



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 17, 2021 – 04:11 AM EDT

PDB ID : 1HR7
Title : Yeast Mitochondrial Processing Peptidase beta-E73Q Mutant
Authors : Taylor, A.B.; Smith, B.S.; Kitada, S.; Kojima, K.; Miyaura, H.; Otwinowski, Z.; Ito, A.; Deisenhofer, J.
Deposited on : 2000-12-21
Resolution : 2.55 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 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	:	2.23.2
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)	:	2.23.2

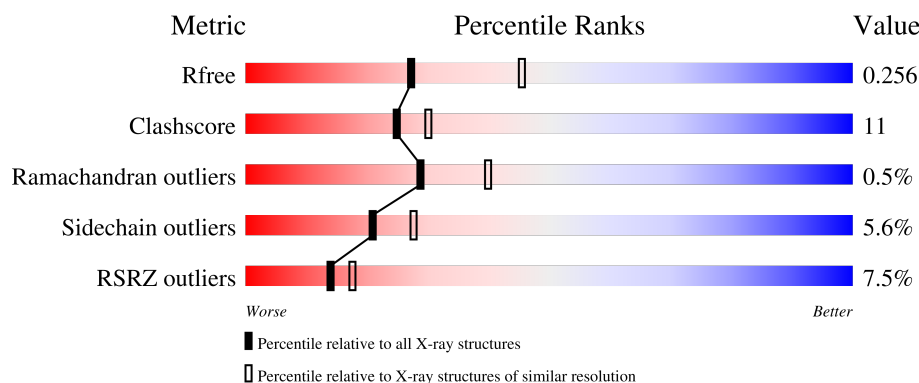
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.55 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	1284 (2.56-2.52)
Clashscore	141614	1332 (2.56-2.52)
Ramachandran outliers	138981	1315 (2.56-2.52)
Sidechain outliers	138945	1315 (2.56-2.52)
RSRZ outliers	127900	1272 (2.56-2.52)

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	475	<div> <div>5%</div> <div>74%</div> <div>20%</div> <div>• •</div> </div>
1	C	475	<div> <div>3%</div> <div>74%</div> <div>17%</div> <div>• 7%</div> </div>
1	E	475	<div> <div>5%</div> <div>72%</div> <div>20%</div> <div>• 6%</div> </div>
1	G	475	<div> <div>4%</div> <div>71%</div> <div>20%</div> <div>• 5%</div> </div>
2	B	443	<div> <div>2%</div> <div>75%</div> <div>21%</div> <div>• •</div> </div>

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Mol	Chain	Length	Quality of chain
2	D	443	<div><div></div><div>3%</div><div>74%</div><div>22%</div><div></div><div>.</div></div>
2	F	443	<div><div></div><div>7%</div><div>75%</div><div>21%</div><div></div><div>..</div></div>
2	H	443	<div><div></div><div>30%</div><div>73%</div><div>23%</div><div></div><div>..</div></div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 27725 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 MITOCHONDRIAL PROCESSING PEPTIDASE ALPHA SUBUNIT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	457	Total	C	N	O	S	0	0	0
			3531	2233	599	680	19			
1	C	444	Total	C	N	O	S	0	0	0
			3447	2183	582	663	19			
1	E	448	Total	C	N	O	S	0	0	0
			3478	2201	590	668	19			
1	G	450	Total	C	N	O	S	0	0	0
			3485	2206	592	668	19			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	177	GLY	GLU	SEE REMARK 999	UNP P11914
A	217	GLY	GLU	SEE REMARK 999	UNP P11914
A	483	HIS	-	expression tag	UNP P11914
A	484	HIS	-	expression tag	UNP P11914
A	485	HIS	-	expression tag	UNP P11914
A	486	HIS	-	expression tag	UNP P11914
A	487	HIS	-	expression tag	UNP P11914
A	488	HIS	-	expression tag	UNP P11914
C	177	GLY	GLU	SEE REMARK 999	UNP P11914
C	217	GLY	GLU	SEE REMARK 999	UNP P11914
C	483	HIS	-	expression tag	UNP P11914
C	484	HIS	-	expression tag	UNP P11914
C	485	HIS	-	expression tag	UNP P11914
C	486	HIS	-	expression tag	UNP P11914
C	487	HIS	-	expression tag	UNP P11914
C	488	HIS	-	expression tag	UNP P11914
E	177	GLY	GLU	SEE REMARK 999	UNP P11914
E	217	GLY	GLU	SEE REMARK 999	UNP P11914
E	483	HIS	-	expression tag	UNP P11914
E	484	HIS	-	expression tag	UNP P11914

