



wwPDB X-ray Structure Validation Summary Report

Feb 27, 2014 – 08:28 AM GMT

PDB ID : 2CEA
Title : CELL DIVISION PROTEIN FTSH
Authors : Bieniossek, C.; Baumann, U.
Deposited on : 2006-02-03
Resolution : 2.75 Å(reported)

This is a wwPDB validation summary report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

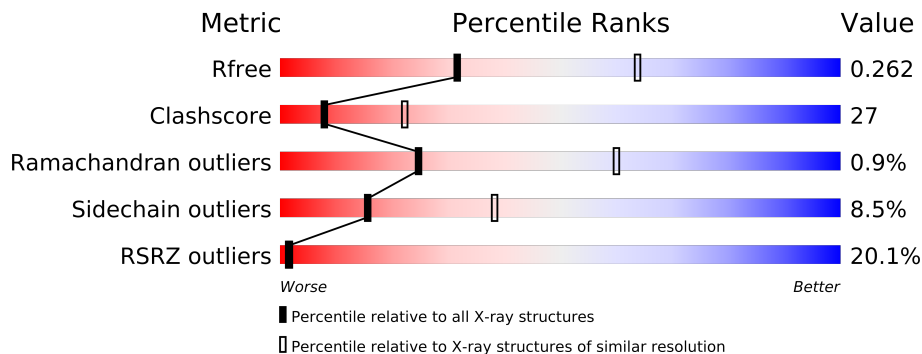
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.75 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}	66092	2406 (2.80-2.72)
Clashscore	79885	2995 (2.80-2.72)
Ramachandran outliers	78287	2941 (2.80-2.72)
Sidechain outliers	78261	2944 (2.80-2.72)
RSRZ outliers	66119	2409 (2.80-2.72)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	476	
1	B	476	
1	C	476	
1	D	476	
1	E	476	
1	F	476	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 19564 atoms, of which 0 are hydrogen and 0 are deuterium.

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 CELL DIVISION PROTEIN FTSH.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	407	Total	C	N	O	S	0	0	1
			3160	1996	559	595	10			
1	B	411	Total	C	N	O	S	0	0	0
			3191	2017	560	604	10			
1	C	421	Total	C	N	O	S	0	0	0
			3280	2076	573	621	10			
1	D	413	Total	C	N	O	S	0	0	0
			3212	2032	562	608	10			
1	E	406	Total	C	N	O	S	0	0	1
			3144	1986	557	591	10			
1	F	412	Total	C	N	O	S	0	0	0
			3204	2024	564	606	10			

There are 82 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	146	MET	-	EXPRESSION TAG	UNP Q9WZ49
A	611	ALA	-	EXPRESSION TAG	UNP Q9WZ49
A	612	ALA	-	EXPRESSION TAG	UNP Q9WZ49
A	613	ALA	-	EXPRESSION TAG	UNP Q9WZ49
A	614	LEU	-	EXPRESSION TAG	UNP Q9WZ49
A	615	GLU	-	EXPRESSION TAG	UNP Q9WZ49
A	616	HIS	-	EXPRESSION TAG	UNP Q9WZ49
A	617	HIS	-	EXPRESSION TAG	UNP Q9WZ49
A	618	HIS	-	EXPRESSION TAG	UNP Q9WZ49
A	619	HIS	-	EXPRESSION TAG	UNP Q9WZ49
A	620	HIS	-	EXPRESSION TAG	UNP Q9WZ49
A	621	HIS	-	EXPRESSION TAG	UNP Q9WZ49
A	410	LEU	LYS	ENGINEERED MUTATION	UNP Q9WZ49
A	415	ALA	LYS	ENGINEERED MUTATION	UNP Q9WZ49
B	146	MET	-	EXPRESSION TAG	UNP Q9WZ49
B	611	ALA	-	EXPRESSION TAG	UNP Q9WZ49
B	612	ALA	-	EXPRESSION TAG	UNP Q9WZ49

