44	0 100 100	72, 110, 184, 244	0
2	G	204/245 (83%)	-0.51	0 100 100	75, 110, 178, 217	0
2	H	191/245 (77%)	-0.51	0 100 100	79, 111, 171, 222	0
2	Y	205/245 (83%)	-0.51	0 100 100	57, 94, 168, 205	0
2	Z	188/245 (76%)	-0.45	0 100 100	64, 108, 169, 264	0
All	All	2103/2850 (73%)	-0.36	9 (0%) 88 70	57, 123, 200, 294	0

The worst 5 of 9 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	119	GLU	3.6
2	D	110	ALA	2.9
2	D	141	SER	2.8
1	A	31	PHE	2.6
1	B	177	LEU	2.5

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.