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Chain	Residue	Modelled	Actual	Comment	Reference
E	485	HIS	-	expression tag	UNP P11914
E	486	HIS	-	expression tag	UNP P11914
E	487	HIS	-	expression tag	UNP P11914
E	488	HIS	-	expression tag	UNP P11914
G	177	GLY	GLU	SEE REMARK 999	UNP P11914
G	217	GLY	GLU	SEE REMARK 999	UNP P11914
G	483	HIS	-	expression tag	UNP P11914
G	484	HIS	-	expression tag	UNP P11914
G	485	HIS	-	expression tag	UNP P11914
G	486	HIS	-	expression tag	UNP P11914
G	487	HIS	-	expression tag	UNP P11914
G	488	HIS	-	expression tag	UNP P11914

- Molecule 2 is a protein called MITOCHONDRIAL PROCESSING PEPTIDASE BETA SUB-UNIT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	439	Total	C	N	O	S	0	0	0
			3414	2148	591	668	7			
2	D	441	Total	C	N	O	S	0	0	0
			3431	2159	594	671	7			
2	F	440	Total	C	N	O	S	0	0	0
			3422	2154	592	669	7			
2	H	440	Total	C	N	O	S	0	0	0
			3422	2154	592	669	7			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	20	ALA	-	cloning artifact	UNP P10507
B	73	GLN	GLU	engineered mutation	UNP P10507
B	84	PRO	SER	SEE REMARK 999	UNP P10507
B	350	ARG	GLN	SEE REMARK 999	UNP P10507
D	20	ALA	-	cloning artifact	UNP P10507
D	73	GLN	GLU	engineered mutation	UNP P10507
D	84	PRO	SER	SEE REMARK 999	UNP P10507
D	350	ARG	GLN	SEE REMARK 999	UNP P10507
F	20	ALA	-	cloning artifact	UNP P10507
F	73	GLN	GLU	engineered mutation	UNP P10507
F	84	PRO	SER	SEE REMARK 999	UNP P10507
F	350	ARG	GLN	SEE REMARK 999	UNP P10507
H	20	ALA	-	cloning artifact	UNP P10507

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Chain	Residue	Modelled	Actual	Comment	Reference
H	73	GLN	GLU	engineered mutation	UNP P10507
H	84	PRO	SER	SEE REMARK 999	UNP P10507
H	350	ARG	GLN	SEE REMARK 999	UNP P10507

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total Zn 1 1	0	0
3	D	1	Total Zn 1 1	0	0
3	F	1	Total Zn 1 1	0	0
3	H	1	Total Zn 1 1	0	0