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	613	ALA	-	EXPRESSION TAG	UNP Q9WZ49
B	614	LEU	-	EXPRESSION TAG	UNP Q9WZ49
B	615	GLU	-	EXPRESSION TAG	UNP Q9WZ49
B	616	HIS	-	EXPRESSION TAG	UNP Q9WZ49
B	617	HIS	-	EXPRESSION TAG	UNP Q9WZ49
B	618	HIS	-	EXPRESSION TAG	UNP Q9WZ49
B	619	HIS	-	EXPRESSION TAG	UNP Q9WZ49
B	620	HIS	-	EXPRESSION TAG	UNP Q9WZ49
B	621	HIS	-	EXPRESSION TAG	UNP Q9WZ49
B	410	LEU	LYS	ENGINEERED MUTATION	UNP Q9WZ49
B	415	ALA	LYS	ENGINEERED MUTATION	UNP Q9WZ49
C	146	MET	-	EXPRESSION TAG	UNP Q9WZ49
C	611	ALA	-	EXPRESSION TAG	UNP Q9WZ49
C	612	ALA	-	EXPRESSION TAG	UNP Q9WZ49
C	613	ALA	-	EXPRESSION TAG	UNP Q9WZ49
C	614	LEU	-	EXPRESSION TAG	UNP Q9WZ49
C	615	GLU	-	EXPRESSION TAG	UNP Q9WZ49
C	616	HIS	-	EXPRESSION TAG	UNP Q9WZ49
C	617	HIS	-	EXPRESSION TAG	UNP Q9WZ49
C	618	HIS	-	EXPRESSION TAG	UNP Q9WZ49
C	619	HIS	-	EXPRESSION TAG	UNP Q9WZ49
C	620	HIS	-	EXPRESSION TAG	UNP Q9WZ49
C	621	HIS	-	EXPRESSION TAG	UNP Q9WZ49
C	410	LEU	LYS	ENGINEERED MUTATION	UNP Q9WZ49
C	415	ALA	LYS	ENGINEERED MUTATION	UNP Q9WZ49
D	146	MET	-	EXPRESSION TAG	UNP Q9WZ49
D	611	ALA	-	EXPRESSION TAG	UNP Q9WZ49
D	612	ALA	-	EXPRESSION TAG	UNP Q9WZ49
D	613	ALA	-	EXPRESSION TAG	UNP Q9WZ49
D	614	LEU	-	EXPRESSION TAG	UNP Q9WZ49
D	615	GLU	-	EXPRESSION TAG	UNP Q9WZ49
D	616	HIS	-	EXPRESSION TAG	UNP Q9WZ49
D	617	HIS	-	EXPRESSION TAG	UNP Q9WZ49
D	618	HIS	-	EXPRESSION TAG	UNP Q9WZ49
D	619	HIS	-	EXPRESSION TAG	UNP Q9WZ49
D	620	HIS	-	EXPRESSION TAG	UNP Q9WZ49
D	621	HIS	-	EXPRESSION TAG	UNP Q9WZ49
D	410	LEU	LYS	ENGINEERED MUTATION	UNP Q9WZ49
D	415	ALA	LYS	ENGINEERED MUTATION	UNP Q9WZ49
E	146	MET	-	EXPRESSION TAG	UNP Q9WZ49
E	611	ALA	-	EXPRESSION TAG	UNP Q9WZ49
E	612	ALA	-	EXPRESSION TAG	UNP Q9WZ49

Continued on next page...

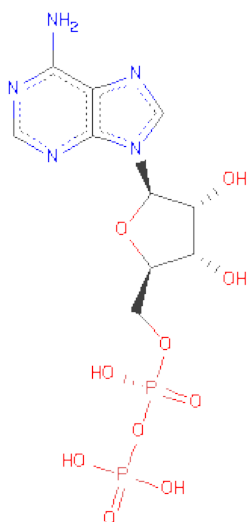
Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
E	613	ALA	-	EXPRESSION TAG	UNP Q9WZ49
E	614	LEU	-	EXPRESSION TAG	UNP Q9WZ49
E	615	GLU	-	EXPRESSION TAG	UNP Q9WZ49
E	616	HIS	-	EXPRESSION TAG	UNP Q9WZ49
E	617	HIS	-	EXPRESSION TAG	UNP Q9WZ49
E	618	HIS	-	EXPRESSION TAG	UNP Q9WZ49
E	619	HIS	-	EXPRESSION TAG	UNP Q9WZ49
E	620	HIS	-	EXPRESSION TAG	UNP Q9WZ49
E	621	HIS	-	EXPRESSION TAG	UNP Q9WZ49
E	410	LEU	LYS	ENGINEERED MUTATION	UNP Q9WZ49
E	415	ALA	LYS	ENGINEERED MUTATION	UNP Q9WZ49
F	146	MET	-	EXPRESSION TAG	UNP Q9WZ49
F	611	ALA	-	EXPRESSION TAG	UNP Q9WZ49
F	612	ALA	-	EXPRESSION TAG	UNP Q9WZ49
F	613	ALA	-	EXPRESSION TAG	UNP Q9WZ49
F	614	LEU	-	EXPRESSION TAG	UNP Q9WZ49
F	615	GLU	-	EXPRESSION TAG	UNP Q9WZ49
F	616	HIS	-	EXPRESSION TAG	UNP Q9WZ49
F	617	HIS	-	EXPRESSION TAG	UNP Q9WZ49
F	618	HIS	-	EXPRESSION TAG	UNP Q9WZ49
F	619	HIS	-	EXPRESSION TAG	UNP Q9WZ49
F	620	HIS	-	EXPRESSION TAG	UNP Q9WZ49
F	621	HIS	-	EXPRESSION TAG	UNP Q9WZ49

