



Full wwPDB NMR Structure Validation Report ⓘ

Mar 9, 2026 – 06:57 PM UTC

PDB ID : 2L0Y / pdb_00002l0y
BMRB ID : 17067
Title : Complex hMia40-hCox17
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Deposited on : 2010-07-20

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A user guide is available at

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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
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
wwPDB-RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
wwPDB-ShiftChecker : v1.2
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

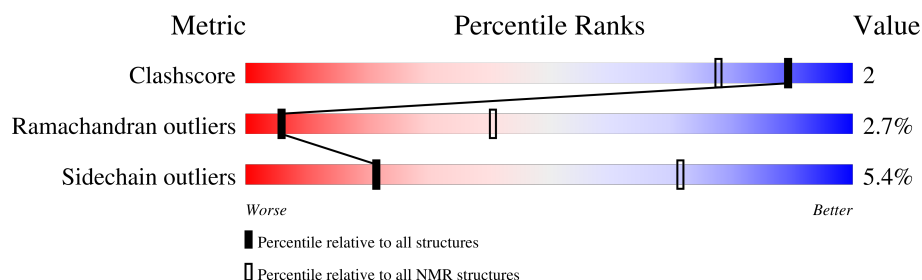
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 64%.

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)	NMR archive (#Entries)
Clashscore	229148	14424
Ramachandran outliers	224038	12848
Sidechain outliers	223484	12823

The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A cyan segment indicates the fraction of residues that are not part of the well-defined cores, and 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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	146	
2	B	67	

2 Ensemble composition and analysis

This entry contains 20 models. Model 14 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *lowest energy*.

The following residues are included in the computation of the global validation metrics.

Well-defined (core) protein residues			
Well-defined core	Residue range (total)	Backbone RMSD (Å)	Medoid model
1	A:3-A:7, A:11-A:53, B:66-B:77 (60)	0.68	14

Ill-defined regions of proteins are excluded from the global statistics.

Ligands and non-protein polymers are included in the analysis.

The models can be grouped into 4 clusters and 3 single-model clusters were found.

Cluster number	Models
1	1, 7, 9, 13, 17, 18, 20
2	4, 5, 6, 10, 14
3	3, 12, 16
4	2, 19
Single-model clusters	8; 11; 15

3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 1214 atoms, of which 580 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Mitochondrial intermembrane space import and assembly protein 40.

Mol	Chain	Residues	Atoms						Trace
1	A	60	Total	C	H	N	O	S	0
			881	289	415	77	92	8	

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-48	GLY	-	expression tag	UNP Q8N4Q1
A	-47	SER	-	expression tag	UNP Q8N4Q1
A	-46	PHE	-	expression tag	UNP Q8N4Q1
A	-45	THR	-	expression tag	UNP Q8N4Q1
A	8	SER	CYS	engineered mutation	UNP Q8N4Q1

- Molecule 2 is a protein called COX17 cytochrome c oxidase assembly homolog (S. cerevisiae) pseudogene (COX17).

Mol	Chain	Residues	Atoms						Trace
2	B	21	Total	C	H	N	O	S	0
			333	105	165	32	29	2	

There are 5 discrepancies between the modelled and reference sequences:

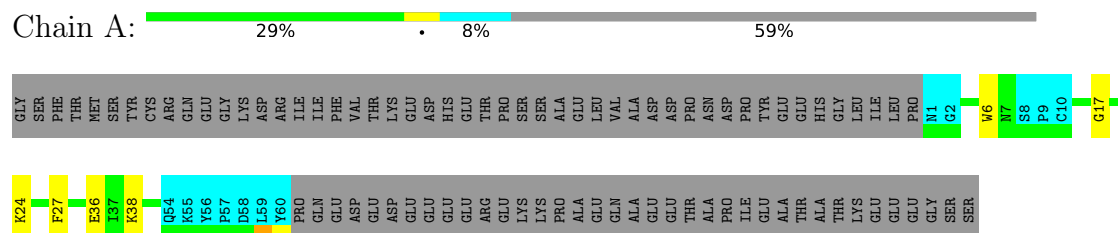
Chain	Residue	Modelled	Actual	Comment	Reference
B	15	GLY	-	expression tag	UNP Q5W0Q5
B	16	SER	-	expression tag	UNP Q5W0Q5
B	17	PHE	-	expression tag	UNP Q5W0Q5
B	18	THR	-	expression tag	UNP Q5W0Q5
B	73	SER	CYS	engineered mutation	UNP Q5W0Q5

4 Residue-property plots

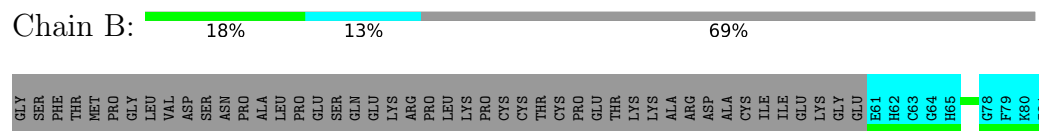
4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-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. Stretches of 2 or more consecutive residues without any outliers are shown as green connectors. Residues which are classified as ill-defined in the NMR ensemble, are shown in cyan with an underline colour-coded according to the previous scheme. Residues which were present in the experimental sample, but not modelled in the final structure are shown in grey.

- Molecule 1: Mitochondrial intermembrane space import and assembly protein 40



- Molecule 2: COX17 cytochrome c oxidase assembly homolog (*S. cerevisiae*) pseudogene (COX17)

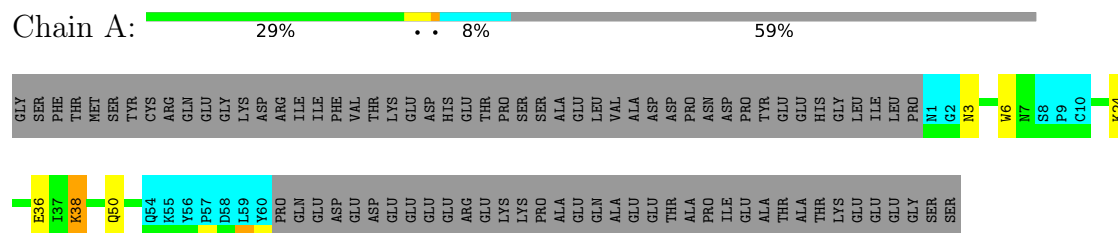


4.2 Scores per residue for each member of the ensemble

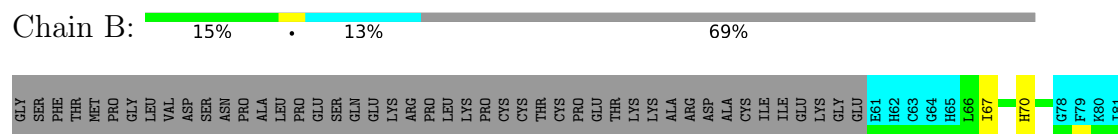
Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

- Molecule 1: Mitochondrial intermembrane space import and assembly protein 40

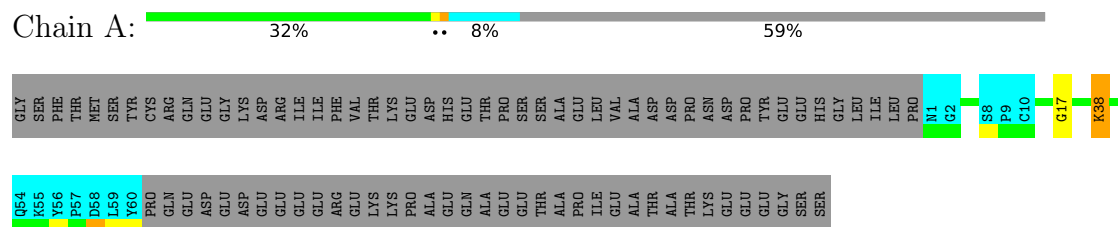


- Molecule 2: COX17 cytochrome c oxidase assembly homolog (*S. cerevisiae*) pseudogene (COX17)

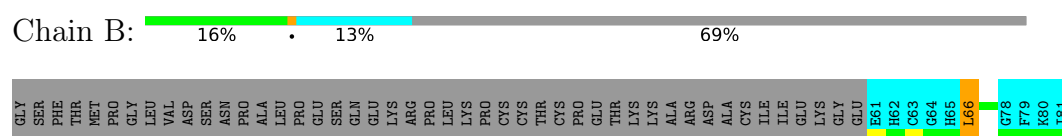


4.2.2 Score per residue for model 2

- Molecule 1: Mitochondrial intermembrane space import and assembly protein 40

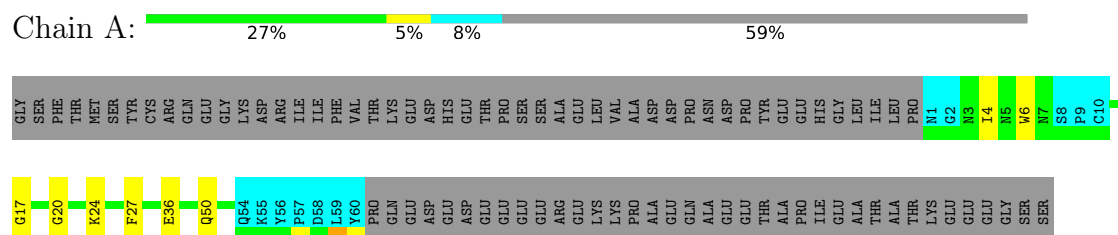


- Molecule 2: COX17 cytochrome c oxidase assembly homolog (*S. cerevisiae*) pseudogene (COX17)