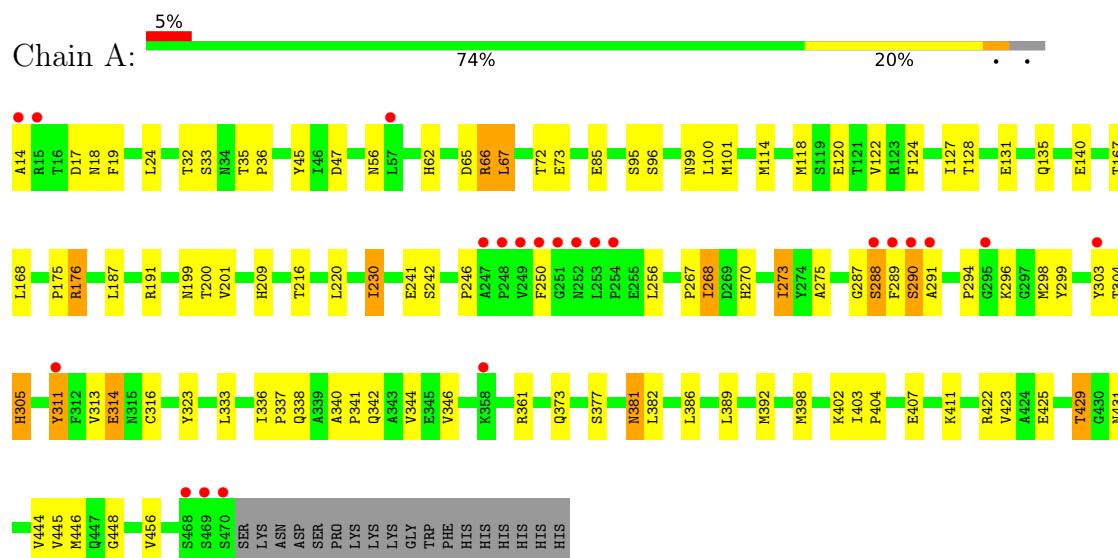
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	20	Total O 20 20	0	0
4	B	27	Total O 27 27	0	0
4	C	13	Total O 13 13	0	0
4	D	10	Total O 10 10	0	0
4	E	9	Total O 9 9	0	0
4	F	4	Total O 4 4	0	0
4	G	7	Total O 7 7	0	0
4	H	1	Total O 1 1	0	0