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	D	1	Total Zn 1 1	0	0
2	E	1	Total Zn 1 1	0	0
2	B	1	Total Zn 1 1	0	0
2	C	1	Total Zn 1 1	0	0
2	A	1	Total Zn 1 1	0	0
2	F	1	Total Zn 1 1	0	0

- Molecule 3 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	B	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	C	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	D	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	E	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	F	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	D	1	Total	Mg	0	0
			1	1		
4	E	1	Total	Mg	0	0
			1	1		
4	B	1	Total	Mg	0	0
			1	1		
4	C	1	Total	Mg	0	0
			1	1		
4	A	1	Total	Mg	0	0
			1	1		
4	F	1	Total	Mg	0	0
			1	1		

- Molecule 5 is water.

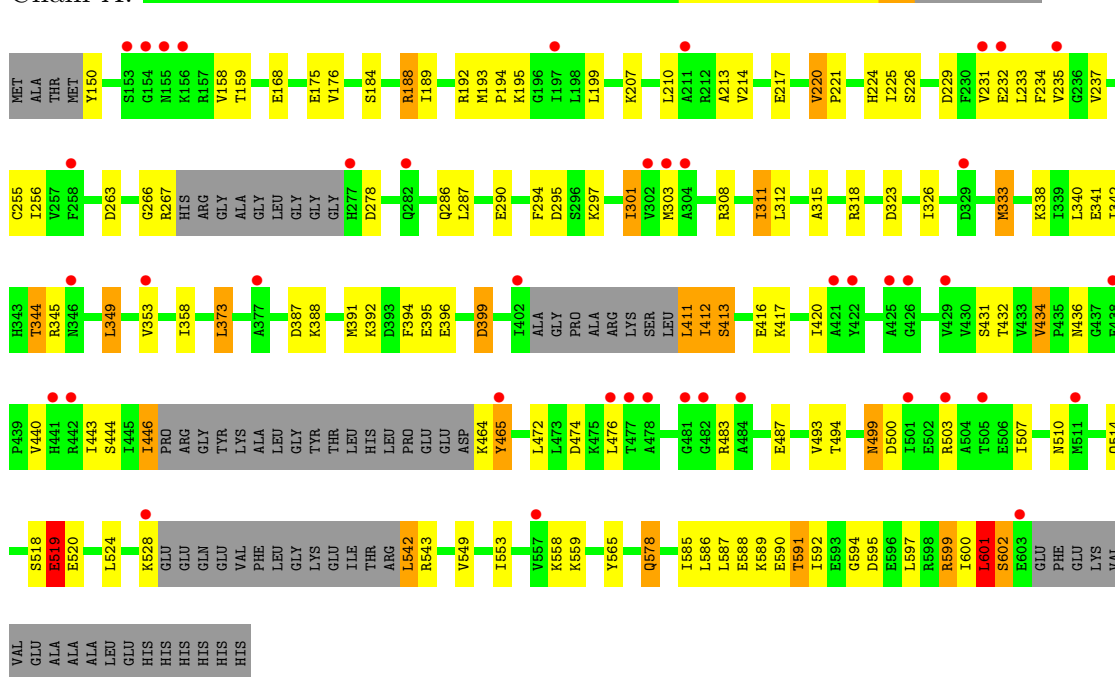
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	46	Total 46	O 46	0	0
5	B	35	Total 35	O 35	0	0
5	C	26	Total 26	O 26	0	0
5	D	34	Total 34	O 34	0	0
5	E	34	Total 34	O 34	0	0
5	F	24	Total 24	O 24	0	0

