



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 05:55 PM UTC

PDB ID : 7BUV / pdb_00007buv
Title : Eucommia ulmoides TPT3, crystal form 2
Authors : Kajiura, H.; Yoshizawa, T.; Tokumoto, Y.; Suzuki, N.; Takeno, S.; Takeno, K.J.; Yamashita, T.; Tanaka, S.; Kaneko, Y.; Fujiyama, K.; Matsumura, H.; Nakazawa, Y.
Deposited on : 2020-04-08
Resolution : 3.30 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

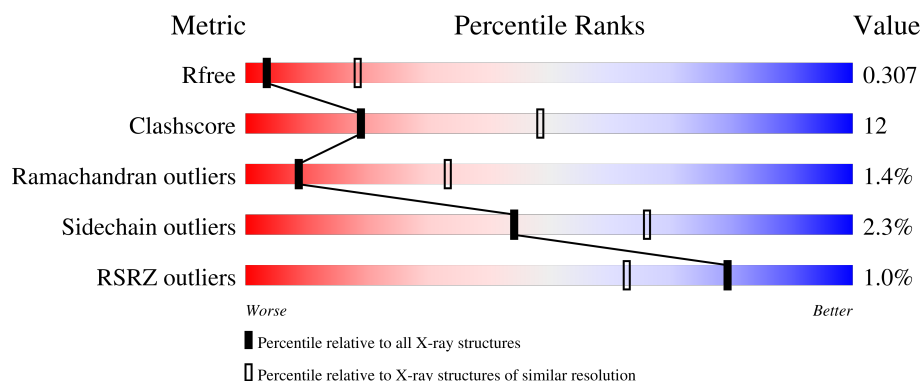
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.30 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	1169 (3.32-3.28)
Clashscore	190562	1209 (3.32-3.28)
Ramachandran outliers	187476	1188 (3.32-3.28)
Sidechain outliers	187428	1187 (3.32-3.28)
RSRZ outliers	180081	1169 (3.32-3.28)

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	364	64% 25% 9%
1	B	364	60% 27% 12%
1	C	364	66% 21% 12%
1	D	364	67% 21% 11%
1	E	364	63% 21% 13%

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Mol	Chain	Length	Quality of chain
1	F	364	% 66%23%10%
1	G	364	69%20%10%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 18385 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 FPS3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	330	Total	C	N	O	S	0	0	0
			2674	1721	436	503	14			
1	B	321	Total	C	N	O	S	0	0	0
			2605	1678	422	491	14			
1	C	322	Total	C	N	O	S	0	0	0
			2603	1673	425	491	14			
1	D	325	Total	C	N	O	S	0	0	0
			2633	1696	429	494	14			
1	E	316	Total	C	N	O	S	0	0	0
			2569	1655	417	483	14			
1	F	329	Total	C	N	O	S	0	0	0
			2663	1714	432	502	15			
1	G	326	Total	C	N	O	S	0	0	0
			2638	1699	432	492	15			

There are 112 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-15	MET	-	initiating methionine	UNP A0A1L3KPU1
A	-14	ASN	-	expression tag	UNP A0A1L3KPU1
A	-13	HIS	-	expression tag	UNP A0A1L3KPU1
A	-12	LYS	-	expression tag	UNP A0A1L3KPU1
A	-11	VAL	-	expression tag	UNP A0A1L3KPU1
A	-10	HIS	-	expression tag	UNP A0A1L3KPU1
A	-9	HIS	-	expression tag	UNP A0A1L3KPU1
A	-8	HIS	-	expression tag	UNP A0A1L3KPU1
A	-7	HIS	-	expression tag	UNP A0A1L3KPU1
A	-6	HIS	-	expression tag	UNP A0A1L3KPU1
A	-5	HIS	-	expression tag	UNP A0A1L3KPU1
A	-4	ILE	-	expression tag	UNP A0A1L3KPU1
A	-3	GLU	-	expression tag	UNP A0A1L3KPU1
A	-2	GLY	-	expression tag	UNP A0A1L3KPU1
A	-1	ARG	-	expression tag	UNP A0A1L3KPU1