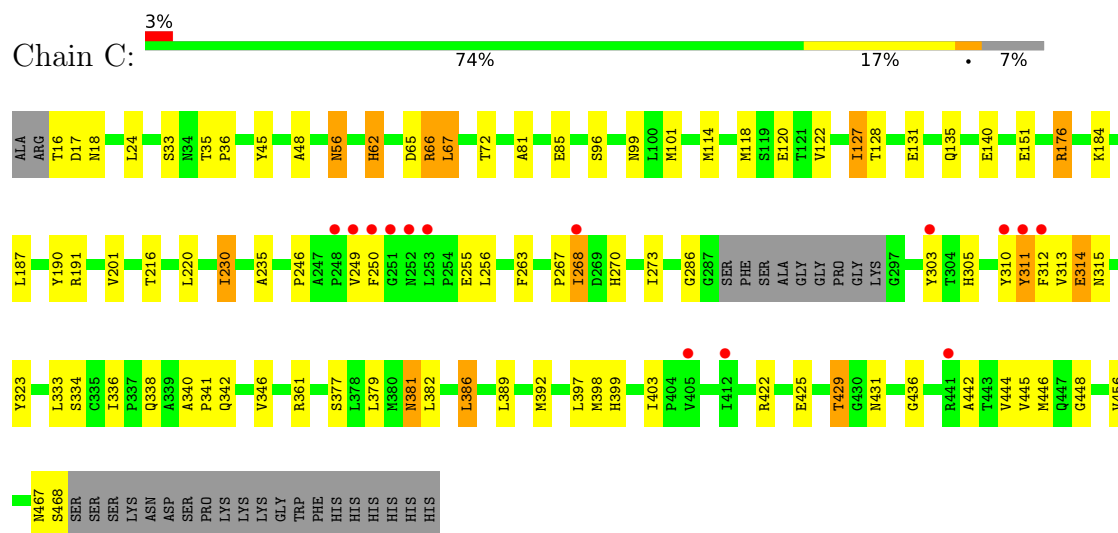
3 Residue-property plots

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: MITOCHONDRIAL PROCESSING PEPTIDASE ALPHA SUBUNIT

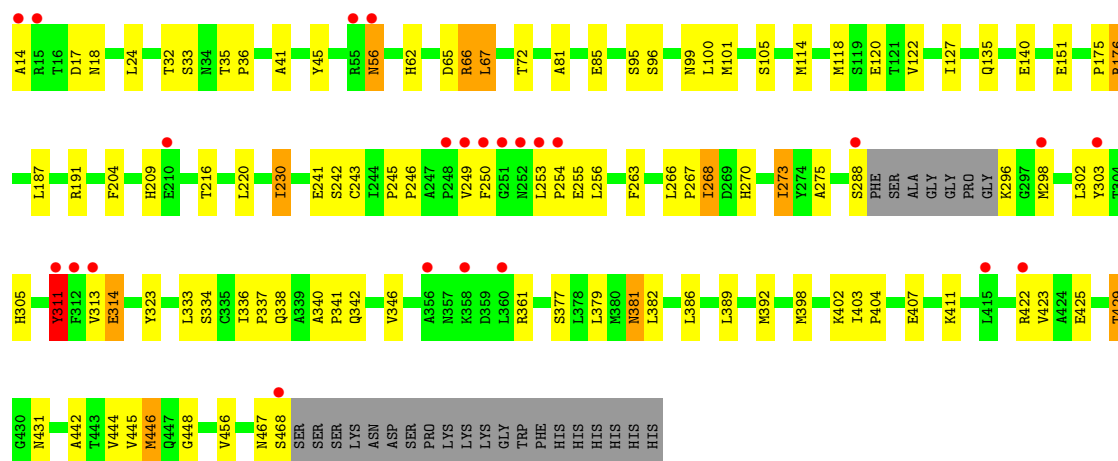


• Molecule 1: MITOCHONDRIAL PROCESSING PEPTIDASE ALPHA SUBUNIT