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

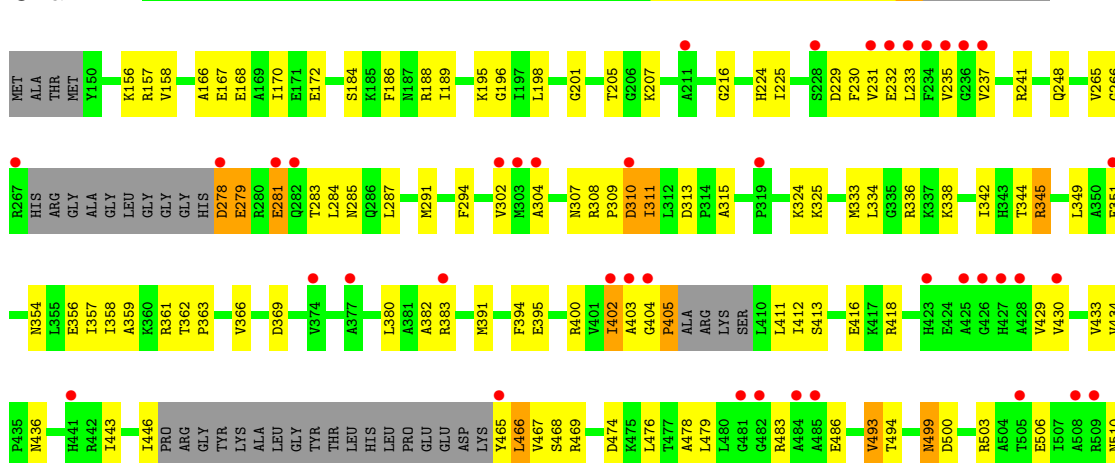
• Molecule 1: CELL DIVISION PROTEIN FTSH

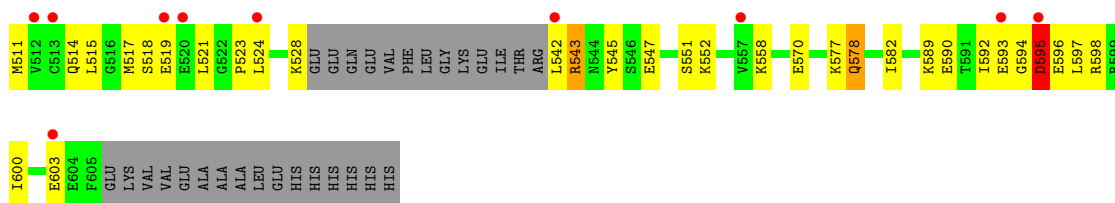
Chain A:



• Molecule 1: CELL DIVISION PROTEIN FTSH

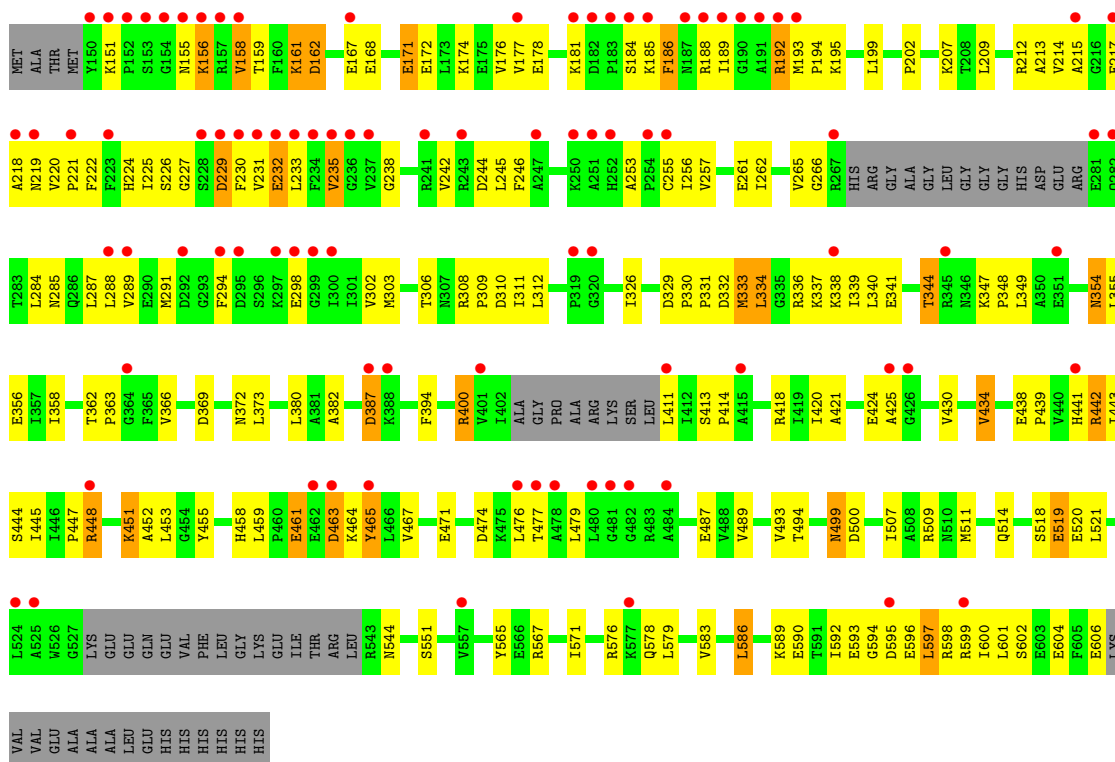
Chain B:





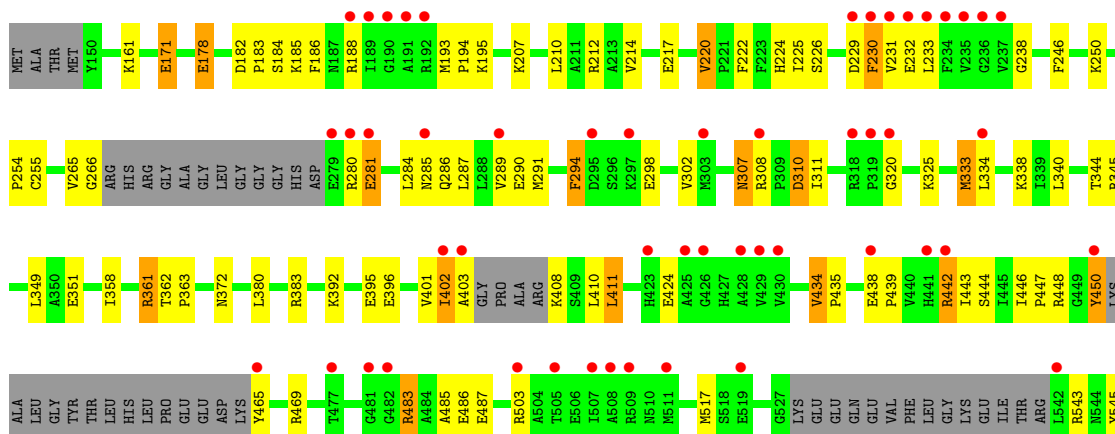
• Molecule 1: CELL DIVISION PROTEIN FTSH

Chain C:



• Molecule 1: CELL DIVISION PROTEIN FTSH

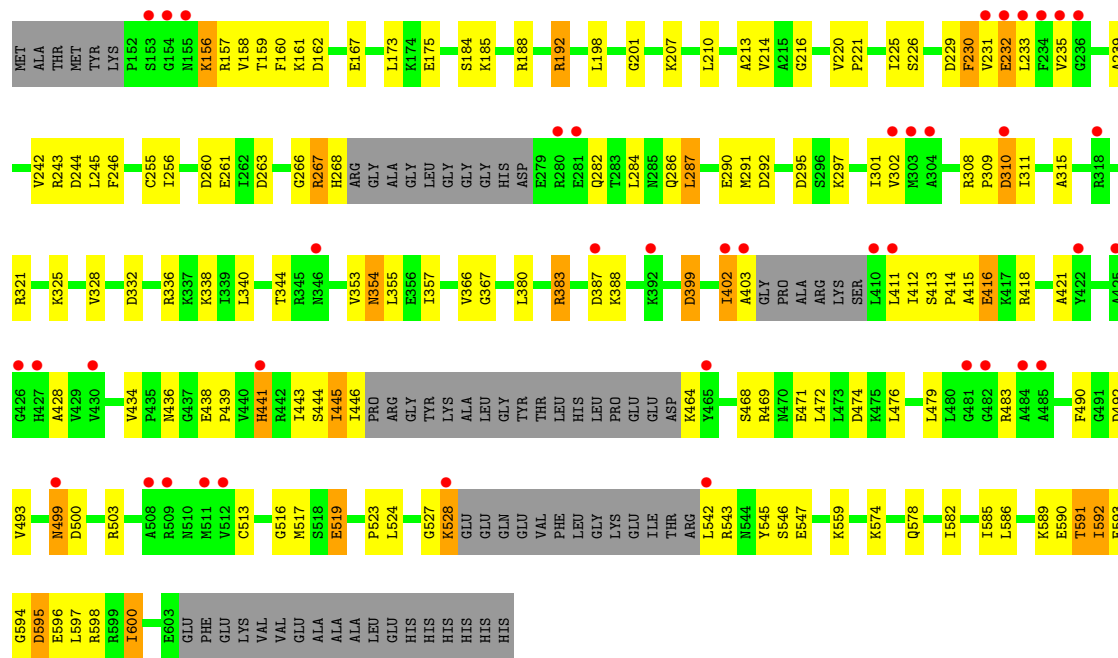
Chain D:





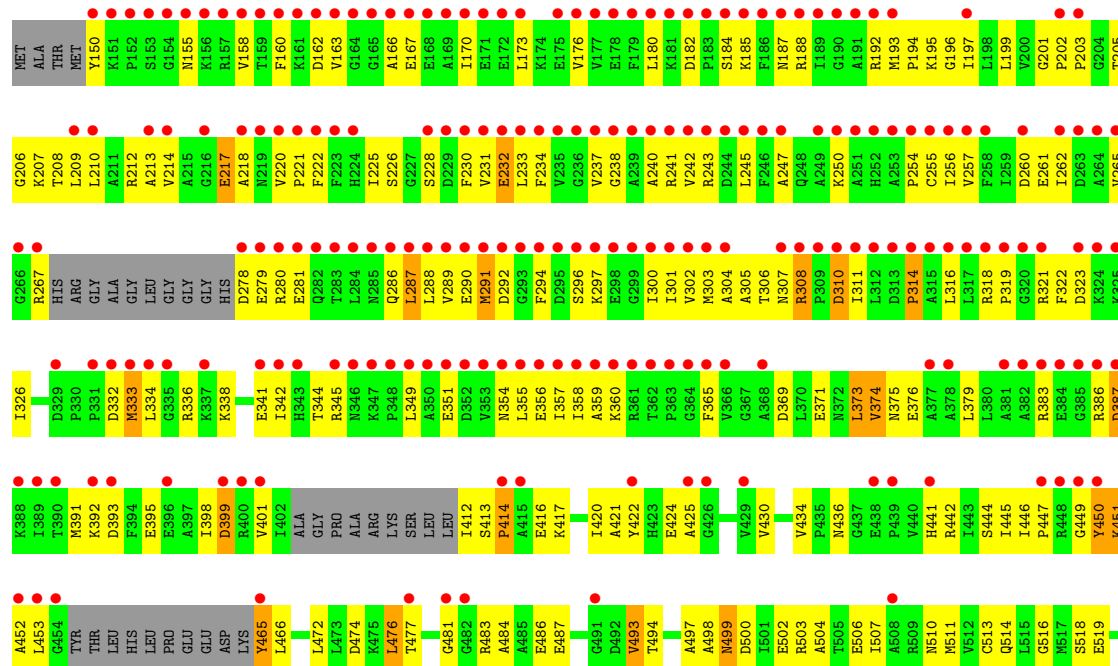
• Molecule 1: CELL DIVISION PROTEIN FTSH

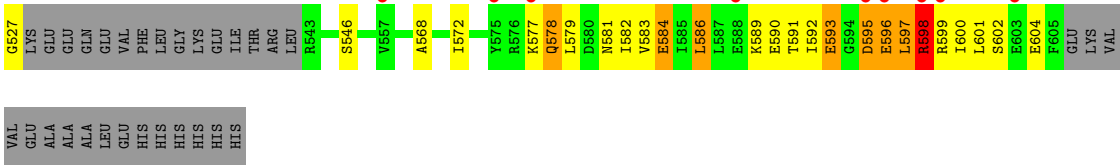
Chain E:



• Molecule 1: CELL DIVISION PROTEIN FTSH

Chain F:





4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	165.32Å 165.32Å 234.75Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	25.00 – 2.75 19.98 – 2.75	Depositor EDS
% Data completeness (in resolution range)	100.0 (25.00-2.75) 97.7 (19.98-2.75)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.15 (at 2.75Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.216 , 0.262 0.216 , 0.262	Depositor DCC
R_{free} test set	1283 reflections (1.58%)	DCC
Wilson B-factor (Å ²)	56.7	Xtriage
Anisotropy	0.047	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 24.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtriage
Outliers	0 of 82694 reflections	Xtriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	19564	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.25% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	0.79	2/3202 (0.1%)	0.57	0/4314
1	B	0.76	2/3233 (0.1%)	0.56	1/4356 (0.0%)
1	C	0.59	0/3328	0.49	0/4488
1	D	0.68	0/3256	0.52	0/4388
1	E	0.72	1/3185 (0.0%)	0.54	0/4291
1	F	0.55	1/3248 (0.0%)	0.47	0/4376
All	All	0.68	6/19452 (0.0%)	0.53	1/26213 (0.0%)

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	513	CYS	CB-SG	-7.17	1.70	1.82
1	A	519	GLU	CG-CD	6.13	1.61	1.51
1	F	513	CYS	CB-SG	-6.08	1.72	1.82
1	B	506	GLU	CG-CD	5.75	1.60	1.51
1	B	172	GLU	CG-CD	5.48	1.60	1.51

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	405	PRO	N-CA-CB	6.36	110.93	103.30

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens

added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3160	0	3240	119	0
1	B	3191	0	3261	143	0
1	C	3280	0	3346	199	0
1	D	3212	0	3283	121	0
1	E	3144	0	3231	172	0
1	F	3204	0	3270	301	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
3	A	27	0	12	1	0
3	B	27	0	12	7	0
3	C	27	0	12	10	0
3	D	27	0	12	6	0
3	E	27	0	12	7	0
3	F	27	0	12	5	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
4	E	1	0	0	0	0
4	F	1	0	0	0	0
5	A	46	0	0	5	0
5	B	35	0	0	13	0
5	C	26	0	0	9	0
5	D	34	0	0	11	0
5	E	34	0	0	6	0
5	F	24	0	0	9	0
All	All	19564	0	19703	1053	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 27.

The worst 5 of 1053 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:519:GLU:HA	5:C:2018:HOH:O	1.15	1.27

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:E:231:VAL:HG12	1:E:232:GLU:OE2	1.11	1.27
1:E:231:VAL:CG1	1:E:232:GLU:OE2	1.84	1.24
1:C:340:LEU:O	1:C:344:THR:HG22	1.38	1.20
1:C:594:GLY:N	5:C:2024:HOH:O	1.74	1.19

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	397/476 (83%)	379 (96%)	13 (3%)	5 (1%)	18	47
1	B	401/476 (84%)	378 (94%)	20 (5%)	3 (1%)	30	67
1	C	413/476 (87%)	393 (95%)	18 (4%)	2 (0%)	38	74
1	D	403/476 (85%)	383 (95%)	19 (5%)	1 (0%)	56	87
1	E	396/476 (83%)	376 (95%)	13 (3%)	7 (2%)	13	36
1	F	402/476 (84%)	372 (92%)	26 (6%)	4 (1%)	22	56
All	All	2412/2856 (84%)	2281 (95%)	109 (4%)	22 (1%)	25	60

5 of 22 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	465	TYR
1	A	602	SER
1	B	595	ASP
1	D	402	ILE
1	F	450	TYR

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	337/390 (86%)	308 (91%)	29 (9%)	15	37
1	B	339/390 (87%)	317 (94%)	22 (6%)	24	54
1	C	349/390 (90%)	312 (89%)	37 (11%)	10	25
1	D	342/390 (88%)	318 (93%)	24 (7%)	21	49
1	E	335/390 (86%)	308 (92%)	27 (8%)	17	41
1	F	340/390 (87%)	305 (90%)	35 (10%)	10	27
All	All	2042/2340 (87%)	1868 (92%)	174 (8%)	15	38

5 of 174 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	476	LEU
1	D	310	ASP
1	F	487	GLU
1	C	514	GLN
1	D	171	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 32 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	307	ASN
1	D	510	ASN
1	F	510	ASN
1	D	499	ASN
1	D	578	GLN

5.3.3 RNA ⓘ

There are no RNA chains 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 carbohydrates in this entry.