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Chain	Residue	Modelled	Actual	Comment	Reference
A	0	HIS	-	expression tag	UNP A0A1L3KPU1
B	-15	MET	-	initiating methionine	UNP A0A1L3KPU1
B	-14	ASN	-	expression tag	UNP A0A1L3KPU1
B	-13	HIS	-	expression tag	UNP A0A1L3KPU1
B	-12	LYS	-	expression tag	UNP A0A1L3KPU1
B	-11	VAL	-	expression tag	UNP A0A1L3KPU1
B	-10	HIS	-	expression tag	UNP A0A1L3KPU1
B	-9	HIS	-	expression tag	UNP A0A1L3KPU1
B	-8	HIS	-	expression tag	UNP A0A1L3KPU1
B	-7	HIS	-	expression tag	UNP A0A1L3KPU1
B	-6	HIS	-	expression tag	UNP A0A1L3KPU1
B	-5	HIS	-	expression tag	UNP A0A1L3KPU1
B	-4	ILE	-	expression tag	UNP A0A1L3KPU1
B	-3	GLU	-	expression tag	UNP A0A1L3KPU1
B	-2	GLY	-	expression tag	UNP A0A1L3KPU1
B	-1	ARG	-	expression tag	UNP A0A1L3KPU1
B	0	HIS	-	expression tag	UNP A0A1L3KPU1
C	-15	MET	-	initiating methionine	UNP A0A1L3KPU1
C	-14	ASN	-	expression tag	UNP A0A1L3KPU1
C	-13	HIS	-	expression tag	UNP A0A1L3KPU1
C	-12	LYS	-	expression tag	UNP A0A1L3KPU1
C	-11	VAL	-	expression tag	UNP A0A1L3KPU1
C	-10	HIS	-	expression tag	UNP A0A1L3KPU1
C	-9	HIS	-	expression tag	UNP A0A1L3KPU1
C	-8	HIS	-	expression tag	UNP A0A1L3KPU1
C	-7	HIS	-	expression tag	UNP A0A1L3KPU1
C	-6	HIS	-	expression tag	UNP A0A1L3KPU1
C	-5	HIS	-	expression tag	UNP A0A1L3KPU1
C	-4	ILE	-	expression tag	UNP A0A1L3KPU1
C	-3	GLU	-	expression tag	UNP A0A1L3KPU1
C	-2	GLY	-	expression tag	UNP A0A1L3KPU1
C	-1	ARG	-	expression tag	UNP A0A1L3KPU1
C	0	HIS	-	expression tag	UNP A0A1L3KPU1
D	-15	MET	-	initiating methionine	UNP A0A1L3KPU1
D	-14	ASN	-	expression tag	UNP A0A1L3KPU1
D	-13	HIS	-	expression tag	UNP A0A1L3KPU1
D	-12	LYS	-	expression tag	UNP A0A1L3KPU1
D	-11	VAL	-	expression tag	UNP A0A1L3KPU1
D	-10	HIS	-	expression tag	UNP A0A1L3KPU1
D	-9	HIS	-	expression tag	UNP A0A1L3KPU1
D	-8	HIS	-	expression tag	UNP A0A1L3KPU1
D	-7	HIS	-	expression tag	UNP A0A1L3KPU1