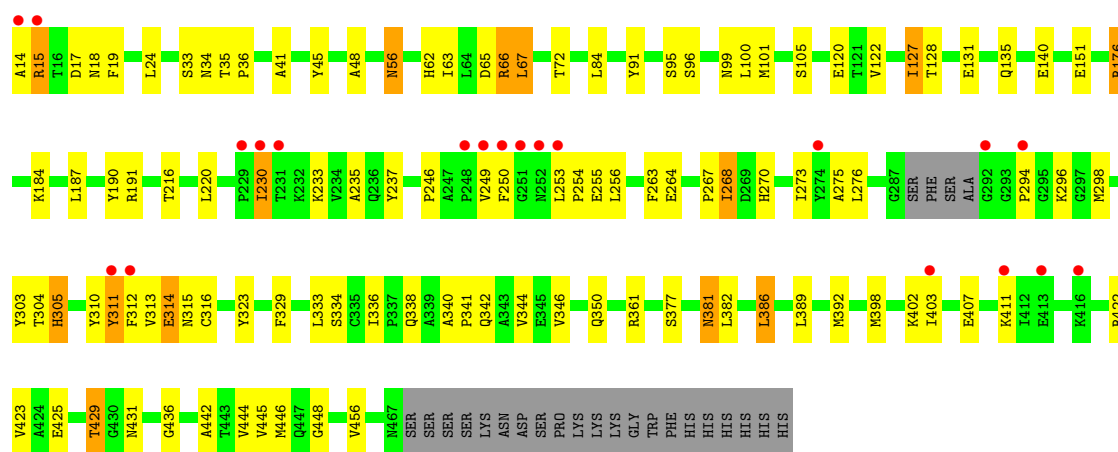


• Molecule 1: MITOCHONDRIAL PROCESSING PEPTIDASE ALPHA SUBUNIT

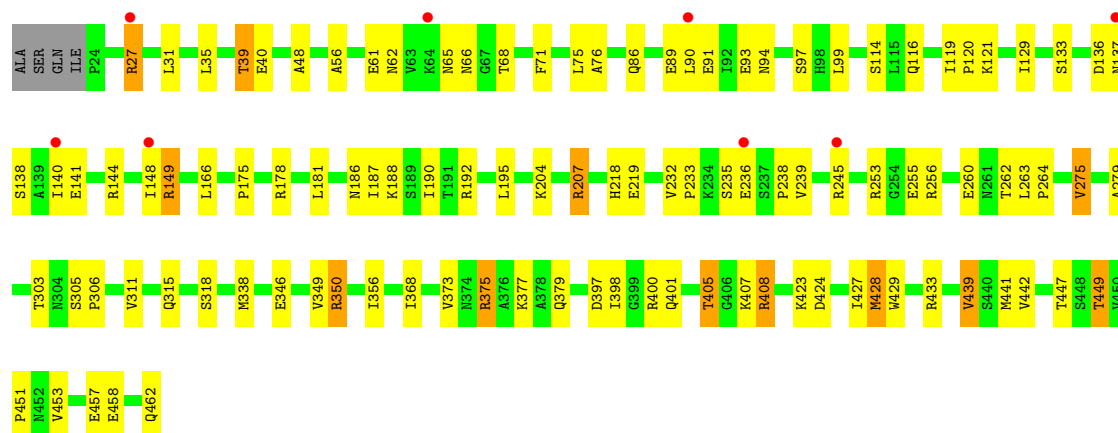
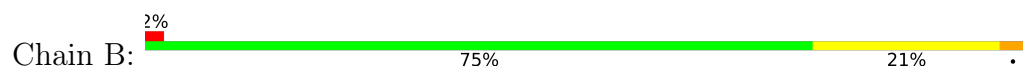




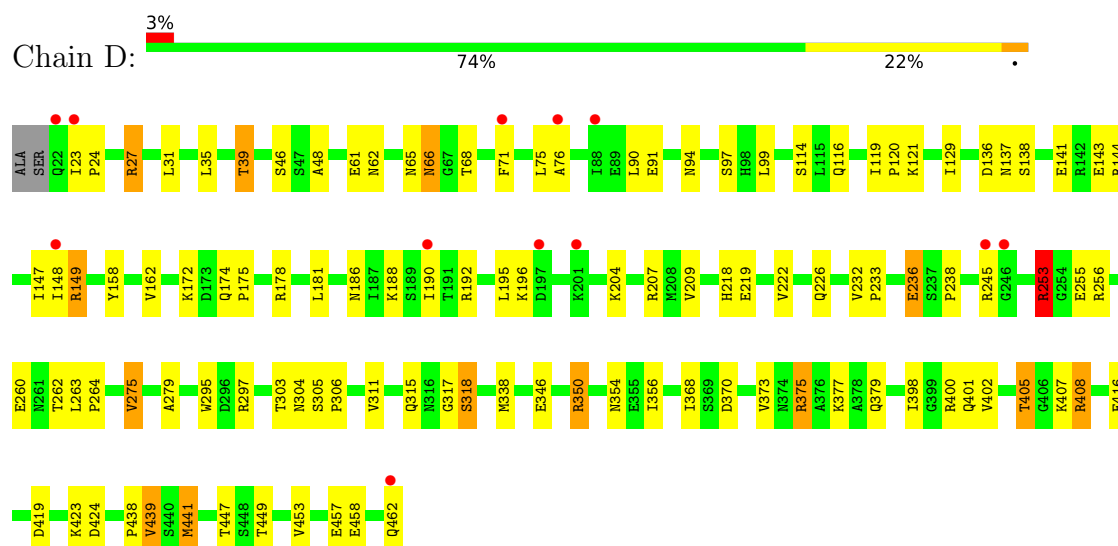
• Molecule 1: MITOCHONDRIAL PROCESSING PEPTIDASE ALPHA SUBUNIT