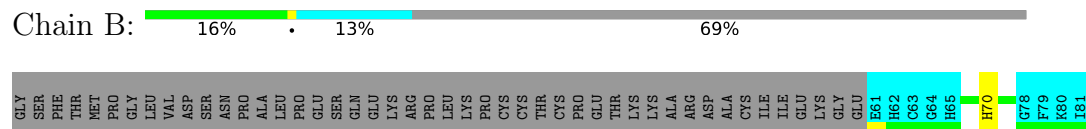


4.2.3 Score per residue for model 3

- Molecule 1: Mitochondrial intermembrane space import and assembly protein 40



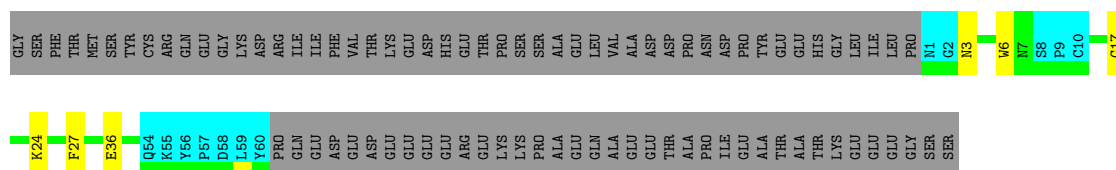
- Molecule 2: COX17 cytochrome c oxidase assembly homolog (*S. cerevisiae*) pseudogene (COX17)



4.2.4 Score per residue for model 4

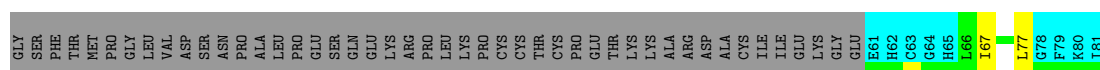
- Molecule 1: Mitochondrial intermembrane space import and assembly protein 40

Chain A:  29% 8% 59%



- Molecule 2: COX17 cytochrome c oxidase assembly homolog (*S. cerevisiae*) pseudogene (COX17)

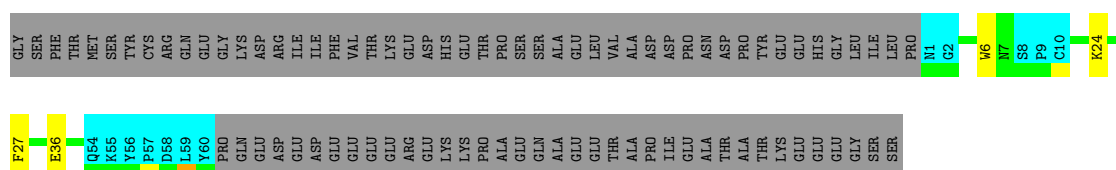
Chain B:  15% 13% 69%



4.2.5 Score per residue for model 5

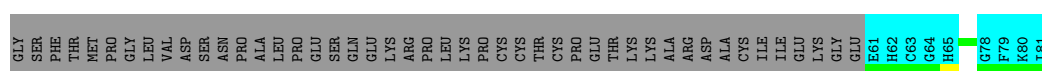
- Molecule 1: Mitochondrial intermembrane space import and assembly protein 40

Chain A:  30% 8% 59%



- Molecule 2: COX17 cytochrome c oxidase assembly homolog (*S. cerevisiae*) pseudogene (COX17)

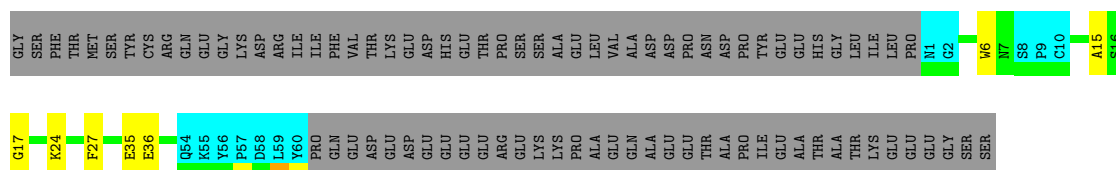
Chain B:  18% 13% 69%



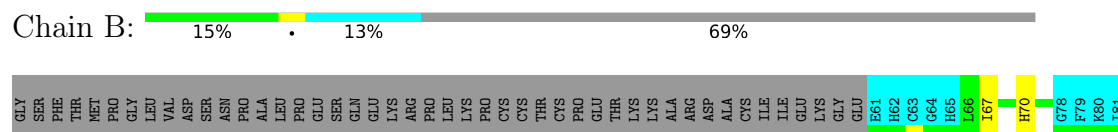
4.2.6 Score per residue for model 6

- Molecule 1: Mitochondrial intermembrane space import and assembly protein 40

Chain A:  28% 5% 8% 59%



- Molecule 2: COX17 cytochrome c oxidase assembly homolog (*S. cerevisiae*) pseudogene (COX17)

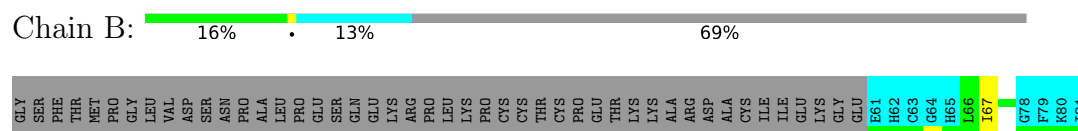


4.2.7 Score per residue for model 7

- Molecule 1: Mitochondrial intermembrane space import and assembly protein 40

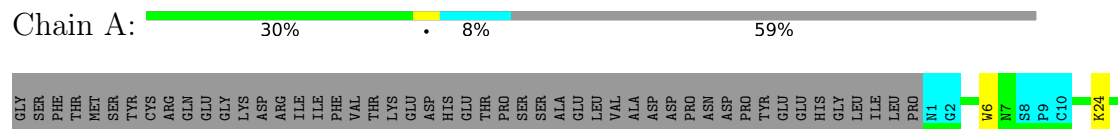


- Molecule 2: COX17 cytochrome c oxidase assembly homolog (*S. cerevisiae*) pseudogene (COX17)

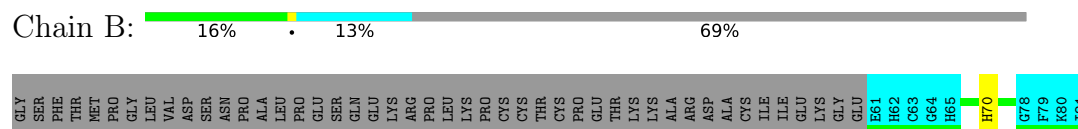


4.2.8 Score per residue for model 8

- Molecule 1: Mitochondrial intermembrane space import and assembly protein 40



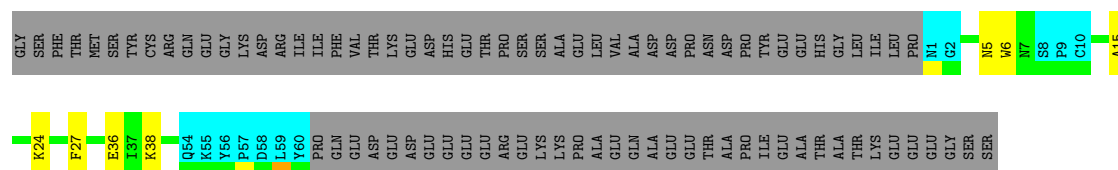
- Molecule 2: COX17 cytochrome c oxidase assembly homolog (*S. cerevisiae*) pseudogene (COX17)



4.2.9 Score per residue for model 9

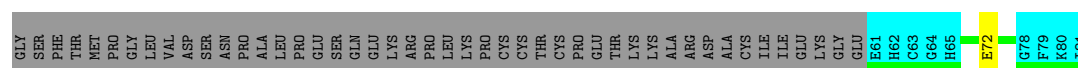
- Molecule 1: Mitochondrial intermembrane space import and assembly protein 40

Chain A:  28% 5% 8% 59%



- Molecule 2: COX17 cytochrome c oxidase assembly homolog (*S. cerevisiae*) pseudogene (COX17)