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-6	HIS	-	expression tag	UNP A0A1L3KPU1
D	-5	HIS	-	expression tag	UNP A0A1L3KPU1
D	-4	ILE	-	expression tag	UNP A0A1L3KPU1
D	-3	GLU	-	expression tag	UNP A0A1L3KPU1
D	-2	GLY	-	expression tag	UNP A0A1L3KPU1
D	-1	ARG	-	expression tag	UNP A0A1L3KPU1
D	0	HIS	-	expression tag	UNP A0A1L3KPU1
E	-15	MET	-	initiating methionine	UNP A0A1L3KPU1
E	-14	ASN	-	expression tag	UNP A0A1L3KPU1
E	-13	HIS	-	expression tag	UNP A0A1L3KPU1
E	-12	LYS	-	expression tag	UNP A0A1L3KPU1
E	-11	VAL	-	expression tag	UNP A0A1L3KPU1
E	-10	HIS	-	expression tag	UNP A0A1L3KPU1
E	-9	HIS	-	expression tag	UNP A0A1L3KPU1
E	-8	HIS	-	expression tag	UNP A0A1L3KPU1
E	-7	HIS	-	expression tag	UNP A0A1L3KPU1
E	-6	HIS	-	expression tag	UNP A0A1L3KPU1
E	-5	HIS	-	expression tag	UNP A0A1L3KPU1
E	-4	ILE	-	expression tag	UNP A0A1L3KPU1
E	-3	GLU	-	expression tag	UNP A0A1L3KPU1
E	-2	GLY	-	expression tag	UNP A0A1L3KPU1
E	-1	ARG	-	expression tag	UNP A0A1L3KPU1
E	0	HIS	-	expression tag	UNP A0A1L3KPU1
F	-15	MET	-	initiating methionine	UNP A0A1L3KPU1
F	-14	ASN	-	expression tag	UNP A0A1L3KPU1
F	-13	HIS	-	expression tag	UNP A0A1L3KPU1
F	-12	LYS	-	expression tag	UNP A0A1L3KPU1
F	-11	VAL	-	expression tag	UNP A0A1L3KPU1
F	-10	HIS	-	expression tag	UNP A0A1L3KPU1
F	-9	HIS	-	expression tag	UNP A0A1L3KPU1
F	-8	HIS	-	expression tag	UNP A0A1L3KPU1
F	-7	HIS	-	expression tag	UNP A0A1L3KPU1
F	-6	HIS	-	expression tag	UNP A0A1L3KPU1
F	-5	HIS	-	expression tag	UNP A0A1L3KPU1
F	-4	ILE	-	expression tag	UNP A0A1L3KPU1
F	-3	GLU	-	expression tag	UNP A0A1L3KPU1
F	-2	GLY	-	expression tag	UNP A0A1L3KPU1
F	-1	ARG	-	expression tag	UNP A0A1L3KPU1
F	0	HIS	-	expression tag	UNP A0A1L3KPU1
G	-15	MET	-	initiating methionine	UNP A0A1L3KPU1
G	-14	ASN	-	expression tag	UNP A0A1L3KPU1
G	-13	HIS	-	expression tag	UNP A0A1L3KPU1

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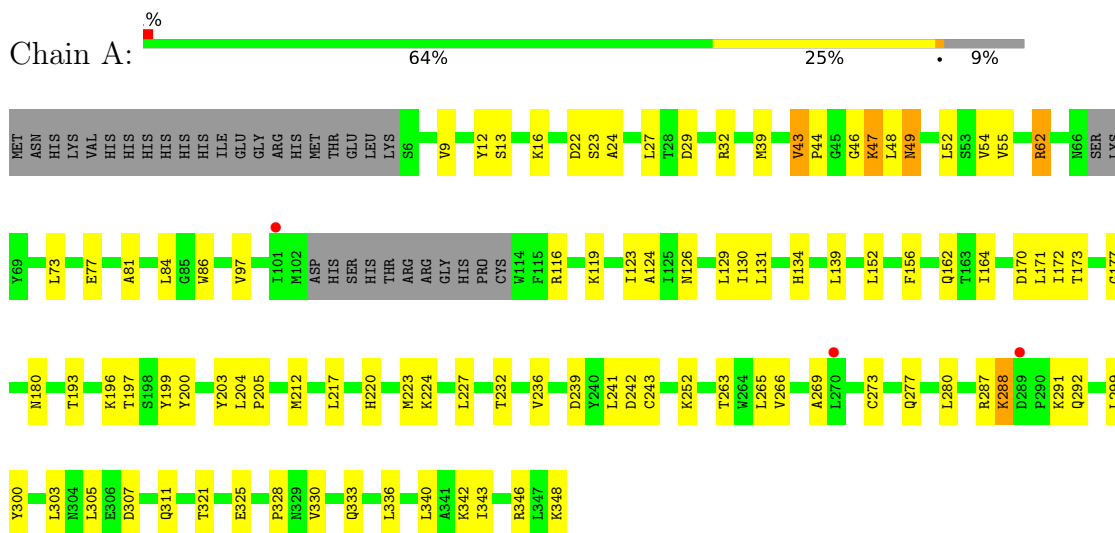
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Chain	Residue	Modelled	Actual	Comment	Reference
G	-12	LYS	-	expression tag	UNP A0A1L3KPU1
G	-11	VAL	-	expression tag	UNP A0A1L3KPU1
G	-10	HIS	-	expression tag	UNP A0A1L3KPU1
G	-9	HIS	-	expression tag	UNP A0A1L3KPU1
G	-8	HIS	-	expression tag	UNP A0A1L3KPU1
G	-7	HIS	-	expression tag	UNP A0A1L3KPU1
G	-6	HIS	-	expression tag	UNP A0A1L3KPU1
G	-5	HIS	-	expression tag	UNP A0A1L3KPU1
G	-4	ILE	-	expression tag	UNP A0A1L3KPU1
G	-3	GLU	-	expression tag	UNP A0A1L3KPU1
G	-2	GLY	-	expression tag	UNP A0A1L3KPU1
G	-1	ARG	-	expression tag	UNP A0A1L3KPU1
G	0	HIS	-	expression tag	UNP A0A1L3KPU1