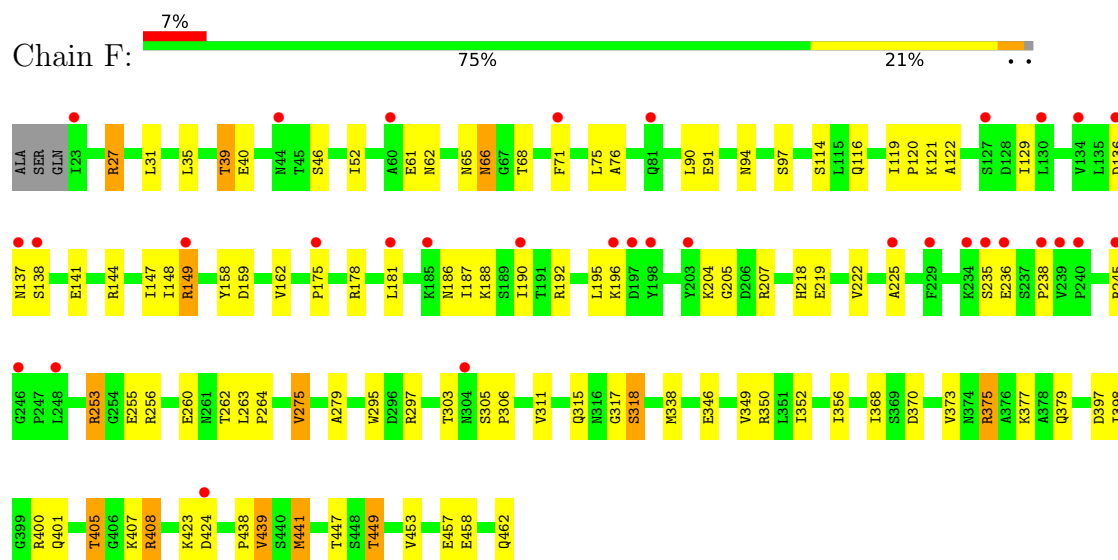
• Molecule 2: MITOCHONDRIAL PROCESSING PEPTIDASE BETA SUBUNIT



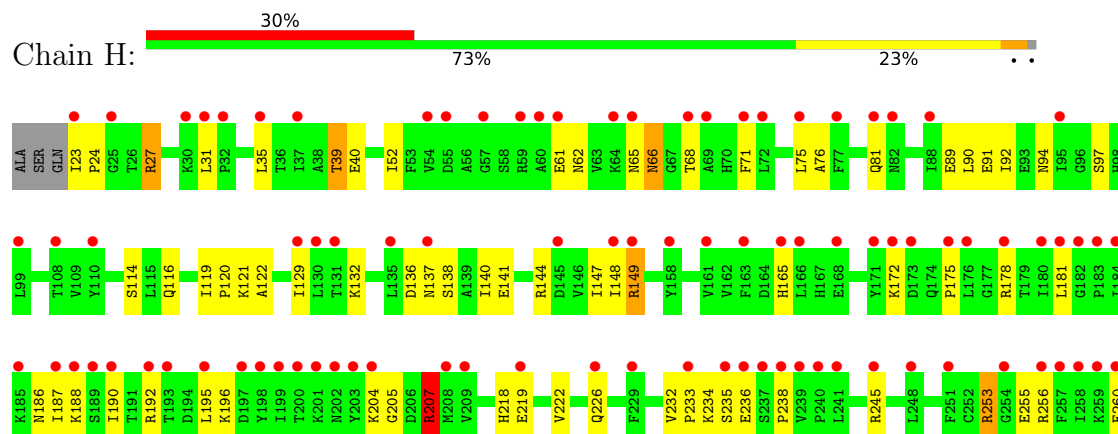
• Molecule 2: MITOCHONDRIAL PROCESSING PEPTIDASE BETA SUBUNIT

