



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 13, 2020 – 05:28 PM BST

PDB ID : 4N0I
Title : Crystal structure of *S. cerevisiae* mitochondrial GatFAB in complex with glutamine
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Deposited on : 2013-10-02
Resolution : 2.00 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : **FAILED**
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.14.4.dev1

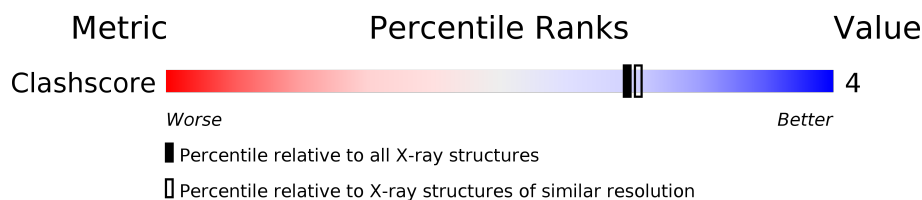
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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))
Clashscore	141614	9178 (2.00-2.00)

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 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 $\leq 5\%$

Note EDS failed to run properly.

Mol	Chain	Length	Quality of chain
1	A	464	 89% 8% .
2	B	325	 79% 9% 12%
3	F	160	 72% 6% 22%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 6933 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 Glutamyl-tRNA(Gln) amidotransferase subunit A, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	450	Total	C	N	O	S	0	5	0
			3439	2202	571	653	13			

- Molecule 2 is a protein called Glutamyl-tRNA(Gln) amidotransferase subunit B, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	285	Total	C	N	O	S	0	0	0
			2199	1397	376	420	6			

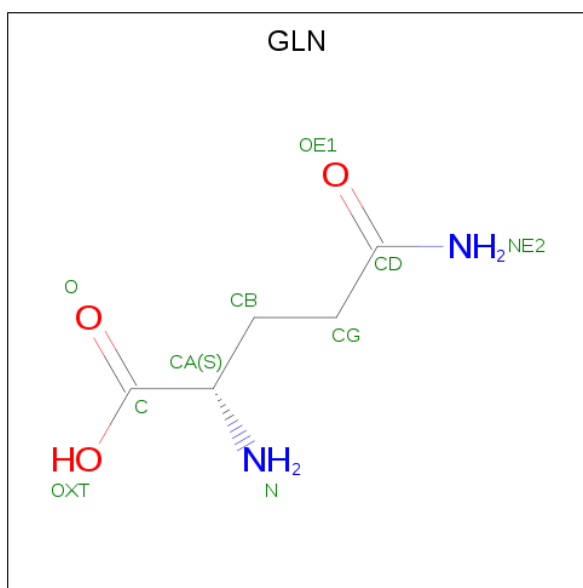
There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	330	LEU	-	EXPRESSION TAG	UNP P33893
B	331	GLU	-	EXPRESSION TAG	UNP P33893
B	332	SER	-	EXPRESSION TAG	UNP P33893
B	333	SER	-	EXPRESSION TAG	UNP P33893
B	334	GLY	-	EXPRESSION TAG	UNP P33893
B	335	GLU	-	EXPRESSION TAG	UNP P33893
B	336	ASN	-	EXPRESSION TAG	UNP P33893
B	337	LEU	-	EXPRESSION TAG	UNP P33893
B	338	TYR	-	EXPRESSION TAG	UNP P33893
B	339	PHE	-	EXPRESSION TAG	UNP P33893
B	340	GLN	-	EXPRESSION TAG	UNP P33893

- Molecule 3 is a protein called Glutamyl-tRNA(Gln) amidotransferase subunit F, mitochondrial.

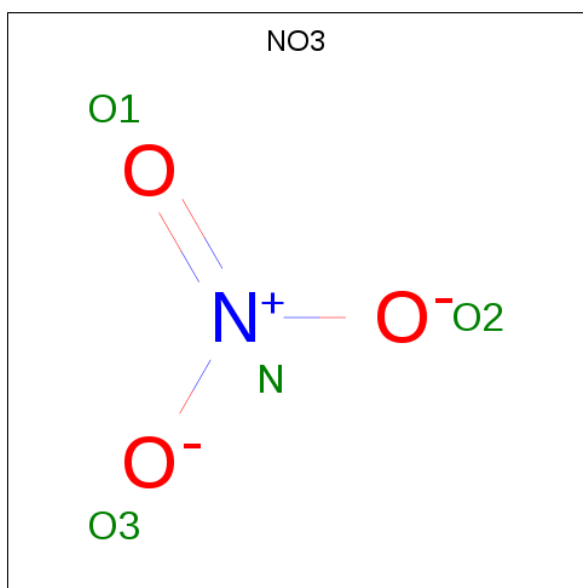
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	F	125	Total	C	N	O	S	0	0	0
			955	611	167	176	1			