5.6 Ligand geometry

Of 18 ligands modelled in this entry, 12 are monoatomic - leaving 6 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$
3	ADP	A	1604	4	29,29,29	1.10	3 (10%)	45,45,45	2.00	10 (22%)
3	ADP	B	1607	4	29,29,29	1.43	3 (10%)	45,45,45	1.96	9 (20%)
3	ADP	C	1608	4	29,29,29	1.11	2 (6%)	45,45,45	1.87	8 (17%)
3	ADP	D	1608	4	29,29,29	1.36	4 (13%)	45,45,45	1.93	9 (20%)
3	ADP	E	1604	4	29,29,29	1.12	2 (6%)	45,45,45	2.07	9 (20%)
3	ADP	F	1607	4	29,29,29	1.12	3 (10%)	45,45,45	1.88	9 (20%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	ADP	A	1604	4	-	0/16/32/32	0/1/3/3
3	ADP	B	1607	4	-	0/16/32/32	0/1/3/3
3	ADP	C	1608	4	-	0/16/32/32	0/1/3/3
3	ADP	D	1608	4	-	0/16/32/32	0/1/3/3
3	ADP	E	1604	4	-	0/16/32/32	0/1/3/3
3	ADP	F	1607	4	-	0/16/32/32	0/1/3/3

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1607	ADP	C4-N9	-4.82	1.30	1.37
3	D	1608	ADP	C4-N9	-4.08	1.31	1.37

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	1604	ADP	C4-N9	-3.28	1.33	1.37
3	A	1604	ADP	C5-C4	2.73	1.46	1.40
3	C	1608	ADP	C5-C4	2.72	1.46	1.40

The worst 5 of 54 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	1608	ADP	N3-C2-N1	-7.35	122.57	128.71
3	A	1604	ADP	N3-C2-N1	-7.15	122.73	128.71
3	B	1607	ADP	N3-C2-N1	-7.13	122.75	128.71
3	C	1608	ADP	N3-C2-N1	-7.12	122.76	128.71
3	F	1607	ADP	N3-C2-N1	-6.92	122.92	128.71

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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(Å ²)	Q<0.9
1	A	407/476 (85%)	0.79	42 (10%) 7 6	35, 44, 54, 66	0
1	B	411/476 (86%)	0.81	50 (12%) 5 4	34, 44, 54, 74	0
1	C	421/476 (88%)	1.26	90 (21%) 1 1	36, 43, 57, 86	0
1	D	413/476 (86%)	0.88	54 (13%) 4 4	35, 44, 56, 78	0
1	E	406/476 (85%)	0.79	41 (10%) 7 7	35, 44, 55, 84	0
1	F	412/476 (86%)	2.72	222 (53%) 0 0	34, 43, 56, 90	0
All	All	2470/2856 (86%)	1.21	499 (20%) 2 1	34, 43, 55, 90	0

The worst 5 of 499 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	230	PHE	13.8
1	F	235	VAL	12.9
1	F	245	LEU	12.7
1	C	235	VAL	10.4
1	F	236	GLY	9.6

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 carbohydrates in this entry.

6.4 Ligands ⓘ

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	RSR	LLDF	B-factors(Å ²)	Q<0.9
4	MG	F	1608	1/1	0.29	0.09	68,68,68,68	0
3	ADP	C	1608	27/27	0.17	-0.41	54,57,59,61	0
4	MG	A	1605	1/1	0.19	-0.62	47,47,47,47	0
4	MG	C	1609	1/1	0.12	-0.96	60,60,60,60	0
3	ADP	E	1604	27/27	0.15	-1.16	34,38,42,48	0
3	ADP	A	1604	27/27	0.15	-1.33	32,34,39,41	0
3	ADP	F	1607	27/27	0.17	-1.48	72,79,80,81	0
3	ADP	D	1608	27/27	0.13	-1.98	21,25,30,31	0
3	ADP	B	1607	27/27	0.12	-2.14	20,26,33,37	0
4	MG	E	1605	1/1	0.11	-2.19	53,53,53,53	0
2	ZN	B	1606	1/1	0.10	-2.34	64,64,64,64	0
4	MG	B	1608	1/1	0.10	-2.64	44,44,44,44	0
2	ZN	D	1607	1/1	0.10	-3.17	79,79,79,79	0
2	ZN	E	1603	1/1	0.05	-3.44	63,63,63,63	0
2	ZN	C	1607	1/1	0.03	-4.08	60,60,60,60	0
2	ZN	F	1606	1/1	0.02	-4.10	69,69,69,69	0
4	MG	D	1609	1/1	0.09	-4.52	41,41,41,41	0
2	ZN	A	1603	1/1	0.04	-4.96	63,63,63,63	0

6.5 Other polymers ⓘ

There are no such residues in this entry.