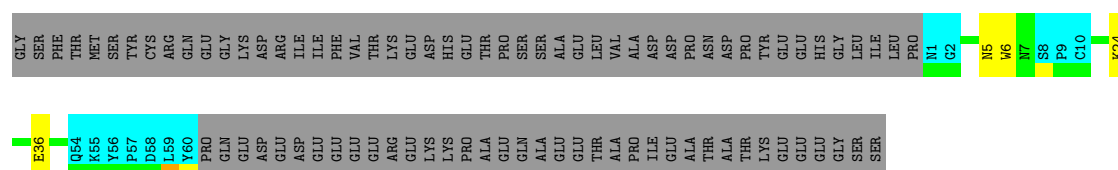
Chain B:  16% 13% 69%



4.2.10 Score per residue for model 10

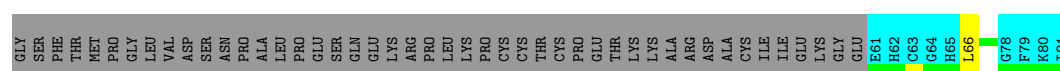
- Molecule 1: Mitochondrial intermembrane space import and assembly protein 40

Chain A:  30% 8% 59%



- Molecule 2: COX17 cytochrome c oxidase assembly homolog (*S. cerevisiae*) pseudogene (COX17)

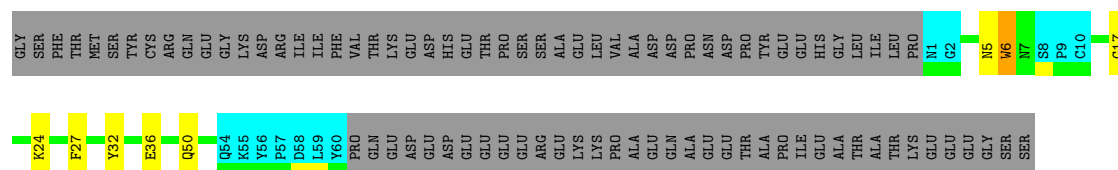
Chain B:  16% 13% 69%



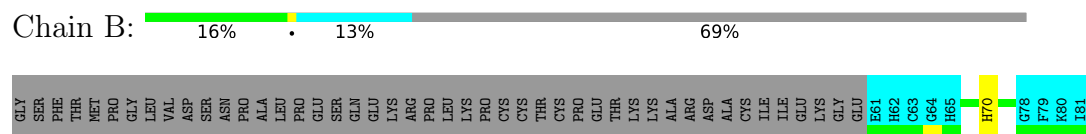
4.2.11 Score per residue for model 11

- Molecule 1: Mitochondrial intermembrane space import and assembly protein 40

Chain A:  27% 5% 8% 59%

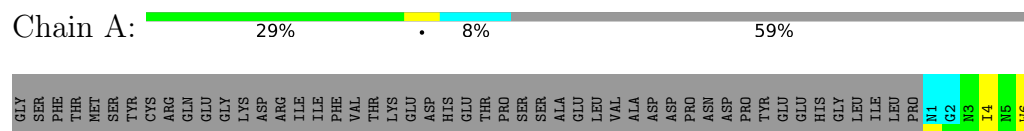


- Molecule 2: COX17 cytochrome c oxidase assembly homolog (*S. cerevisiae*) pseudogene (COX17)

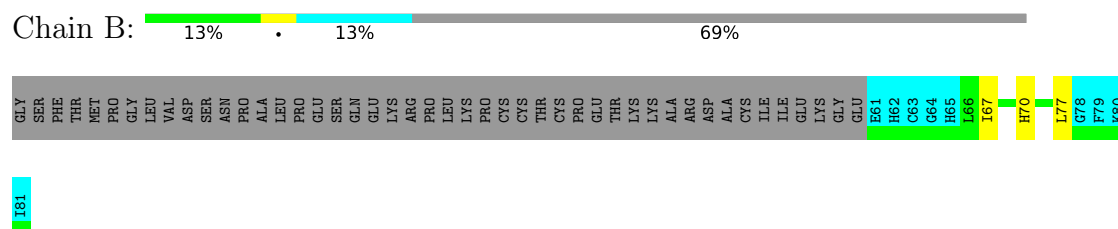


4.2.12 Score per residue for model 12

- Molecule 1: Mitochondrial intermembrane space import and assembly protein 40

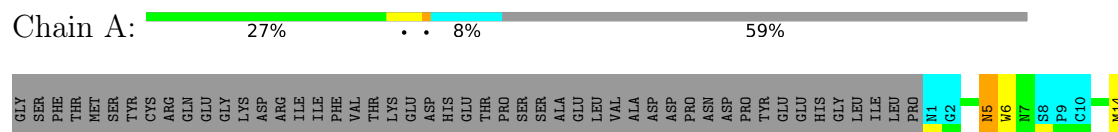


- Molecule 2: COX17 cytochrome c oxidase assembly homolog (*S. cerevisiae*) pseudogene (COX17)

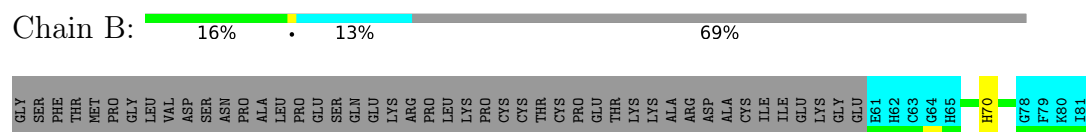


4.2.13 Score per residue for model 13

- Molecule 1: Mitochondrial intermembrane space import and assembly protein 40

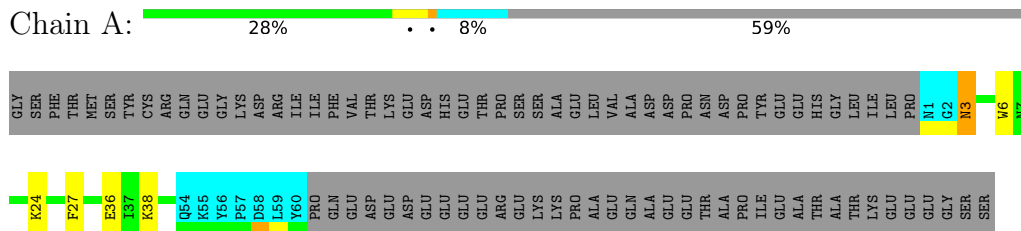


- Molecule 2: COX17 cytochrome c oxidase assembly homolog (*S. cerevisiae*) pseudogene (COX17)

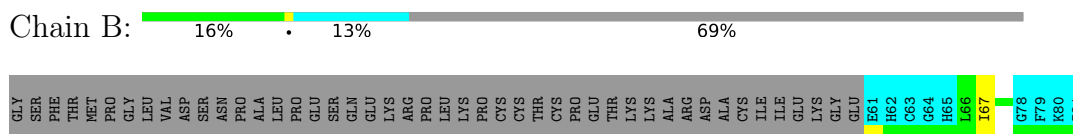


4.2.14 Score per residue for model 14 (medoid)

- Molecule 1: Mitochondrial intermembrane space import and assembly protein 40

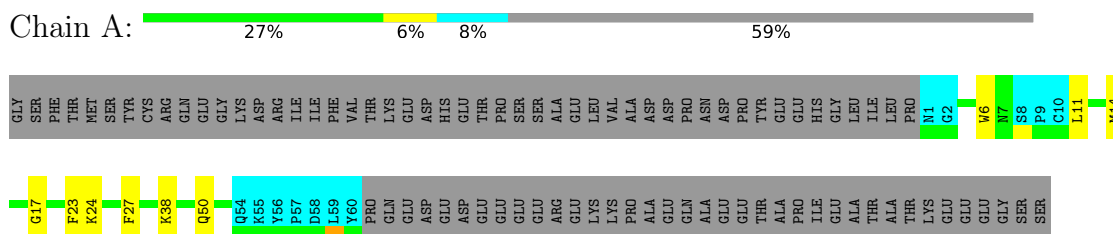


- Molecule 2: COX17 cytochrome c oxidase assembly homolog (*S. cerevisiae*) pseudogene (COX17)

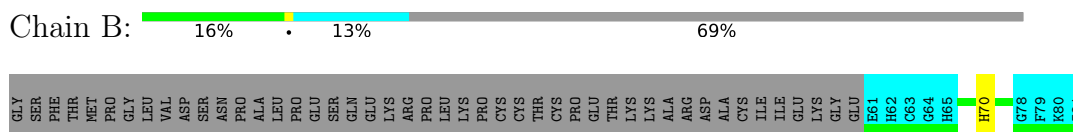


4.2.15 Score per residue for model 15

- Molecule 1: Mitochondrial intermembrane space import and assembly protein 40

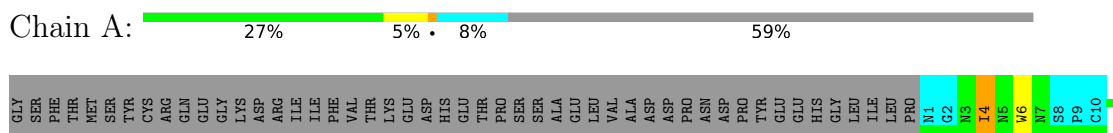


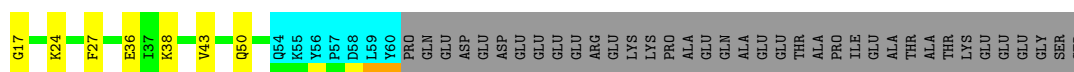
- Molecule 2: COX17 cytochrome c oxidase assembly homolog (*S. cerevisiae*) pseudogene (COX17)