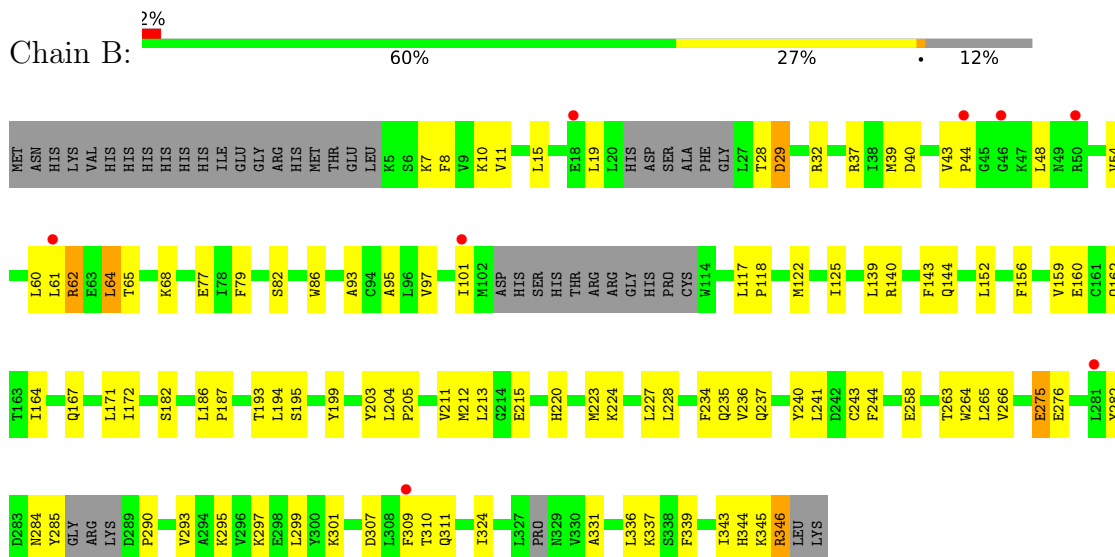
3 Residue-property plots

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: FPS3

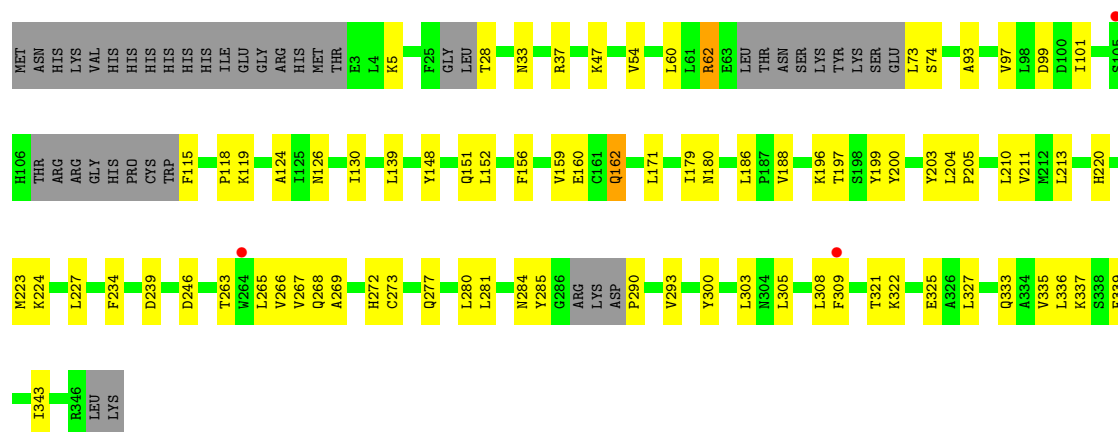


• Molecule 1: FPS3

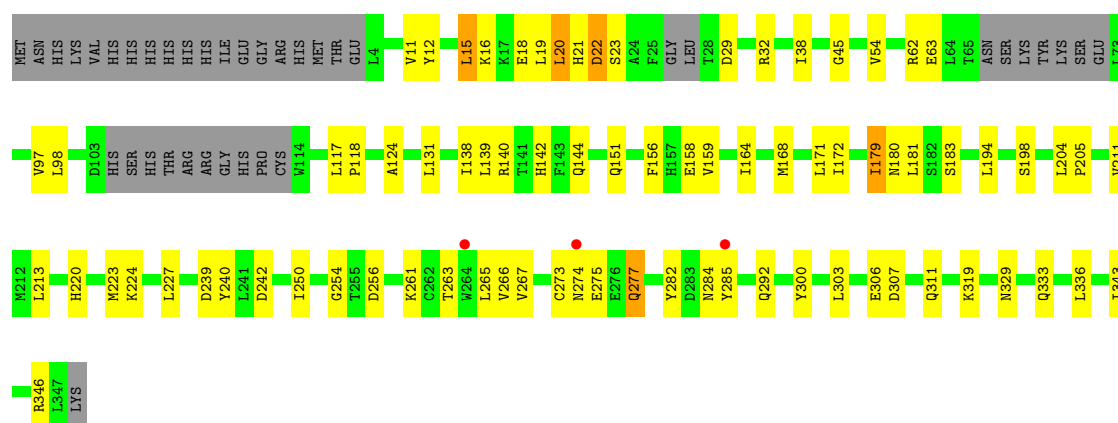


• Molecule 1: FPS3

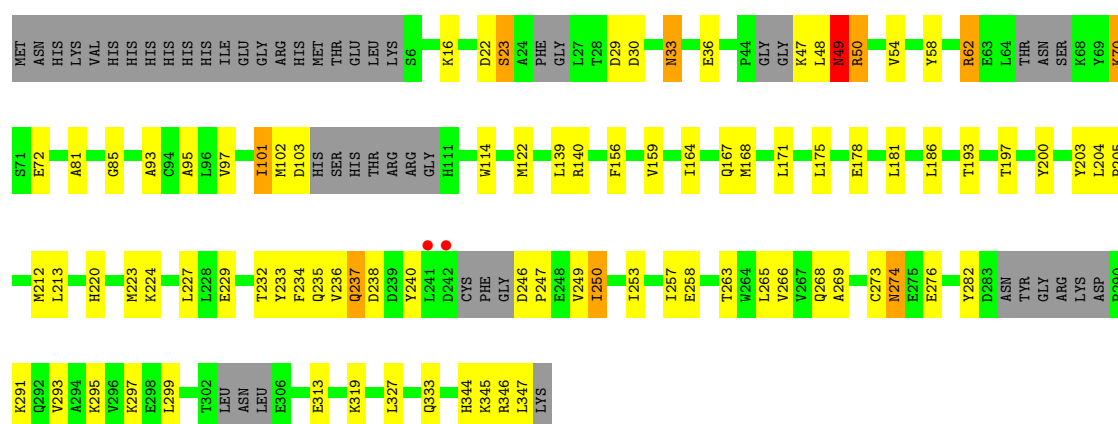




● Molecule 1: FPS3

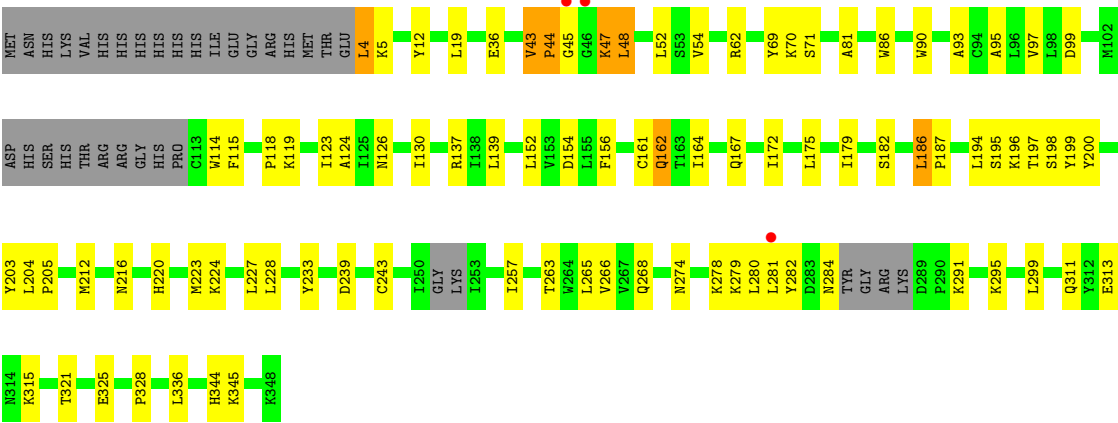


● Molecule 1: FPS3

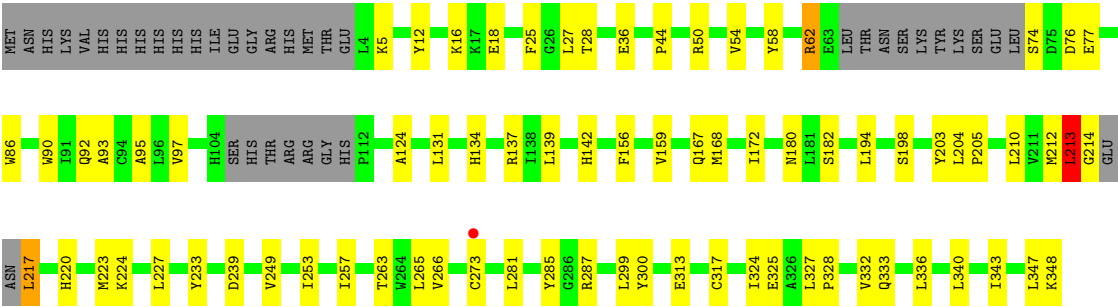


● Molecule 1: FPS3





● Molecule 1: FPS3



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	234.39Å 131.06Å 103.92Å 90.00° 111.98° 90.00°	Depositor
Resolution (Å)	48.19 – 3.30 48.19 – 3.30	Depositor EDS
% Data completeness (in resolution range)	99.9 (48.19-3.30) 99.9 (48.19-3.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.72 (at 3.33Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.282 , 0.304 0.283 , 0.307	Depositor DCC
R_{free} test set	2193 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	116.1	Xtriage
Anisotropy	0.194	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 76.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	18385	wwPDB-VP
Average B, all atoms (Å ²)	113.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.31% 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](#)