- Molecule 4 is GLUTAMINE (three-letter code: GLN) (formula: $C_5H_{10}N_2O_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			9	5	1	3		

- Molecule 5 is NITRATE ION (three-letter code: NO3) (formula: NO_3).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	N	O	0	0
			4	1	3		


- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	218	Total 218	O 218	0	0
6	B	54	Total 54	O 54	0	0
6	F	55	Total 55	O 55	0	0

Note EDS failed to run properly.

- Chain A:
-
- 89% 8%
- Sequence: MET, PRO, LEU, LYS, ARG, S6, L7, S10, I11, Y21, T25, P31, Y32, S33, ILE, THR, ASN, LYS, LYS, GLY, THR, LYS, LYS, GLU, T43, S66, E99, R111, P117, R156, M197, K229, E246, P249, L263, L264, L268, E269, I270, I275, V278, K279, N280

- Chain B:
-
- | Amino Acid | Category |
|------------|----------|
| ILE | Grey |
| HIS | Grey |
| SER | Grey |
| HIS | Grey |
| GLY | Green |
| ALA | Grey |
| PRO | Grey |
| PHE | Green |
| ARG | Green |
| PRO | Grey |
| GLU | Green |
| Y27 | Green |
| A28 | Green |
| L29 | Green |
| K30 | Green |
| G31 | Yellow |
| E34 | Green |
| I35 | Green |
| K36 | Green |
| T37 | Green |
| Q38 | Green |
| M87 | Green |
| R88 | Green |
| L89 | Green |
| Q113 | Green |
| Q118 | Green |
| R128 | Green |
| I141 | Green |
| D142 | Green |
| E143 | Green |
| Q152 | Green |
| L153 | Green |
| Q154 | Green |
| T155 | Green |
| E156 | Green |
| T165 | Green |
| GLU | Grey |
| THR | Grey |
| ASP | Grey |
| LYS | Grey |
| ASP | Green |
| V171 | Green |
| L174 | Yellow |
| L184 | Yellow |
| F193 | Yellow |
| S194 | Yellow |
| D228 | Yellow |

- Chain F: 
- | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|------|------|------|------|-----|-----|-----|-----|
| PHE | VAL | THR | GLY | G29 | Y45 | R48 | Y56 | I59 | ASN | THR | LYS | GLU | LYS | LEU | GLU | P68 | L107 | E113 | G114 | GLU | LYS | HIS | THR | LYS | GLU | TVR | ASP | ARG | ALA | LEU | VAL | GLN | ARG | ASN | T130 | M134 | K137 | G141 | Q145 | V173 | E176 | GLY | LEU | LYS | LYS |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|------|------|------|------|-----|-----|-----|-----|

4 Data and refinement statistics

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	62.44Å 85.43Å 194.78Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	26.46 – 2.00	Depositor
% Data completeness (in resolution range)	96.9 (26.46-2.00)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.88 (at 1.99Å)	Xtriage
Refinement program	PHENIX 1.7.2_869	Depositor
R, R_{free}	0.189 , 0.219	Depositor
Wilson B-factor (Å ²)	30.3	Xtriage
Anisotropy	0.175	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6933	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.90% 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: NO3

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	0.35	0/3518	0.55	0/4772
2	B	0.31	0/2241	0.52	0/3048
3	F	0.30	0/971	0.49	0/1308
All	All	0.33	0/6730	0.53	0/9128

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

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	3439	0	3445	28	0
2	B	2199	0	2147	17	0
3	F	955	0	951	8	0
4	A	9	0	5	1	0
5	A	4	0	0	0	0
6	A	218	0	0	3	0
6	B	54	0	0	1	0
6	F	55	0	0	0	0
All	All	6933	0	6548	49	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 4.

All (49) 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:334:ARG:NH2	4:A:501:GLN:OXT	2.15	0.79
1:A:436:LEU:HD21	1:A:444:LEU:HD22	1.73	0.70
2:B:270:THR:O	2:B:270:THR:OG1	2.12	0.68
1:A:418:ASP:OD2	6:A:684:HOH:O	2.15	0.62
2:B:152:GLN:OE1	2:B:154:GLN:NE2	2.32	0.62
1:A:249:PRO:HB3	1:A:396:LEU:HG	1.83	0.60
1:A:377:ASN:ND2	6:A:779:HOH:O	2.33	0.60
3:F:134:ASN:ND2	3:F:137:LYS:H	2.01	0.59
1:A:283:PRO:HB2	3:F:107:LEU:HD13	1.87	0.57
1:A:229:LYS:NZ	6:A:773:HOH:O	2.39	0.55
1:A:263:LEU:HB3	1:A:268:LEU:HD11	1.88	0.55
2:B:31:CYS:HB3	2:B:193:PHE:HB2	1.89	0.54
2:B:128:ARG:NH2	6:B:429:HOH:O	2.37	0.52
2:B:89:LEU:HD23	2:B:153:LEU:HD21	1.92	0.52
1:A:307:TYR:CE2	1:A:326:LYS:HG3	2.45	0.52
2:B:113:GLN:NE2	2:B:118:GLN:HB2	2.24	0.52
2:B:29:LEU:O	2:B:194:SER:HA	2.11	0.50
1:A:7:LEU:O	1:A:11:ILE:HG12	2.12	0.50
1:A:264:ILE:HG13	1:A:270:ILE:HD12	1.93	0.49
1:A:275:ILE:O	1:A:278:VAL:HG22	2.13	0.49
2:B:113:GLN:HE22	2:B:118:GLN:HB2	1.78	0.48
1:A:438:GLU:HG2	1:A:439:LYS:HD3	1.96	0.48
1:A:156:ARG:HH11	1:A:445:GLN:HE22	1.63	0.47
1:A:66:SER:HB2	1:A:99:GLU:HG3	1.96	0.47
1:A:350:ASN:HD22	1:A:350:ASN:HA	1.58	0.46
1:A:156:ARG:HH11	1:A:445:GLN:NE2	2.13	0.46
3:F:45:TYR:HA	3:F:48:ARG:HD3	1.97	0.46
2:B:87:MET:HE2	2:B:311:LEU:HD13	1.98	0.46
2:B:165:THR:OG1	2:B:165:THR:O	2.34	0.45
1:A:21:TYR:CE1	1:A:117:PRO:HA	2.52	0.45
1:A:197[B]:ASN:H	1:A:197[B]:ASN:ND2	2.14	0.45
2:B:34:GLU:HB2	2:B:228:ASP:HB2	2.00	0.44
2:B:38:GLN:HA	2:B:184:LEU:HD23	2.00	0.43
2:B:231:LEU:HD12	2:B:239:VAL:HG13	2.01	0.43
3:F:141:GLY:O	3:F:145:GLN:HG3	2.18	0.43
1:A:156:ARG:HD2	1:A:445:GLN:HE21	1.83	0.43
2:B:174:LEU:HD23	3:F:173:VAL:HG12	2.00	0.43
1:A:11:ILE:HD12	1:A:31:PRO:HG2	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:246:GLU:HG3	1:A:420:PHE:CZ	2.53	0.43
2:B:141:ILE:HG22	2:B:143:GLU:H	1.84	0.42
1:A:360:ASN:HD21	3:F:113:GLU:H	1.67	0.42
1:A:280:ASN:ND2	3:F:56:TYR:OH	2.45	0.42
1:A:418:ASP:HB3	1:A:422:VAL:HG13	2.02	0.42
3:F:134:ASN:HD21	3:F:137:LYS:HG2	1.84	0.42
1:A:25:THR:O	1:A:111:ARG:NH1	2.45	0.41
2:B:36:HIS:HD2	2:B:156:GLU:OE1	2.03	0.41
1:A:156:ARG:HD2	1:A:445:GLN:NE2	2.36	0.41
2:B:258:TYR:O	2:B:262:VAL:HG23	2.21	0.40
1:A:6:SER:O	1:A:10:SER:N	2.51	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

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

2 ligands are modelled in this entry.

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
5	NO3	A	502	-	1,3,3	3.70	1 (100%)	0,3,3	0.00	-
4	GLN	A	501	-	4,8,9	0.59	0	2,9,11	1.11	0

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
4	GLN	A	501	-	-	0/3/8/9	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	502	NO3	O1-N	3.70	1.41	1.24

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	501	GLN	1	0

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 ⓘ

EDS failed to run properly - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

EDS failed to run properly - this section is therefore empty.

6.3 Carbohydrates ⓘ

EDS failed to run properly - this section is therefore empty.

6.4 Ligands ⓘ

EDS failed to run properly - this section is therefore empty.

6.5 Other polymers ⓘ

EDS failed to run properly - this section is therefore empty.