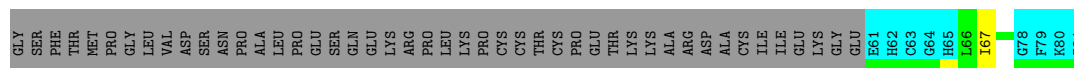
4.2.16 Score per residue for model 16

- Molecule 1: Mitochondrial intermembrane space import and assembly protein 40



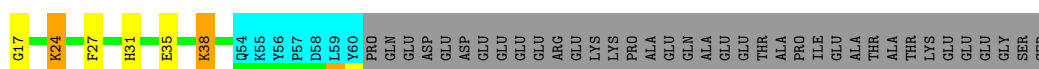
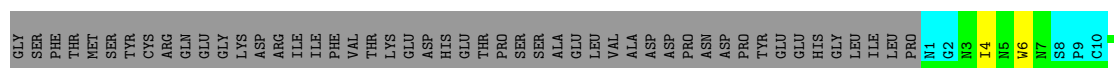


- Molecule 2: COX17 cytochrome c oxidase assembly homolog (*S. cerevisiae*) pseudogene (COX17)

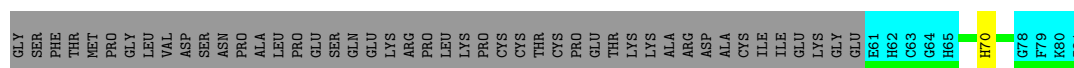


4.2.17 Score per residue for model 17

- Molecule 1: Mitochondrial intermembrane space import and assembly protein 40

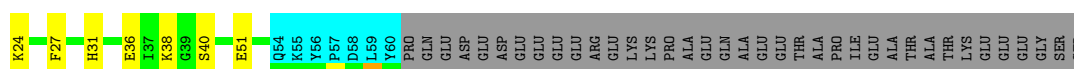
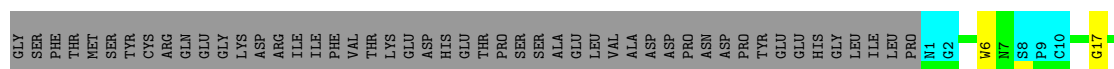


- Molecule 2: COX17 cytochrome c oxidase assembly homolog (*S. cerevisiae*) pseudogene (COX17)

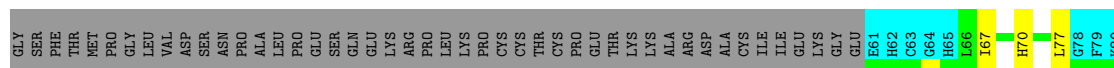


4.2.18 Score per residue for model 18

- Molecule 1: Mitochondrial intermembrane space import and assembly protein 40



- Molecule 2: COX17 cytochrome c oxidase assembly homolog (*S. cerevisiae*) pseudogene (COX17)



I81

4.2.19 Score per residue for model 19

- Molecule 1: Mitochondrial intermembrane space import and assembly protein 40

Chain A: 

GLY SER PHE THR MET SER TYR CYS ARG GLN GLY LYS ASP ARG ILE ILE PHE VAL GLN THR LYS GLU ASP ASP HIS GLU THR PRO GLU SER LYS ALA LEU VAL ALA ASP PRO ASN ASP THR PRO TYR GLU HIS GLY THR GLY LEU ILE LEU PRO N1 G2 N3 I4 N5 N6 N7 S8 P9 C10 L11

F23 F24 F27 E36 F37 K38 Q54 K55 Y56 P57 D58 L59 Y60 PRO GLN GLU ASP ASP ASP GLU GLU THR PRO GLU SER LYS ALA LEU VAL ALA ASP PRO ASN ASP THR PRO TYR GLU HIS GLY THR GLY LEU ILE LEU PRO N1 G2 N3 I4 N5 N6 N7 S8 P9 C10 L11

- Molecule 2: COX17 cytochrome c oxidase assembly homolog (*S. cerevisiae*) pseudogene (COX17)

Chain B: 

GLY SER PHE THR MET SER TYR CYS ARG GLN GLU ASP ASP HIS GLU THR PRO GLU SER LYS ALA LEU VAL ALA ASP PRO ASN ASP THR PRO TYR GLU HIS GLY THR GLY LEU ILE LEU PRO N1 G2 N3 I4 N5 N6 N7 S8 P9 C10 L11

4.2.20 Score per residue for model 20

- Molecule 1: Mitochondrial intermembrane space import and assembly protein 40

Chain A: 

GLY SER PHE THR MET SER TYR CYS ARG GLN GLU ASP ASP HIS GLU THR PRO GLU SER LYS ALA LEU VAL ALA ASP PRO ASN ASP THR PRO TYR GLU HIS GLY THR GLY LEU ILE LEU PRO N1 G2 N3 I4 N5 N6 N7 S8 P9 C10 L11

F27 F35 E36 K38 E51 Q54 K55 Y56 P57 D58 L59 Y60 PRO GLN GLU ASP ASP ASP ASP GLU GLU THR PRO GLU SER LYS ALA LEU VAL ALA ASP PRO ASN ASP THR PRO TYR GLU HIS GLY THR GLY LEU ILE LEU PRO N1 G2 N3 I4 N5 N6 N7 S8 P9 C10 L11

- Molecule 2: COX17 cytochrome c oxidase assembly homolog (*S. cerevisiae*) pseudogene (COX17)

Chain B: 

GLY SER PHE THR MET SER TYR CYS ARG GLN GLU ASP ASP HIS GLU THR PRO GLU SER LYS ALA LEU VAL ALA ASP PRO ASN ASP THR PRO TYR GLU HIS GLY THR GLY LEU ILE LEU PRO N1 G2 N3 I4 N5 N6 N7 S8 P9 C10 L11

5 Refinement protocol and experimental data overview

The models were refined using the following method: *simulated annealing, molecular dynamics*.

Of the 400 calculated structures, 20 were deposited, based on the following criterion: *target function*.

The following table shows the software used for structure solution, optimisation and refinement.

Software name	Classification	Version
Amber	refinement	10.0
CYANA	structure solution	2.1

The following table shows chemical shift validation statistics as aggregates over all chemical shift files. Detailed validation can be found in section 7 of this report.

Chemical shift file(s)	working_cs.cif
Number of chemical shift lists	1
Total number of shifts	1135
Number of shifts mapped to atoms	624
Number of unparsed shifts	0
Number of shifts with mapping errors	511
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	64%

6 Model quality i

6.1 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 (average) 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	0.82±0.02	0±0/379 (0.0± 0.0%)	1.53±0.04	2±2/508 (0.5± 0.3%)
2	B	0.84±0.03	0±0/97 (0.0± 0.0%)	1.49±0.09	1±1/129 (0.5± 0.6%)
All	All	0.82	0/9520 (0.0%)	1.53	62/12740 (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	Planarity
1	A	0.0±0.0	0.1±0.5
All	All	0	3

There are no bond-length outliers.

All unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	17	GLY	CA-C-N	6.82	127.38	119.47	14	12
1	A	17	GLY	C-N-CA	6.82	127.38	119.47	14	12
2	B	70	HIS	CA-CB-CG	6.50	120.30	113.80	1	9
1	A	20	GLY	CA-C-N	5.93	128.82	120.28	3	2
1	A	20	GLY	C-N-CA	5.93	128.82	120.28	3	2
1	A	3	ASN	CA-CB-CG	5.72	118.32	112.60	14	1
1	A	50	GLN	CA-C-N	5.68	128.46	120.28	12	6
1	A	50	GLN	C-N-CA	5.68	128.46	120.28	12	6
2	B	70	HIS	CB-CG-CD2	-5.58	123.95	131.20	12	2
1	A	24	LYS	CA-C-N	5.43	127.50	120.44	17	1
1	A	24	LYS	C-N-CA	5.43	127.50	120.44	17	1
1	A	35	GLU	CA-C-N	5.17	131.41	121.54	13	1
1	A	35	GLU	C-N-CA	5.17	131.41	121.54	13	1
2	B	77	LEU	CA-C-N	5.06	125.60	119.98	4	1

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
2	B	77	LEU	C-N-CA	5.06	125.60	119.98	4	1
1	A	19	CYS	CA-C-N	5.01	125.65	119.99	7	1
1	A	19	CYS	C-N-CA	5.01	125.65	119.99	7	1
1	A	5	ASN	CA-C-N	5.00	127.69	120.38	13	1
1	A	5	ASN	C-N-CA	5.00	127.69	120.38	13	1

There are no chirality outliers.

All unique planar outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Group	Models (Total)
1	A	6	TRP	Peptide	1
1	A	32	TYR	Sidechain	1
1	A	30	PHE	Sidechain	1

6.2 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 each 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 averaged over the ensemble.

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	370	329	329	2±1
2	B	96	102	102	0±0
All	All	9320	8620	8620	33

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 2.

All unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:66:LEU:H	2:B:66:LEU:HD23	0.55	1.60	2	1
1:A:11:LEU:HD23	1:A:23:PHE:CE2	0.53	2.39	19	2
1:A:6:TRP:CH2	1:A:24:LYS:HA	0.52	2.40	3	13
1:A:4:ILE:HG21	1:A:11:LEU:HD22	0.49	1.85	19	1
1:A:15:ALA:HB1	1:A:24:LYS:CE	0.48	2.38	6	2
1:A:6:TRP:CE2	1:A:24:LYS:HD2	0.48	2.44	8	11
1:A:4:ILE:HG21	1:A:6:TRP:CE3	0.47	2.44	12	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:66:LEU:H	2:B:66:LEU:CD2	0.42	2.27	2	1

6.3 Torsion angles [i](#)

6.3.1 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 PDB entries followed by that with respect to all NMR entries. 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	48/146 (33%)	42±1 (87±3%)	5±1 (10±3%)	2±1 (3±1%)	5	35
2	B	12/67 (18%)	12±0 (99±2%)	0±0 (1±3%)	0±0 (0±0%)	100	100
All	All	1200/4260 (28%)	1070 (89%)	98 (8%)	32 (3%)	6	41

All 5 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	36	GLU	15
1	A	38	LYS	12
1	A	5	ASN	3
1	A	3	ASN	1
1	A	35	GLU	1

6.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all NMR entries. 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	40/126 (32%)	38±1 (95±3%)	2±1 (5±3%)	24	74
2	B	10/57 (18%)	9±1 (92±6%)	1±1 (8±6%)	14	62
All	All	1000/3660 (27%)	946 (95%)	54 (5%)	21	71

All 16 unique residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	27	PHE	14
2	B	67	ILE	8
1	A	38	LYS	5
1	A	3	ASN	3
2	B	66	LEU	3
1	A	4	ILE	3
1	A	35	GLU	3
1	A	51	GLU	3
1	A	43	VAL	2
2	B	77	LEU	2
1	A	14	MET	2
1	A	31	HIS	2
2	B	72	GLU	1
1	A	5	ASN	1
2	B	70	HIS	1
1	A	40	SER	1

6.3.3 RNA [i](#)

There are no RNA molecules in this entry.

6.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.6 Ligand geometry [i](#)

There are no ligands in this entry.

6.7 Other polymers [i](#)

There are no such molecules in this entry.

6.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

7 Chemical shift validation

The completeness of assignment taking into account all chemical shift lists is 64% for the well-defined parts and 60% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *assigned_chem_shift_list_1*

7.1.1 Bookkeeping

The following table shows the results of parsing the chemical shift list and reports the number of nuclei with statistically unusual chemical shifts.

Total number of shifts	1135
Number of shifts mapped to atoms	624
Number of unparsed shifts	0
Number of shifts with mapping errors	511
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	13

The following assigned chemical shifts were not mapped to the molecules present in the coordinate file.

- No matching atom found in the structure. All 511 occurrences are reported below.