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	0.18	0/2725	0.45	0/3684
1	B	0.20	0/2651	0.49	0/3582
1	C	0.17	0/2651	0.42	0/3582
1	D	0.17	0/2682	0.42	1/3627 (0.0%)
1	E	0.18	0/2614	0.44	0/3530
1	F	0.16	0/2712	0.46	2/3666 (0.1%)
1	G	0.19	0/2689	0.46	1/3633 (0.0%)
All	All	0.18	0/18724	0.45	4/25304 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	213	LEU	N-CA-C	-6.49	103.42	112.12
1	F	43	VAL	CA-C-N	6.00	127.34	119.84
1	F	43	VAL	C-N-CA	6.00	127.34	119.84
1	D	22	ASP	CB-CA-C	-5.71	108.20	116.54

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	2674	0	2690	66	0
1	B	2605	0	2626	80	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	2603	0	2607	62	0
1	D	2633	0	2651	54	0
1	E	2569	0	2585	66	0
1	F	2663	0	2682	62	0
1	G	2638	0	2657	61	0
All	All	18385	0	18498	434	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 12.

The worst 5 of 434 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:G:58:TYR:CE1	1:G:213:LEU:HD21	1.79	1.15
1:G:58:TYR:HE1	1:G:213:LEU:HD21	0.89	1.03
1:G:212:MET:C	1:G:213:LEU:HD23	1.90	0.97
1:A:346:ARG:HG2	1:A:348:LYS:H	1.35	0.92
1:F:43:VAL:HB	1:F:44:PRO:HD3	1.54	0.89

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	324/364 (89%)	300 (93%)	18 (6%)	6 (2%)	6	28
1	B	311/364 (85%)	291 (94%)	17 (6%)	3 (1%)	12	40
1	C	312/364 (86%)	292 (94%)	17 (5%)	3 (1%)	12	40
1	D	317/364 (87%)	292 (92%)	20 (6%)	5 (2%)	7	31
1	E	300/364 (82%)	273 (91%)	21 (7%)	6 (2%)	6	27

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	F	321/364 (88%)	300 (94%)	17 (5%)	4 (1%)	10	37
1	G	318/364 (87%)	294 (92%)	20 (6%)	4 (1%)	9	35
All	All	2203/2548 (86%)	2042 (93%)	130 (6%)	31 (1%)	9	33

5 of 31 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	29	ASP
1	A	47	LYS
1	A	242	ASP
1	C	47	LYS
1	D	20	LEU

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	300/332 (90%)	292 (97%)	8 (3%)	39	63
1	B	294/332 (89%)	287 (98%)	7 (2%)	43	65
1	C	293/332 (88%)	288 (98%)	5 (2%)	53	71
1	D	296/332 (89%)	289 (98%)	7 (2%)	43	65
1	E	291/332 (88%)	283 (97%)	8 (3%)	39	63
1	F	301/332 (91%)	295 (98%)	6 (2%)	48	68
1	G	296/332 (89%)	289 (98%)	7 (2%)	43	65
All	All	2071/2324 (89%)	2023 (98%)	48 (2%)	44	66

5 of 48 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	49	ASN
1	F	4	LEU
1	E	50	ARG
1	E	102	MET

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Mol	Chain	Res	Type
1	F	48	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 21 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	42	ASN
1	F	92	GLN
1	G	333	GLN
1	F	268	GLN
1	E	167	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 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	330/364 (90%)	0.14	3 (0%) 81 65	30, 115, 139, 162	0
1	B	321/364 (88%)	0.32	8 (2%) 58 39	77, 121, 149, 159	0
1	C	322/364 (88%)	0.08	3 (0%) 81 65	78, 120, 149, 166	0
1	D	325/364 (89%)	0.03	3 (0%) 81 65	81, 119, 143, 163	0
1	E	316/364 (86%)	0.08	2 (0%) 85 73	84, 120, 159, 170	0
1	F	329/364 (90%)	0.01	3 (0%) 81 65	30, 97, 135, 154	0
1	G	326/364 (89%)	0.05	1 (0%) 90 82	63, 103, 132, 158	0
All	All	2269/2548 (89%)	0.10	23 (1%) 79 63	30, 114, 149, 170	0

The worst 5 of 23 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	46	GLY	6.0
1	A	289	ASP	4.2
1	B	61	LEU	3.8
1	F	281	LEU	3.8
1	A	101	ILE	3.6

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.