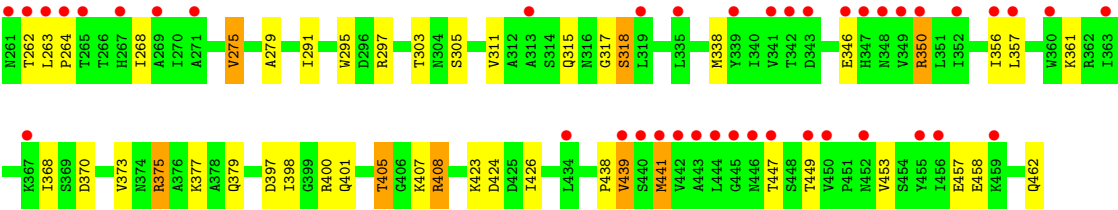


• Molecule 2: MITOCHONDRIAL PROCESSING PEPTIDASE BETA SUBUNIT



• Molecule 2: MITOCHONDRIAL PROCESSING PEPTIDASE BETA SUBUNIT





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	134.20Å 178.62Å 201.97Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.53 – 2.55 47.53 – 2.54	Depositor EDS
% Data completeness (in resolution range)	98.7 (47.53-2.55) 98.2 (47.53-2.54)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.22 (at 2.54Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.243 , 0.256 0.242 , 0.256	Depositor DCC
R_{free} test set	2025 reflections (1.29%)	wwPDB-VP
Wilson B-factor (Å ²)	53.7	Xtriage
Anisotropy	0.471	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 44.3	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	0.93	EDS
Total number of atoms	27725	wwPDB-VP
Average B, all atoms (Å ²)	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.08% 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 ⓘ

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

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	0.64	0/3604	0.76	2/4877 (0.0%)
1	C	0.63	0/3517	0.75	1/4760 (0.0%)
1	E	0.61	0/3548	0.82	4/4800 (0.1%)
1	G	0.59	0/3556	0.75	2/4811 (0.0%)
2	B	0.61	0/3478	0.78	5/4720 (0.1%)
2	D	0.61	1/3495 (0.0%)	0.91	10/4744 (0.2%)
2	F	0.53	0/3486	0.74	5/4732 (0.1%)
2	H	0.53	0/3486	0.87	9/4732 (0.2%)
All	All	0.60	1/28170 (0.0%)	0.80	38/38176 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	236	GLU	CB-CG	-6.03	1.40	1.52

The worst 5 of 38 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	149	ARG	NE-CZ-NH2	-17.07	111.76	120.30
2	D	253	ARG	NE-CZ-NH2	16.87	128.73	120.30
2	H	207	ARG	NE-CZ-NH1	-16.50	112.05	120.30
2	H	149	ARG	NE-CZ-NH1	16.43	128.52	120.30
2	D	253	ARG	NE-CZ-NH1	-16.30	112.15	120.30

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	3531	0	3488	78	0
1	C	3447	0	3406	64	0
1	E	3478	0	3442	77	0
1	G	3485	0	3448	82	0
2	B	3414	0	3414	77	0
2	D	3431	0	3432	74	0
2	F	3422	0	3424	75	0
2	H	3422	0	3424	85	0
3	B	1	0	0	0	0
3	D	1	0	0	0	0
3	F	1	0	0	0	0
3	H	1	0	0	0	0
4	A	20	0	0	0	0
4	B	27	0	0	0	0
4	C	13	0	0	0	0
4	D	10	0	0	0	0
4	E	9	0	0	0	0
4	F	4	0	0	0	0
4	G	7	0	0	0	0
4	H	1	0	0	0	0
All	All	27725	0	27478	597	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 11.

The worst 5 of 597 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:E:33:SER:HB3	1:E:392:MET:HE1	1.30	1.08
1:C:33:SER:HB3	1:C:392:MET:HE1	1.36	1.06
1:G:33:SER:HB3	1:G:392:MET:HE1	1.38	1.04
1:A:33:SER:HB3	1:A:392:MET:HE1	1.40	1.03
1:A:230:ILE:HD12	1:A:230:ILE:H	1.29	0.98

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	455/475 (96%)	435 (96%)	16 (4%)	4 (1%)	17	24
1	C	440/475 (93%)	421 (96%)	17 (4%)	2 (0%)	29	40
1	E	444/475 (94%)	422 (95%)	20 (4%)	2 (0%)	29	40
1	G	446/475 (94%)	425 (95%)	19 (4%)	2 (0%)	34	46
2	B	437/443 (99%)	423 (97%)	12 (3%)	2 (0%)	29	40
2	D	439/443 (99%)	423 (96%)	15 (3%)	1 (0%)	47	60
2	F	438/443 (99%)	421 (96%)	16 (4%)	1 (0%)	47	60
2	H	438/443 (99%)	420 (96%)	16 (4%)	2 (0%)	29	40
All	All	3537/3672 (96%)	3390 (96%)	131 (4%)	16 (0%)	29	40

5 of 16 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	250	PHE
1	G	250	PHE
2	H	24	PRO
1	A	250	PHE
1	A	288	SER

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	384/401 (96%)	364 (95%)	20 (5%)	23	30

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	376/401 (94%)	353 (94%)	23 (6%)	18	24
1	E	379/401 (94%)	357 (94%)	22 (6%)	20	26
1	G	378/401 (94%)	356 (94%)	22 (6%)	20	26
2	B	376/379 (99%)	356 (95%)	20 (5%)	22	30
2	D	378/379 (100%)	358 (95%)	20 (5%)	22	30
2	F	377/379 (100%)	357 (95%)	20 (5%)	22	30
2	H	377/379 (100%)	356 (94%)	21 (6%)	21	28
All	All	3025/3120 (97%)	2857 (94%)	168 (6%)	21	28

5 of 168 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	F	350	ARG
1	G	386	LEU
2	F	408	ARG
1	G	151	GLU
2	H	71	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 58 such sidechains are listed below:

Mol	Chain	Res	Type
2	D	374	ASN
2	H	186	ASN
2	F	44	ASN
2	H	165	HIS
2	H	44	ASN

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 [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	457/475 (96%)	0.59	22 (4%)	30	37	31, 49, 83, 101	0
1	C	444/475 (93%)	0.36	14 (3%)	47	55	30, 50, 75, 101	0
1	E	448/475 (94%)	0.55	24 (5%)	25	30	34, 53, 80, 101	0
1	G	450/475 (94%)	0.53	20 (4%)	34	41	35, 54, 82, 101	0
2	B	439/443 (99%)	0.45	8 (1%)	68	74	30, 51, 76, 95	0
2	D	441/443 (99%)	0.39	12 (2%)	54	61	33, 58, 79, 97	0
2	F	440/443 (99%)	0.60	33 (7%)	14	17	44, 67, 86, 97	0
2	H	440/443 (99%)	1.41	133 (30%)	0	0	52, 75, 91, 99	0
All	All	3559/3672 (96%)	0.61	266 (7%)	14	17	30, 58, 85, 101	0

The worst 5 of 266 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	250	PHE	9.2
1	E	250	PHE	8.5
1	C	252	ASN	7.7
2	H	456	ILE	7.5
2	H	198	TYR	7.5

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 monosaccharides in this entry.

6.4 Ligands [i](#)

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. 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	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	ZN	H	504	1/1	0.84	0.10	100,100,100,100	0
3	ZN	D	502	1/1	0.94	0.14	64,64,64,64	0
3	ZN	F	503	1/1	0.96	0.14	73,73,73,73	0
3	ZN	B	501	1/1	0.98	0.17	46,46,46,46	0

6.5 Other polymers [i](#)

There are no such residues in this entry.