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	-23	THR	H	8.27	0.02	1
1	A	-23	THR	C	170.0	0.3	1
1	A	-23	THR	CA	57.1	0.3	1
1	A	-23	THR	CB	66.9	0.3	1
1	A	-23	THR	N	118.4	0.3	1
1	A	-21	SER	H	8.43	0.02	1
1	A	-21	SER	HA	4.31	0.02	1
1	A	-21	SER	C	172.1	0.3	1
1	A	-21	SER	CA	55.5	0.3	1
1	A	-21	SER	CB	61.1	0.3	1
1	A	-21	SER	N	116.5	0.3	1
1	A	-20	SER	H	8.27	0.02	1
1	A	-20	SER	HA	4.29	0.02	1
1	A	-20	SER	C	171.6	0.3	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	-20	SER	CA	55.7	0.3	1
1	A	-20	SER	CB	60.9	0.3	1
1	A	-20	SER	N	117.6	0.3	1
1	A	-19	ALA	H	8.2	0.02	1
1	A	-19	ALA	HA	4.18	0.02	1
1	A	-19	ALA	C	174.9	0.3	1
1	A	-19	ALA	CA	50.0	0.3	1
1	A	-19	ALA	CB	16.3	0.3	1
1	A	-19	ALA	N	125.5	0.3	1
1	A	-18	GLU	H	8.14	0.02	1
1	A	-18	GLU	HA	4.12	0.02	1
1	A	-18	GLU	HB2	1.83	0.02	2
1	A	-18	GLU	HB3	1.92	0.02	2
1	A	-18	GLU	HG2	2.14	0.02	2
1	A	-18	GLU	HG3	2.12	0.02	2
1	A	-18	GLU	C	173.5	0.3	1
1	A	-18	GLU	CA	53.8	0.3	1
1	A	-18	GLU	CB	27.3	0.3	1
1	A	-18	GLU	CG	33.4	0.3	1
1	A	-18	GLU	N	119.3	0.3	1
1	A	-17	LEU	H	8.05	0.02	1
1	A	-17	LEU	HA	4.23	0.02	1
1	A	-17	LEU	HB2	1.41	0.02	2
1	A	-17	LEU	HB3	1.49	0.02	2
1	A	-17	LEU	HG	1.47	0.02	1
1	A	-17	LEU	C	174.3	0.3	1
1	A	-17	LEU	CA	52.3	0.3	1
1	A	-17	LEU	CB	39.5	0.3	1
1	A	-17	LEU	CD1	22.0	0.3	1
1	A	-17	LEU	CD2	20.8	0.3	1
1	A	-17	LEU	CG	24.2	0.3	1
1	A	-17	LEU	N	123.1	0.3	1
1	A	-16	VAL	H	8.05	0.02	1
1	A	-16	VAL	HA	3.96	0.02	1
1	A	-16	VAL	HB	1.92	0.02	1
1	A	-16	VAL	C	172.9	0.3	1
1	A	-16	VAL	CA	59.1	0.3	1
1	A	-16	VAL	CB	29.9	0.3	1
1	A	-16	VAL	CG1	17.8	0.3	1
1	A	-16	VAL	CG2	18.5	0.3	1
1	A	-16	VAL	N	122.0	0.3	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	-15	ALA	H	8.29	0.02	1
1	A	-15	ALA	HA	4.18	0.02	1
1	A	-15	ALA	C	174.3	0.3	1
1	A	-15	ALA	CA	49.4	0.3	1
1	A	-15	ALA	CB	16.6	0.3	1
1	A	-15	ALA	N	128.4	0.3	1
1	A	-14	ASP	H	8.18	0.02	1
1	A	-14	ASP	HA	4.34	0.02	1
1	A	-14	ASP	C	172.8	0.3	1
1	A	-14	ASP	CA	51.4	0.3	1
1	A	-14	ASP	CB	38.4	0.3	1
1	A	-14	ASP	N	120.2	0.3	1
1	A	-13	ASP	H	8.23	0.02	1
1	A	-13	ASP	HA	4.74	0.02	1
1	A	-13	ASP	HB2	2.7	0.02	2
1	A	-13	ASP	HB3	2.43	0.02	2
1	A	-13	ASP	C	172.4	0.3	1
1	A	-13	ASP	CA	49.1	0.3	1
1	A	-13	ASP	CB	38.6	0.3	1
1	A	-13	ASP	N	121.9	0.3	1
1	A	-12	PRO	HA	4.26	0.02	1
1	A	-12	PRO	HB2	2.1	0.02	2
1	A	-12	PRO	HB3	1.82	0.02	2
1	A	-12	PRO	HD2	3.7	0.02	2
1	A	-12	PRO	HD3	3.6	0.02	2
1	A	-12	PRO	HG2	1.9	0.02	2
1	A	-12	PRO	HG3	1.83	0.02	2
1	A	-12	PRO	CA	60.7	0.3	1
1	A	-12	PRO	CB	29.2	0.3	1
1	A	-12	PRO	CD	47.9	0.3	1
1	A	-12	PRO	CG	24.0	0.3	1
1	A	-11	ASN	H	8.39	0.02	1
1	A	-11	ASN	HA	4.51	0.02	1
1	A	-11	ASN	HB2	2.65	0.02	2
1	A	-11	ASN	HB3	2.61	0.02	2
1	A	-11	ASN	HD21	6.84	0.02	1
1	A	-11	ASN	HD22	7.72	0.02	1
1	A	-11	ASN	C	171.8	0.3	1
1	A	-11	ASN	CA	50.5	0.3	1
1	A	-11	ASN	CB	36.2	0.3	1
1	A	-11	ASN	N	117.9	0.3	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	-10	ASP	H	8.04	0.02	1
1	A	-10	ASP	HA	4.72	0.02	1
1	A	-10	ASP	HB2	2.41	0.02	2
1	A	-10	ASP	HB3	2.66	0.02	2
1	A	-10	ASP	C	171.7	0.3	1
1	A	-10	ASP	CA	49.5	0.3	1
1	A	-10	ASP	CB	38.3	0.3	1
1	A	-10	ASP	N	121.6	0.3	1
1	A	-8	TYR	H	8.21	0.02	1
1	A	-8	TYR	C	173.1	0.3	1
1	A	-8	TYR	CA	55.3	0.3	1
1	A	-8	TYR	CB	35.5	0.3	1
1	A	-8	TYR	N	119.8	0.3	1
1	A	-7	GLU	H	7.86	0.02	1
1	A	-7	GLU	C	173.2	0.3	1
1	A	-7	GLU	CA	53.6	0.3	1
1	A	-7	GLU	CB	27.6	0.3	1
1	A	-7	GLU	N	122.3	0.3	1
1	A	-5	HIS	HA	4.51	0.02	1
1	A	-5	HIS	HB2	3.05	0.02	2
1	A	-5	HIS	HB3	2.95	0.02	2
1	A	-5	HIS	CA	53.1	0.3	1
1	A	-5	HIS	CB	27.6	0.3	1
1	A	-4	GLY	H	8.23	0.02	1
1	A	-4	GLY	HA2	3.78	0.02	2
1	A	-4	GLY	HA3	3.93	0.02	2
1	A	-4	GLY	C	171.0	0.3	1
1	A	-4	GLY	CA	42.7	0.3	1
1	A	-4	GLY	N	108.8	0.3	1
1	A	-3	LEU	HA	3.99	0.02	1
1	A	-3	LEU	HB2	1.43	0.02	2
1	A	-3	LEU	HB3	1.49	0.02	2
1	A	-3	LEU	HG	0.74	0.02	1
1	A	-3	LEU	CA	54.8	0.3	1
1	A	-3	LEU	CB	40.2	0.3	1
1	A	-3	LEU	CD1	21.3	0.3	1
1	A	-3	LEU	CD2	21.1	0.3	1
1	A	-3	LEU	CG	22.7	0.3	1
1	A	-2	ILE	H	7.62	0.02	1
1	A	-2	ILE	HA	4.21	0.02	1
1	A	-2	ILE	HB	1.71	0.02	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	-2	ILE	HG12	1.26	0.02	2
1	A	-2	ILE	HG13	1.09	0.02	2
1	A	-2	ILE	C	174.4	0.3	1
1	A	-2	ILE	CA	54.8	0.3	1
1	A	-2	ILE	CB	33.9	0.3	1
1	A	-2	ILE	CD1	6.8	0.3	1
1	A	-2	ILE	CG1	23.5	0.3	1
1	A	-2	ILE	CG2	14.0	0.3	1
1	A	-2	ILE	N	115.3	0.3	1
1	A	-1	LEU	H	8.73	0.02	1
1	A	-1	LEU	HA	4.21	0.02	1
1	A	-1	LEU	HB2	1.49	0.02	2
1	A	-1	LEU	HB3	1.41	0.02	2
1	A	-1	LEU	HG	0.66	0.02	1
1	A	-1	LEU	C	174.4	0.3	1
1	A	-1	LEU	CA	51.4	0.3	1
1	A	-1	LEU	CB	37.4	0.3	1
1	A	-1	LEU	CD1	17.7	0.3	1
1	A	-1	LEU	CD2	19.6	0.3	1
1	A	-1	LEU	CG	22.7	0.3	1
1	A	-1	LEU	N	127.5	0.3	1
1	A	0	PRO	HA	4.15	0.02	1
1	A	0	PRO	HB2	2.24	0.02	2
1	A	0	PRO	HB3	1.72	0.02	2
1	A	0	PRO	HG2	2.01	0.02	2
1	A	0	PRO	HG3	1.91	0.02	2
1	A	0	PRO	CA	62.7	0.3	1
1	A	0	PRO	CB	29.2	0.3	1
1	A	0	PRO	CD	47.5	0.3	1
1	A	0	PRO	CG	24.7	0.3	1
1	A	62	GLN	H	8.57	0.02	1
1	A	62	GLN	C	173.2	0.3	1
1	A	62	GLN	CA	52.1	0.3	1
1	A	62	GLN	CB	27.4	0.3	1
1	A	62	GLN	N	121.6	0.3	1
1	A	76	ALA	H	8.34	0.02	1
1	A	76	ALA	C	175.2	0.3	1
1	A	76	ALA	CA	49.8	0.3	1
1	A	76	ALA	CB	16.2	0.3	1
1	A	76	ALA	N	124.5	0.3	1
1	A	77	GLU	H	8.32	0.02	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	77	GLU	C	173.7	0.3	1
1	A	77	GLU	CA	53.7	0.3	1
1	A	77	GLU	CB	27.5	0.3	1
1	A	77	GLU	N	120.1	0.3	1
1	A	78	GLN	H	8.28	0.02	1
1	A	78	GLN	C	172.7	0.3	1
1	A	78	GLN	CA	52.8	0.3	1
1	A	78	GLN	CB	26.9	0.3	1
1	A	78	GLN	N	121.4	0.3	1
1	A	79	ALA	H	8.3	0.02	1
1	A	79	ALA	HA	4.17	0.02	1
1	A	79	ALA	C	174.8	0.3	1
1	A	79	ALA	CA	49.6	0.3	1
1	A	79	ALA	CB	16.4	0.3	1
1	A	79	ALA	N	126.1	0.3	1
1	A	80	GLU	H	8.34	0.02	1
1	A	80	GLU	HA	4.16	0.02	1
1	A	80	GLU	HB2	1.8	0.02	2
1	A	80	GLU	HB3	2.11	0.02	2
1	A	80	GLU	C	173.4	0.3	1
1	A	80	GLU	CA	53.7	0.3	1
1	A	80	GLU	CB	27.5	0.3	1
1	A	80	GLU	CG	33.4	0.3	1
1	A	80	GLU	N	120.5	0.3	1
1	A	81	GLU	H	8.38	0.02	1
1	A	81	GLU	HA	4.13	0.02	1
1	A	81	GLU	HB2	1.84	0.02	2
1	A	81	GLU	HB3	2.12	0.02	2
1	A	81	GLU	C	173.7	0.3	1
1	A	81	GLU	CA	53.7	0.3	1
1	A	81	GLU	CB	27.5	0.3	1
1	A	81	GLU	CG	33.4	0.3	1
1	A	81	GLU	N	121.9	0.3	1
1	A	82	THR	H	8.14	0.02	1
1	A	82	THR	HA	4.19	0.02	1
1	A	82	THR	HB	1.88	0.02	1
1	A	82	THR	C	171.1	0.3	1
1	A	82	THR	CA	58.9	0.3	1
1	A	82	THR	CB	67.1	0.3	1
1	A	82	THR	CG2	18.9	0.3	1
1	A	82	THR	N	116.2	0.3	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	83	ALA	H	8.28	0.02	1
1	A	83	ALA	HA	4.69	0.02	1
1	A	83	ALA	C	172.7	0.3	1
1	A	83	ALA	CA	47.8	0.3	1
1	A	83	ALA	CB	15.1	0.3	1
1	A	83	ALA	N	128.3	0.3	1
1	A	84	PRO	HA	4.29	0.02	1
1	A	84	PRO	HB2	2.16	0.02	2
1	A	84	PRO	HB3	1.76	0.02	2
1	A	84	PRO	HD2	3.7	0.02	2
1	A	84	PRO	HD3	3.52	0.02	2
1	A	84	PRO	HG2	1.9	0.02	2
1	A	84	PRO	HG3	1.08	0.02	2
1	A	84	PRO	CA	60.0	0.3	1
1	A	84	PRO	CB	29.2	0.3	1
1	A	84	PRO	CD	47.9	0.3	1
1	A	84	PRO	CG	24.6	0.3	1
1	A	85	ILE	H	8.18	0.02	1
1	A	85	ILE	HA	4.01	0.02	1
1	A	85	ILE	HB	1.71	0.02	1
1	A	85	ILE	HG12	1.38	0.02	2
1	A	85	ILE	HG13	1.09	0.02	2
1	A	85	ILE	C	173.7	0.3	1
1	A	85	ILE	CA	58.4	0.3	1
1	A	85	ILE	CB	35.9	0.3	1
1	A	85	ILE	CD1	24.5	0.3	1
1	A	85	ILE	CG1	14.7	0.3	1
1	A	85	ILE	CG2	10.1	0.3	1
1	A	85	ILE	N	121.3	0.3	1
1	A	86	GLU	H	8.41	0.02	1
1	A	86	GLU	HA	4.16	0.02	1
1	A	86	GLU	HB2	1.83	0.02	2
1	A	86	GLU	HB3	1.92	0.02	2
1	A	86	GLU	C	173.3	0.3	1
1	A	86	GLU	CA	53.6	0.3	1
1	A	86	GLU	CB	27.4	0.3	1
1	A	86	GLU	CG	33.4	0.3	1
1	A	86	GLU	N	125.3	0.3	1
1	A	87	ALA	H	8.31	0.02	1
1	A	87	ALA	HA	4.18	0.02	1
1	A	87	ALA	C	175.1	0.3	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	87	ALA	CA	49.7	0.3	1
1	A	87	ALA	CB	16.3	0.3	1
1	A	87	ALA	N	126.0	0.3	1
1	A	88	THR	H	8.03	0.02	1
1	A	88	THR	HA	4.23	0.02	1
1	A	88	THR	HB	4.05	0.02	1
1	A	88	THR	C	171.5	0.3	1
1	A	88	THR	CA	59.0	0.3	1
1	A	88	THR	CB	67.0	0.3	1
1	A	88	THR	CG2	18.8	0.3	1
1	A	88	THR	N	113.6	0.3	1
1	A	89	ALA	H	8.23	0.02	1
1	A	89	ALA	HA	4.16	0.02	1
1	A	89	ALA	C	175.1	0.3	1
1	A	89	ALA	CA	49.6	0.3	1
1	A	89	ALA	CB	16.4	0.3	1
1	A	89	ALA	N	126.8	0.3	1
1	A	90	THR	H	8.11	0.02	1
1	A	90	THR	HA	4.09	0.02	1
1	A	90	THR	HB	4.08	0.02	1
1	A	90	THR	C	171.6	0.3	1
1	A	90	THR	CA	59.1	0.3	1
1	A	90	THR	CB	67.1	0.3	1
1	A	90	THR	CG2	18.8	0.3	1
1	A	90	THR	N	114.5	0.3	1
1	A	91	LYS	H	8.31	0.02	1
1	A	91	LYS	HA	4.21	0.02	1
1	A	91	LYS	HB2	1.71	0.02	2
1	A	91	LYS	HB3	1.65	0.02	2
1	A	91	LYS	HD2	1.55	0.02	2
1	A	91	LYS	HD3	2.87	0.02	2
1	A	91	LYS	HE2	1.55	0.02	2
1	A	91	LYS	HE3	2.87	0.02	2
1	A	91	LYS	HG2	1.31	0.02	2
1	A	91	LYS	HG3	1.56	0.02	2
1	A	91	LYS	C	173.7	0.3	1
1	A	91	LYS	CA	53.4	0.3	1
1	A	91	LYS	CB	30.1	0.3	1
1	A	91	LYS	CD	26.2	0.3	1
1	A	91	LYS	CE	39.3	0.3	1
1	A	91	LYS	CG	21.8	0.3	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	91	LYS	N	124.1	0.3	1
1	A	92	GLU	H	8.45	0.02	1
1	A	92	GLU	HA	4.12	0.02	1
1	A	92	GLU	HB2	1.93	0.02	2
1	A	92	GLU	HB3	1.83	0.02	2
1	A	92	GLU	C	174.0	0.3	1
1	A	92	GLU	CA	53.9	0.3	1
1	A	92	GLU	CB	27.2	0.3	1
1	A	92	GLU	CG	33.4	0.3	1
1	A	92	GLU	N	122.8	0.3	1
1	A	93	GLU	H	8.15	0.02	1
1	A	93	GLU	HA	4.11	0.02	1
1	A	93	GLU	HB2	1.86	0.02	2
1	A	93	GLU	HB3	1.91	0.02	2
1	A	93	GLU	C	173.8	0.3	1
1	A	93	GLU	CA	53.8	0.3	1
1	A	93	GLU	CB	27.8	0.3	1
1	A	93	GLU	CG	33.4	0.3	1
1	A	93	GLU	N	122.2	0.3	1
1	A	94	GLU	H	8.42	0.02	1
1	A	94	GLU	HA	4.16	0.02	1
1	A	94	GLU	C	174.4	0.3	1
1	A	94	GLU	CA	54.2	0.3	1
1	A	94	GLU	CB	27.4	0.3	1
1	A	94	GLU	CG	33.4	0.3	1
1	A	94	GLU	N	122.6	0.3	1
1	A	95	GLY	H	8.4	0.02	1
1	A	95	GLY	HA2	4.2	0.02	2
1	A	95	GLY	HA3	3.87	0.02	2
1	A	95	GLY	C	171.4	0.3	1
1	A	95	GLY	CA	42.5	0.3	1
1	A	95	GLY	N	110.2	0.3	1
1	A	96	SER	H	8.12	0.02	1
1	A	96	SER	C	171.1	0.3	1
1	A	96	SER	CA	55.5	0.3	1
1	A	96	SER	CB	61.3	0.3	1
1	A	96	SER	N	115.6	0.3	1
1	A	97	SER	H	7.97	0.02	1
1	A	97	SER	C	175.9	0.3	1
1	A	97	SER	CA	57.1	0.3	1
1	A	97	SER	CB	61.8	0.3	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	97	SER	N	122.9	0.3	1
1	B	18	THR	H	7.99	0.02	1
1	B	18	THR	C	170.9	0.3	1
1	B	18	THR	CA	58.8	0.3	1
1	B	18	THR	CB	67.2	0.3	1
1	B	18	THR	N	117.3	0.3	1
1	B	19	MET	H	8.25	0.02	1
1	B	19	MET	C	171.2	0.3	1
1	B	19	MET	CA	50.5	0.3	1
1	B	19	MET	CB	29.7	0.3	1
1	B	19	MET	N	124.4	0.3	1
1	B	21	GLY	H	8.37	0.02	1
1	B	21	GLY	C	171.2	0.3	1
1	B	21	GLY	CA	42.4	0.3	1
1	B	21	GLY	N	108.9	0.3	1
1	B	22	LEU	H	7.92	0.02	1
1	B	22	LEU	C	174.6	0.3	1
1	B	22	LEU	CA	52.4	0.3	1
1	B	22	LEU	CB	39.6	0.3	1
1	B	22	LEU	N	121.6	0.3	1
1	B	23	VAL	H	8.05	0.02	1
1	B	23	VAL	C	173.0	0.3	1
1	B	23	VAL	CA	59.4	0.3	1
1	B	23	VAL	CB	30.1	0.3	1
1	B	23	VAL	N	120.8	0.3	1
1	B	24	ASP	H	8.3	0.02	1
1	B	24	ASP	C	173.3	0.3	1
1	B	24	ASP	CA	51.5	0.3	1
1	B	24	ASP	CB	38.5	0.3	1
1	B	24	ASP	N	124.2	0.3	1
1	B	25	SER	H	8.13	0.02	1
1	B	25	SER	C	171.2	0.3	1
1	B	25	SER	CA	55.5	0.3	1
1	B	25	SER	CB	61.1	0.3	1
1	B	25	SER	N	116.2	0.3	1
1	B	26	ASN	H	8.37	0.02	1
1	B	26	ASN	C	170.0	0.3	1
1	B	26	ASN	CA	48.8	0.3	1
1	B	26	ASN	CB	36.1	0.3	1
1	B	26	ASN	N	121.4	0.3	1
1	B	28	ALA	H	8.26	0.02	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	B	28	ALA	C	172.2	0.3	1
1	B	28	ALA	CA	47.5	0.3	1
1	B	28	ALA	CB	15.2	0.3	1
1	B	28	ALA	N	125.7	0.3	1
1	B	31	GLU	H	8.55	0.02	1
1	B	31	GLU	C	173.9	0.3	1
1	B	31	GLU	CA	54.1	0.3	1
1	B	31	GLU	CB	27.2	0.3	1
1	B	31	GLU	N	120.5	0.3	1
1	B	32	SER	H	8.24	0.02	1
1	B	32	SER	C	172.0	0.3	1
1	B	32	SER	CA	55.6	0.3	1
1	B	32	SER	CB	61.0	0.3	1
1	B	32	SER	N	116.3	0.3	1
1	B	33	GLN	H	8.3	0.02	1
1	B	33	GLN	C	173.1	0.3	1
1	B	33	GLN	CA	53.1	0.3	1
1	B	33	GLN	CB	26.8	0.3	1
1	B	33	GLN	N	122.2	0.3	1
1	B	34	GLU	H	8.25	0.02	1
1	B	34	GLU	C	173.5	0.3	1
1	B	34	GLU	CA	53.9	0.3	1
1	B	34	GLU	CB	27.3	0.3	1
1	B	34	GLU	N	121.7	0.3	1
1	B	35	LYS	H	8.27	0.02	1
1	B	35	LYS	C	173.5	0.3	1
1	B	35	LYS	CA	53.2	0.3	1
1	B	35	LYS	CB	29.9	0.3	1
1	B	35	LYS	N	122.8	0.3	1
1	B	22	LYS	H	8.22	0.02	1
1	B	22	LYS	C	171.6	0.3	1
1	B	22	LYS	CA	51.3	0.3	1
1	B	22	LYS	CB	29.7	0.3	1
1	B	22	LYS	N	124.0	0.3	1
1	B	38	LEU	H	8.26	0.02	1
1	B	38	LEU	C	174.4	0.3	1
1	B	38	LEU	CA	52.3	0.3	1
1	B	38	LEU	CB	39.8	0.3	1
1	B	38	LEU	N	122.7	0.3	1
1	B	39	LYS	H	8.18	0.02	1
1	B	39	LYS	C	171.6	0.3	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	B	39	LYS	CA	51.2	0.3	1
1	B	39	LYS	CB	29.9	0.3	1
1	B	39	LYS	N	123.2	0.3	1
1	B	29	ALA	H	8.35	0.02	1
1	B	29	ALA	C	174.5	0.3	1
1	B	29	ALA	CA	49.6	0.3	1
1	B	29	ALA	CB	16.6	0.3	1
1	B	29	ALA	N	126.6	0.3	1
1	B	30	SER	H	8.26	0.02	1
1	B	30	SER	C	170.2	0.3	1
1	B	30	SER	CA	53.5	0.3	1
1	B	30	SER	CB	60.6	0.3	1
1	B	30	SER	N	116.7	0.3	1
1	B	46	GLU	H	8.48	0.02	1
1	B	46	GLU	C	174.2	0.3	1
1	B	46	GLU	CA	54.2	0.3	1
1	B	46	GLU	CB	27.2	0.3	1
1	B	46	GLU	N	120.4	0.3	1
1	B	47	THR	H	8.04	0.02	1
1	B	47	THR	C	171.9	0.3	1
1	B	47	THR	CA	59.5	0.3	1
1	B	47	THR	CB	66.9	0.3	1
1	B	47	THR	N	115.6	0.3	1
1	B	48	LYS	H	8.19	0.02	1
1	B	48	LYS	C	173.6	0.3	1
1	B	48	LYS	CA	53.8	0.3	1
1	B	48	LYS	CB	30.3	0.3	1
1	B	48	LYS	N	123.9	0.3	1
1	B	49	LYS	H	8.18	0.02	1
1	B	49	LYS	C	173.7	0.3	1
1	B	49	LYS	CA	53.6	0.3	1
1	B	49	LYS	CB	30.4	0.3	1
1	B	49	LYS	N	122.4	0.3	1
1	B	50	ALA	H	8.21	0.02	1
1	B	50	ALA	C	175.2	0.3	1
1	B	50	ALA	CA	49.8	0.3	1
1	B	50	ALA	CB	16.3	0.3	1
1	B	50	ALA	N	125.3	0.3	1
1	B	51	ARG	H	8.25	0.02	1
1	B	51	ARG	C	173.5	0.3	1
1	B	51	ARG	CA	53.7	0.3	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	B	51	ARG	CB	28.2	0.3	1
1	B	51	ARG	N	120.4	0.3	1
1	B	52	ASP	H	8.23	0.02	1
1	B	52	ASP	C	173.4	0.3	1
1	B	52	ASP	CA	51.6	0.3	1
1	B	52	ASP	CB	38.3	0.3	1
1	B	52	ASP	N	121.5	0.3	1
1	B	53	ALA	H	8.18	0.02	1
1	B	53	ALA	C	175.1	0.3	1
1	B	53	ALA	CA	50.1	0.3	1
1	B	53	ALA	CB	16.2	0.3	1
1	B	53	ALA	N	124.7	0.3	1
1	B	40	SER	H	8.27	0.02	1
1	B	40	SER	C	171.8	0.3	1
1	B	40	SER	CA	56.2	0.3	1
1	B	40	SER	CB	60.9	0.3	1
1	B	40	SER	N	114.6	0.3	1
1	B	55	ILE	H	7.82	0.02	1
1	B	55	ILE	C	173.4	0.3	1
1	B	55	ILE	CA	58.6	0.3	1
1	B	55	ILE	CB	35.6	0.3	1
1	B	55	ILE	N	121.9	0.3	1
1	B	56	ILE	H	7.98	0.02	1
1	B	56	ILE	C	173.5	0.3	1
1	B	56	ILE	CA	58.4	0.3	1
1	B	56	ILE	CB	35.6	0.3	1
1	B	56	ILE	N	124.5	0.3	1
1	B	57	GLU	H	8.34	0.02	1
1	B	57	GLU	C	173.6	0.3	1
1	B	57	GLU	CA	53.8	0.3	1
1	B	57	GLU	CB	27.4	0.3	1
1	B	57	GLU	N	125.3	0.3	1
1	B	58	LYS	H	8.29	0.02	1
1	B	58	LYS	C	174.3	0.3	1
1	B	58	LYS	CA	53.8	0.3	1
1	B	58	LYS	CB	30.2	0.3	1
1	B	58	LYS	N	122.3	0.3	1
1	B	59	GLY	H	8.37	0.02	1
1	B	59	GLY	C	171.4	0.3	1
1	B	59	GLY	CA	42.5	0.3	1
1	B	59	GLY	N	110.0	0.3	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	B	60	GLU	H	8.25	0.02	1
1	B	60	GLU	C	173.9	0.3	1
1	B	60	GLU	CA	53.8	0.3	1
1	B	60	GLU	CB	27.6	0.3	1
1	B	60	GLU	N	120.4	0.3	1

7.1.2 Chemical shift referencing [i](#)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	155	2.39 ± 0.28	Should be checked
$^{13}\text{C}_\beta$	144	3.25 ± 0.12	Should be checked
$^{13}\text{C}'$	148	2.34 ± 0.16	Should be applied
^{15}N	148	0.33 ± 0.47	None needed (< 0.5 ppm)

7.1.3 Completeness of resonance assignments [i](#)

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 64%, i.e. 495 atoms were assigned a chemical shift out of a possible 771. 0 out of 4 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	290/303 (96%)	112/124 (90%)	119/120 (99%)	59/59 (100%)
Sidechain	192/393 (49%)	103/254 (41%)	89/124 (72%)	0/15 (0%)
Aromatic	13/75 (17%)	13/38 (34%)	0/34 (0%)	0/3 (0%)
Overall	495/771 (64%)	228/416 (55%)	208/278 (75%)	59/77 (77%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 60%, i.e. 624 atoms were assigned a chemical shift out of a possible 1039. 0 out of 5 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	366/407 (90%)	139/167 (83%)	152/162 (94%)	75/78 (96%)
Sidechain	245/515 (48%)	132/332 (40%)	113/164 (69%)	0/19 (0%)
Aromatic	13/117 (11%)	13/59 (22%)	0/53 (0%)	0/5 (0%)
Overall	624/1039 (60%)	284/558 (51%)	265/379 (70%)	75/102 (74%)

7.1.4 Statistically unusual chemical shifts [i](#)

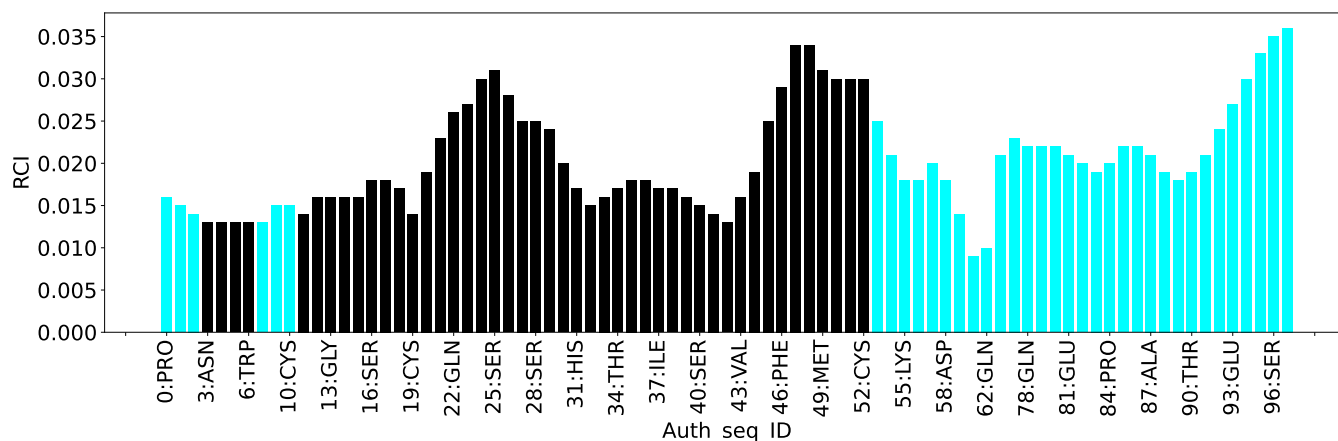
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	53	MET	CE	47.90	8.39 – 25.85	17.6
1	A	49	MET	CE	39.30	8.39 – 25.85	12.7
1	A	11	LEU	CD2	6.80	15.73 – 32.47	-10.3
1	A	85	ILE	CG1	14.70	19.24 – 36.26	-7.7
1	A	82	THR	HB	1.88	2.57 – 5.77	-7.1
1	A	91	LYS	HE2	1.55	1.95 – 3.88	-7.1
1	A	11	LEU	CD1	13.90	16.71 – 32.55	-6.8
1	A	85	ILE	CD1	24.50	5.18 – 21.60	6.8
1	A	91	LYS	HD3	2.87	0.54 – 2.65	6.0
1	A	59	LEU	CD2	14.10	15.73 – 32.47	-6.0
1	A	8	SER	HB3	2.27	2.49 – 5.20	-5.8
1	A	36	GLU	CG	29.40	30.20 – 42.01	-5.7
1	A	85	ILE	CG2	10.10	10.93 – 24.12	-5.6

7.1.5 Random Coil Index (RCI) plots [i](#)

The image below reports *random coil index* values for the protein chains in the structure. The height of each bar gives a probability of a given residue to be disordered, as predicted from the available chemical shifts and the amino acid sequence. A value above 0.2 is an indication of significant predicted disorder. The colour of the bar shows whether the residue is in the well-defined core (black) or in the ill-defined residue ranges (cyan), as described in section 2 on ensemble composition. If well-defined core and ill-defined regions are not identified then it is shown as gray bars.

Random coil index (RCI) for chain A:



Random coil index (RCI) for chain B:

