



Full wwPDB NMR Structure Validation Report ⓘ

Feb 12, 2017 – 10:00 pm GMT

PDB ID : 2GQK
Title : Solution structure of Human Ni(II)-Sco1
Authors : Banci, L.; Bertini, I.; Calderone, V.; Ciofi-Baffoni, S.; Mangani, S.; Palumaa, P.; Martinelli, M.; Wang, S.; Structural Proteomics in Europe (SPINE)
Deposited on : 2006-04-21

This is a Full wwPDB NMR Structure Validation Report for a publicly released PDB entry.

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

A user guide is available at

<http://wwpdb.org/validation/2016/NMRValidationReportHelp>

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:

Cyrange : Kirchner and Güntert (2011)
NmrClust : Kelley et al. (1996)
MolProbity : 4.02b-467
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
ShiftChecker : trunk28760
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : recalc28949

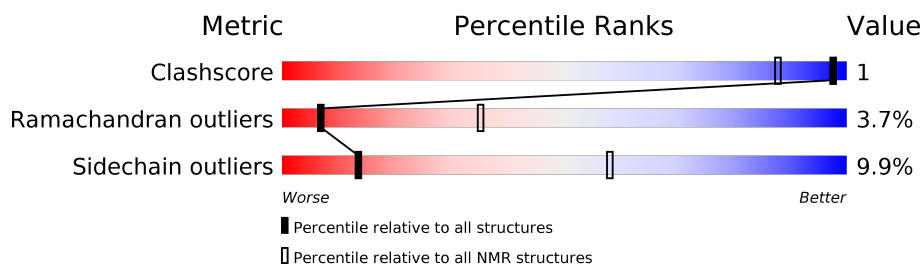
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment was not calculated.

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	125131	11601
Ramachandran outliers	121729	10391
Sidechain outliers	121581	10367

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	173	 81% 6% • 12%

2 Ensemble composition and analysis

This entry contains 30 models. Model 6 is the overall representative, medoid model (most similar to other models).

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:139-A:248, A:257-A:298 (152)	0.75	6

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 7 clusters and 8 single-model clusters were found.

Cluster number	Models
1	4, 7, 10, 12, 18, 20, 23, 24
2	3, 6, 21
3	9, 15, 26
4	1, 2
5	28, 30
6	13, 17
7	27, 29
Single-model clusters	5; 8; 11; 14; 16; 19; 22; 25

3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2750 atoms, of which 1360 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called SCO1 protein homolog, mitochondrial.

Mol	Chain	Residues	Atoms						Trace
1	A	173	Total	C	H	N	O	S	0
			2749	890	1360	224	270	5	

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	129	SER	-	CLONING ARTIFACT	UNP O75880
A	130	PHE	-	CLONING ARTIFACT	UNP O75880
A	131	THR	-	CLONING ARTIFACT	UNP O75880

- Molecule 2 is NICKEL (II) ION (three-letter code: NI) (formula: Ni).

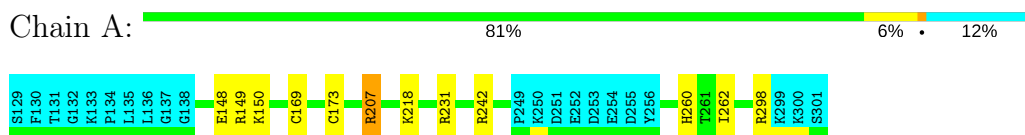
Mol	Chain	Residues	Atoms	
2	A	1	Total	Ni
			1	1

4 Residue-property plots

4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA and DNA 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: SCO1 protein homolog, mitochondrial

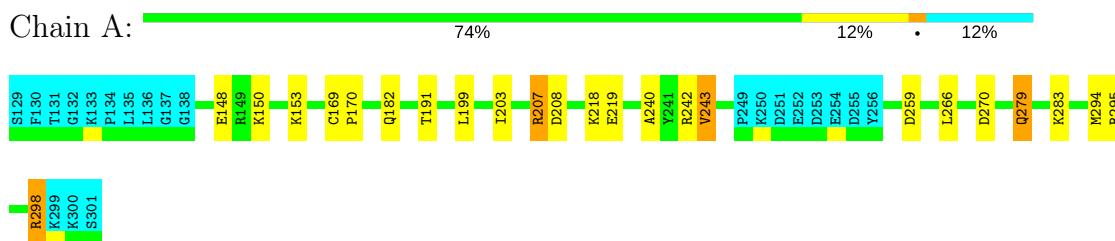


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

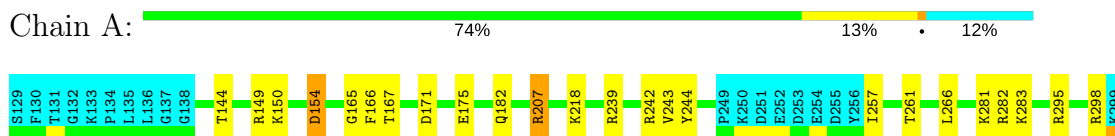
4.2.1 Score per residue for model 1

- Molecule 1: SCO1 protein homolog, mitochondrial



4.2.2 Score per residue for model 2

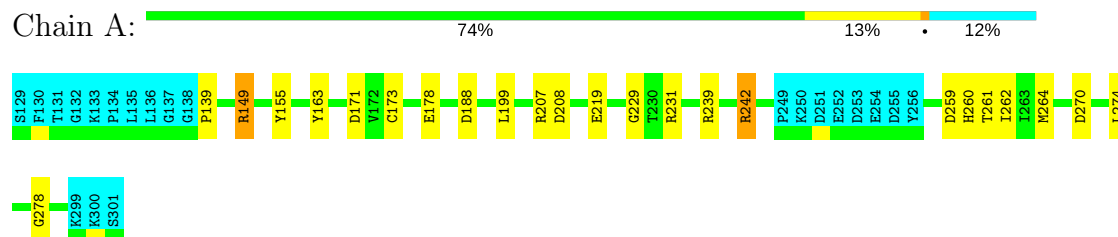
- Molecule 1: SCO1 protein homolog, mitochondrial





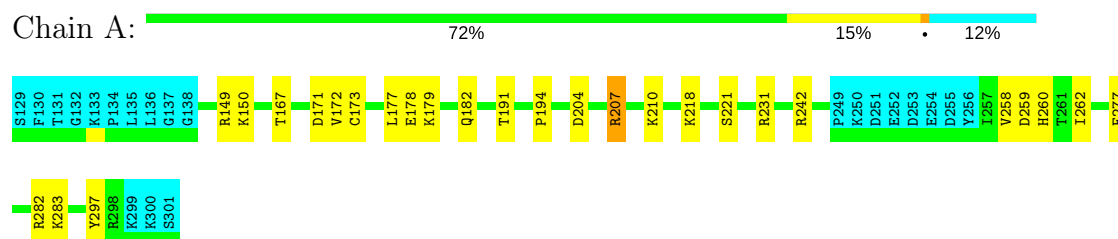
4.2.3 Score per residue for model 3

- Molecule 1: SCO1 protein homolog, mitochondrial



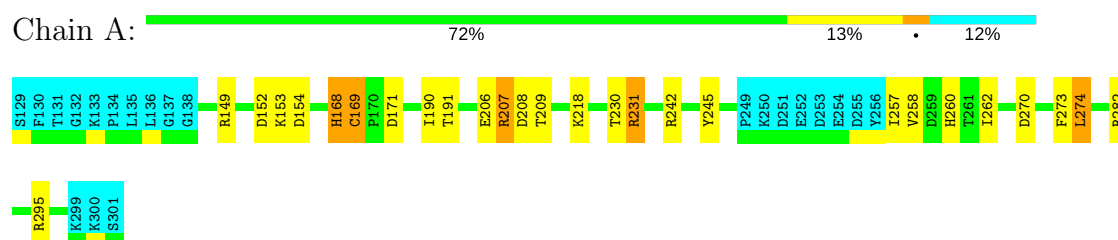
4.2.4 Score per residue for model 4

- Molecule 1: SCO1 protein homolog, mitochondrial



4.2.5 Score per residue for model 5

- Molecule 1: SCO1 protein homolog, mitochondrial



4.2.6 Score per residue for model 6 (medoid)

- Molecule 1: SCO1 protein homolog, mitochondrial

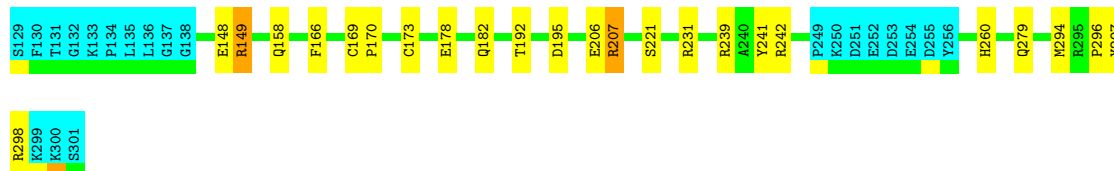




4.2.7 Score per residue for model 7

- Molecule 1: SCO1 protein homolog, mitochondrial

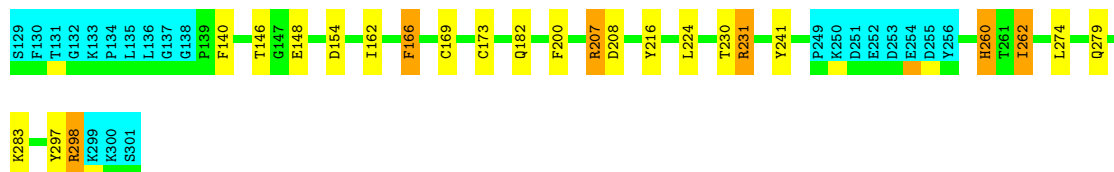
Chain A: 74% 13% 12%



4.2.8 Score per residue for model 8

- Molecule 1: SCO1 protein homolog, mitochondrial

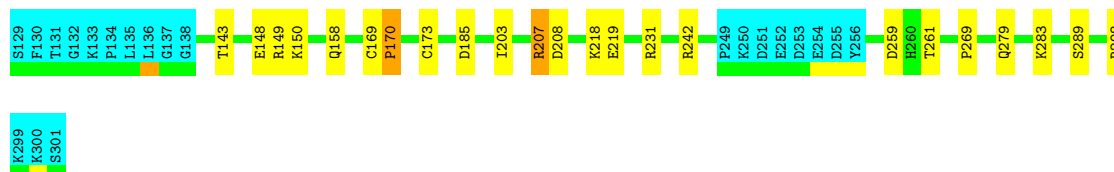
Chain A: 74% 10% 12%



4.2.9 Score per residue for model 9

- Molecule 1: SCO1 protein homolog, mitochondrial

Chain A: 75% 12% 12%



4.2.10 Score per residue for model 10

- Molecule 1: SCO1 protein homolog, mitochondrial

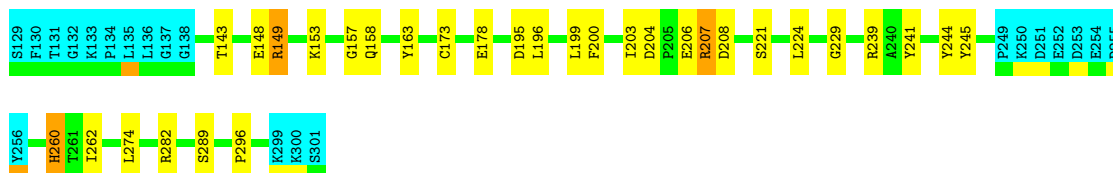
Chain A: 76% 10% 12%



4.2.11 Score per residue for model 11

- Molecule 1: SCO1 protein homolog, mitochondrial

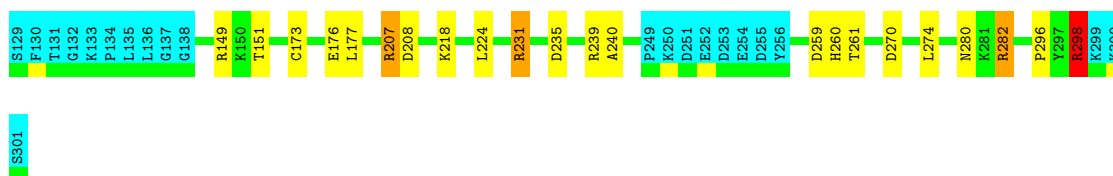
Chain A: 70% 16% 12%



4.2.12 Score per residue for model 12

- Molecule 1: SCO1 protein homolog, mitochondrial

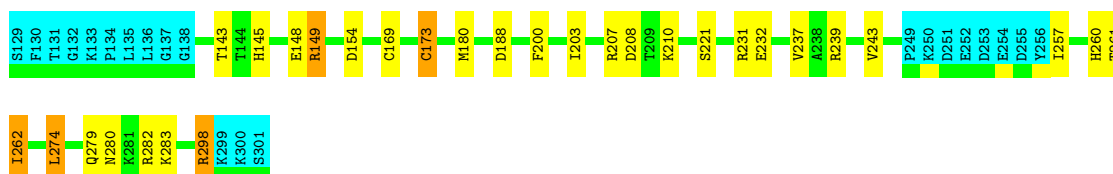
Chain A: 75% 10% 12%



4.2.13 Score per residue for model 13

- Molecule 1: SCO1 protein homolog, mitochondrial

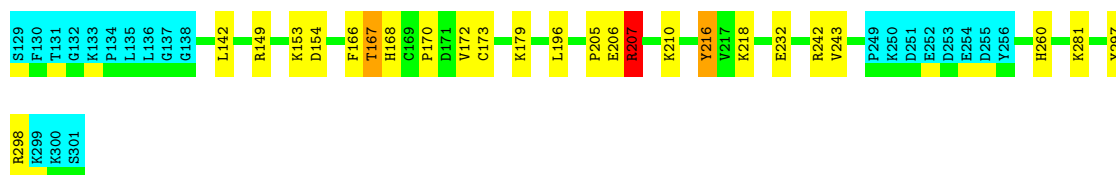
Chain A: 71% 14% 12%



4.2.14 Score per residue for model 14

- Molecule 1: SCO1 protein homolog, mitochondrial

Chain A: 73% 13% 12%



4.2.15 Score per residue for model 15

- Molecule 1: SCO1 protein homolog, mitochondrial

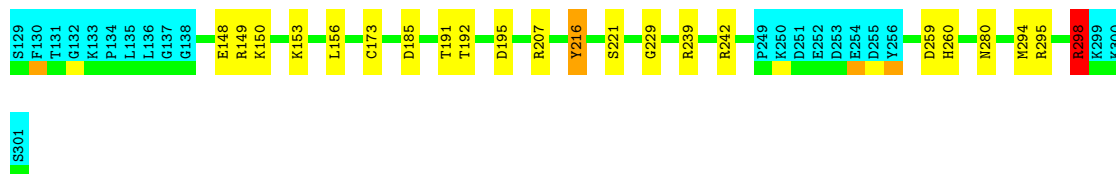
Chain A: 76% 10% 12%



4.2.16 Score per residue for model 16

- Molecule 1: SCO1 protein homolog, mitochondrial

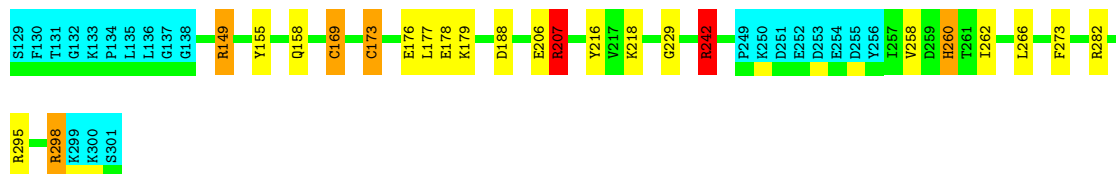
Chain A: 75% 12% 12%



4.2.17 Score per residue for model 17

- Molecule 1: SCO1 protein homolog, mitochondrial

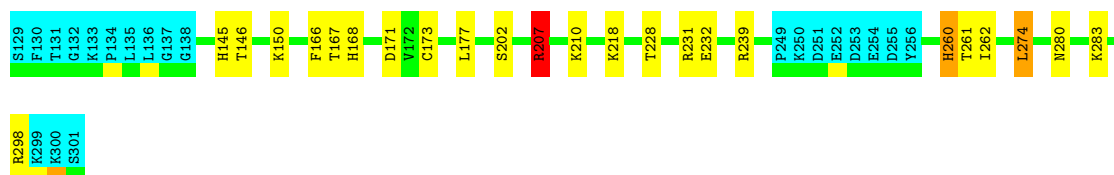
Chain A: 74% 10% 12%



4.2.18 Score per residue for model 18

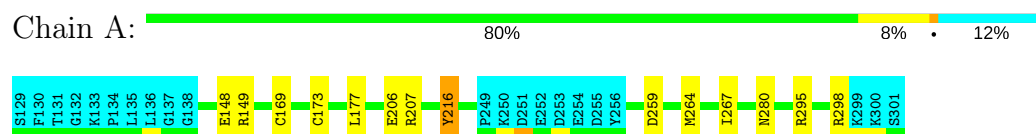
- Molecule 1: SCO1 protein homolog, mitochondrial

Chain A: 74% 12% 12%



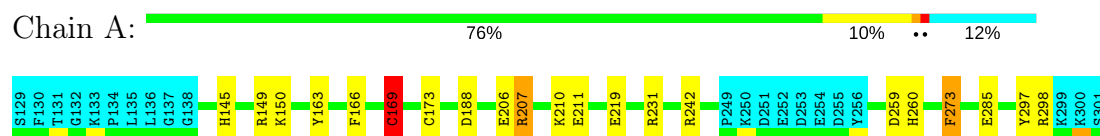
4.2.19 Score per residue for model 19

- Molecule 1: SCO1 protein homolog, mitochondrial



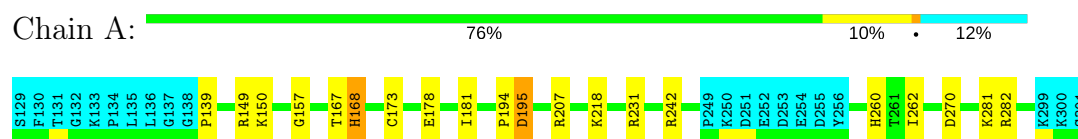
4.2.20 Score per residue for model 20

- Molecule 1: SCO1 protein homolog, mitochondrial



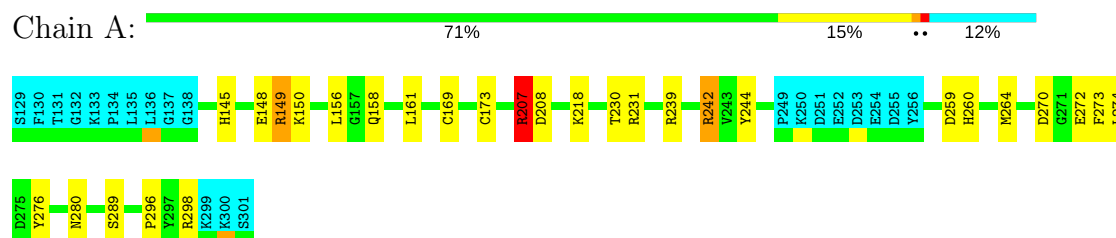
4.2.21 Score per residue for model 21

- Molecule 1: SCO1 protein homolog, mitochondrial



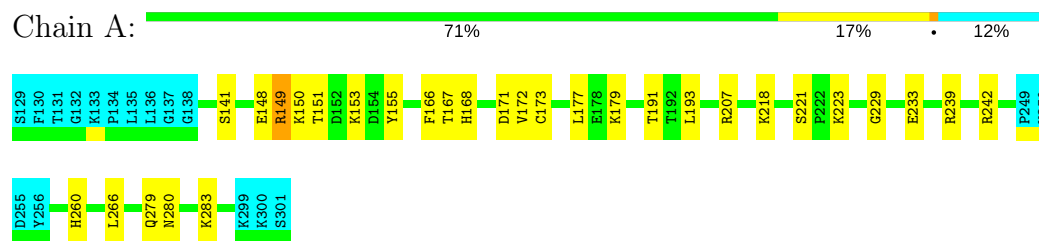
4.2.22 Score per residue for model 22

- Molecule 1: SCO1 protein homolog, mitochondrial



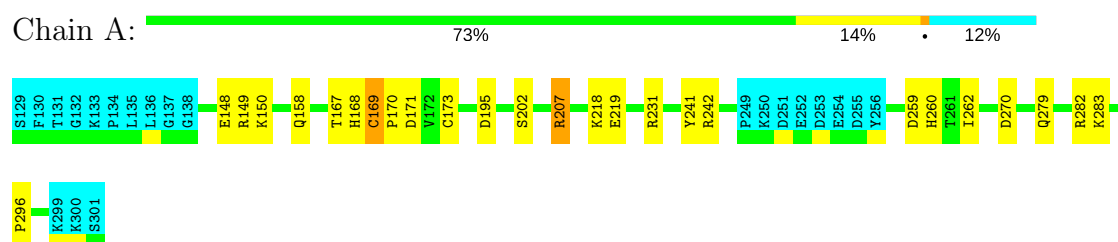
4.2.23 Score per residue for model 23

- Molecule 1: SCO1 protein homolog, mitochondrial



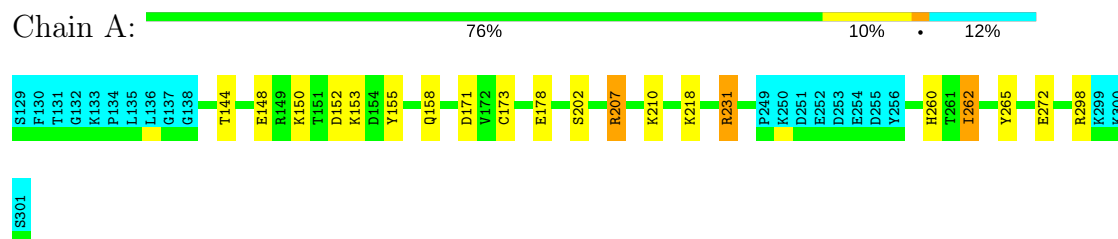
4.2.24 Score per residue for model 24

- Molecule 1: SCO1 protein homolog, mitochondrial



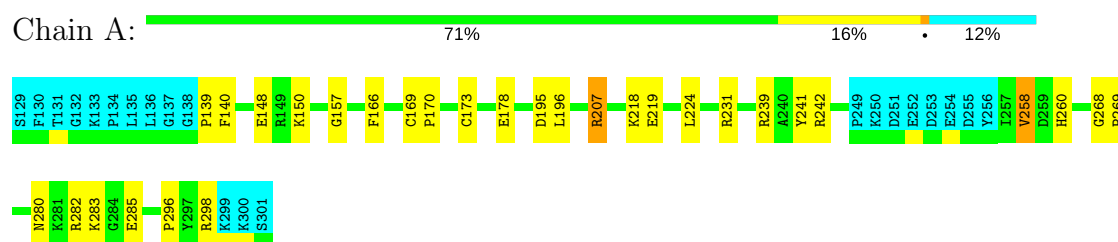
4.2.25 Score per residue for model 25

- Molecule 1: SCO1 protein homolog, mitochondrial



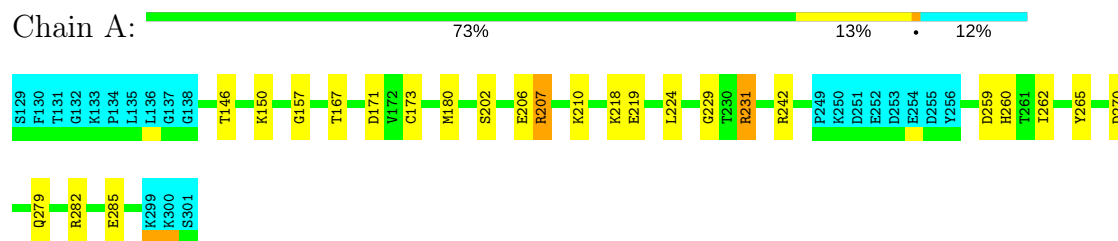
4.2.26 Score per residue for model 26

- Molecule 1: SCO1 protein homolog, mitochondrial



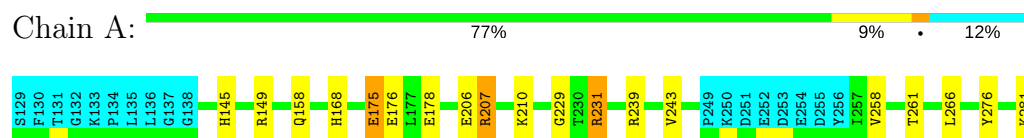
4.2.27 Score per residue for model 27

- Molecule 1: SCO1 protein homolog, mitochondrial



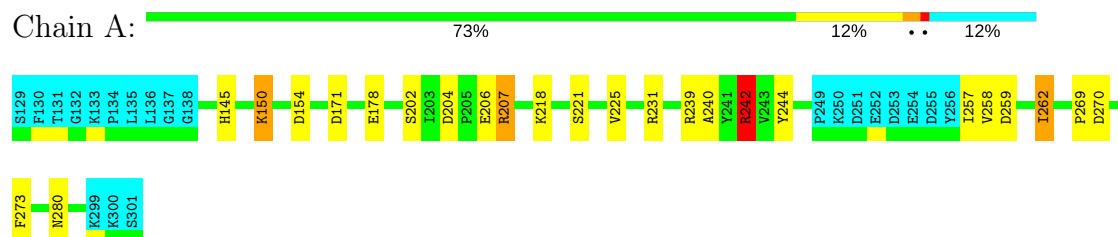
4.2.28 Score per residue for model 28

- Molecule 1: SCO1 protein homolog, mitochondrial



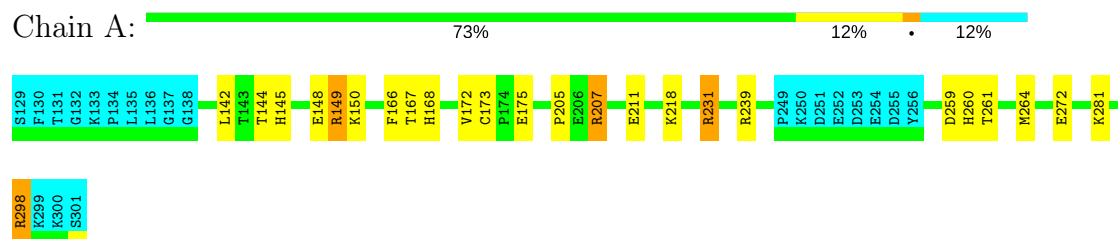
4.2.29 Score per residue for model 29

- Molecule 1: SCO1 protein homolog, mitochondrial



4.2.30 Score per residue for model 30

- Molecule 1: SCO1 protein homolog, mitochondrial



5 Refinement protocol and experimental data overview

The models were refined using the following method: *torsion angle dynamics*.

Of the 350 calculated structures, 30 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
DYANA	structure solution	1.5
AMBER	refinement	8.0

No chemical shift data was provided. No validations of the models with respect to experimental NMR restraints is performed at this time.

6 Model quality i

6.1 Standard geometry i

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

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	0.72±0.01	0±0/1258 (0.0±0.0%)	1.11±0.03	5±2/1711 (0.3±0.1%)
All	All	0.72	0/37740 (0.0%)	1.11	137/51330 (0.3%)

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	2.1±1.5
All	All	0	64

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	231	ARG	NE-CZ-NH1	10.49	125.54	120.30	28	16
1	A	207	ARG	NE-CZ-NH1	9.89	125.25	120.30	6	20
1	A	298	ARG	NE-CZ-NH2	-9.35	115.62	120.30	6	6
1	A	298	ARG	NE-CZ-NH1	8.49	124.55	120.30	10	14
1	A	231	ARG	NE-CZ-NH2	-8.47	116.06	120.30	20	9
1	A	149	ARG	NE-CZ-NH1	8.41	124.51	120.30	22	11
1	A	239	ARG	NE-CZ-NH1	7.62	124.11	120.30	16	13
1	A	282	ARG	NE-CZ-NH1	7.16	123.88	120.30	21	8
1	A	282	ARG	C-N-CA	7.12	139.49	121.70	26	1
1	A	282	ARG	NE-CZ-NH2	-7.11	116.75	120.30	10	2
1	A	207	ARG	NE-CZ-NH2	-7.08	116.76	120.30	12	5
1	A	242	ARG	NE-CZ-NH1	6.95	123.78	120.30	17	2

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	242	ARG	NE-CZ-NH2	-6.70	116.95	120.30	1	3
1	A	295	ARG	NE-CZ-NH1	6.29	123.44	120.30	17	5
1	A	295	ARG	NE-CZ-NH2	-6.18	117.21	120.30	1	2
1	A	231	ARG	CD-NE-CZ	6.13	132.18	123.60	20	3
1	A	216	TYR	CB-CG-CD2	-6.10	117.34	121.00	17	4
1	A	149	ARG	NE-CZ-NH2	-6.04	117.28	120.30	7	1
1	A	173	CYS	N-CA-CB	-5.52	100.66	110.60	17	2
1	A	171	ASP	CB-CG-OD2	5.48	123.23	118.30	2	1
1	A	207	ARG	CD-NE-CZ	5.46	131.25	123.60	6	1
1	A	298	ARG	CD-NE-CZ	5.40	131.16	123.60	17	1
1	A	167	THR	CA-CB-CG2	5.29	119.81	112.40	10	1
1	A	149	ARG	CD-NE-CZ	5.29	131.00	123.60	7	1
1	A	297	TYR	CB-CG-CD2	-5.27	117.84	121.00	20	1
1	A	269	PRO	C-N-CA	5.25	134.82	121.70	29	1
1	A	168	HIS	N-CA-CB	-5.22	101.20	110.60	15	1
1	A	242	ARG	CD-NE-CZ	5.14	130.79	123.60	29	1
1	A	273	PHE	CB-CG-CD2	-5.02	117.28	120.80	20	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	207	ARG	Sidechain,Peptide	8
1	A	169	CYS	Peptide	7
1	A	231	ARG	Sidechain	5
1	A	260	HIS	Sidechain,Peptide	4
1	A	241	TYR	Sidechain	4
1	A	170	PRO	Peptide	3
1	A	298	ARG	Sidechain	3
1	A	295	ARG	Sidechain	2
1	A	149	ARG	Sidechain	2
1	A	244	TYR	Sidechain	2
1	A	229	GLY	Peptide	2
1	A	168	HIS	Sidechain,Peptide	2
1	A	153	LYS	Peptide	2
1	A	268	GLY	Peptide	1
1	A	175	GLU	Peptide	1
1	A	151	THR	Peptide	1
1	A	208	ASP	Peptide	1
1	A	139	PRO	Peptide	1

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Mol	Chain	Res	Type	Group	Models (Total)
1	A	228	THR	Peptide	1
1	A	282	ARG	Peptide	1
1	A	167	THR	Peptide	1
1	A	141	SER	Peptide	1
1	A	258	VAL	Peptide	1
1	A	195	ASP	Peptide	1
1	A	154	ASP	Peptide	1
1	A	242	ARG	Sidechain	1
1	A	190	ILE	Peptide	1
1	A	157	GLY	Peptide	1
1	A	171	ASP	Peptide	1
1	A	165	GLY	Peptide	1
1	A	203	ILE	Peptide	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	1226	1202	1201	2±1
All	All	36810	36060	36031	46

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 1.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:173:CYS:SG	1:A:260:HIS:CE1	0.63	2.92	23	22
1:A:150:LYS:HE2	1:A:155:TYR:CE2	0.51	2.40	25	1
1:A:150:LYS:HE3	1:A:154:ASP:HB2	0.50	1.83	29	1
1:A:166:PHE:CG	1:A:167:THR:N	0.47	2.81	23	1
1:A:150:LYS:HE3	1:A:154:ASP:CB	0.46	2.40	29	1
1:A:166:PHE:H	1:A:260:HIS:CD2	0.45	2.29	26	1
1:A:232:GLU:H	1:A:232:GLU:CD	0.45	2.15	14	1
1:A:171:ASP:CG	1:A:172:VAL:H	0.45	2.15	4	2
1:A:169:CYS:SG	1:A:260:HIS:CD2	0.45	3.10	26	3
1:A:166:PHE:CZ	1:A:260:HIS:CD2	0.44	3.06	8	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:262:ILE:HD11	1:A:279:GLN:HE21	0.44	1.71	13	1
1:A:182:GLN:CB	1:A:283:LYS:HE3	0.43	2.43	8	1
1:A:243:VAL:HG22	1:A:244:TYR:H	0.43	1.74	2	1
1:A:182:GLN:CB	1:A:283:LYS:HE2	0.43	2.44	2	1
1:A:182:GLN:C	1:A:283:LYS:HE2	0.43	2.34	4	2
1:A:207:ARG:HD3	1:A:207:ARG:H	0.43	1.74	14	1
1:A:211:GLU:H	1:A:211:GLU:CD	0.42	2.18	30	1
1:A:172:VAL:HG23	1:A:260:HIS:CE1	0.42	2.50	30	1
1:A:176:GLU:HA	1:A:179:LYS:HE3	0.41	1.91	17	1
1:A:273:PHE:CG	1:A:274:LEU:N	0.41	2.88	5	1
1:A:150:LYS:HE3	1:A:155:TYR:CD2	0.41	2.51	23	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	152/173 (88%)	128±4 (84±3%)	18±4 (12±2%)	6±2 (4±1%)	7	35
All	All	4560/5190 (88%)	3842 (84%)	550 (12%)	168 (4%)	7	35

All 47 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	242	ARG	14
1	A	262	ILE	10
1	A	207	ARG	7
1	A	168	HIS	7
1	A	279	GLN	7
1	A	206	GLU	7
1	A	296	PRO	6
1	A	270	ASP	6
1	A	298	ARG	6
1	A	221	SER	6
1	A	167	THR	5

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Mol	Chain	Res	Type	Models (Total)
1	A	280	ASN	5
1	A	229	GLY	5
1	A	166	PHE	5
1	A	258	VAL	5
1	A	257	ILE	4
1	A	170	PRO	4
1	A	240	ALA	4
1	A	171	ASP	4
1	A	261	THR	3
1	A	157	GLY	3
1	A	274	LEU	3
1	A	243	VAL	3
1	A	273	PHE	3
1	A	208	ASP	3
1	A	205	PRO	2
1	A	169	CYS	2
1	A	194	PRO	2
1	A	278	GLY	2
1	A	148	GLU	2
1	A	203	ILE	2
1	A	282	ARG	2
1	A	139	PRO	2
1	A	272	GLU	2
1	A	191	THR	2
1	A	269	PRO	2
1	A	204	ASP	1
1	A	283	LYS	1
1	A	192	THR	1
1	A	209	THR	1
1	A	173	CYS	1
1	A	195	ASP	1
1	A	156	LEU	1
1	A	182	GLN	1
1	A	175	GLU	1
1	A	281	LYS	1
1	A	241	TYR	1

6.3.2 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 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	135/153 (88%)	122±3 (90±2%)	13±3 (10±2%)	13	58
All	All	4050/4590 (88%)	3650 (90%)	400 (10%)	13	58

All 95 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	207	ARG	23
1	A	218	LYS	20
1	A	149	ARG	16
1	A	150	LYS	15
1	A	148	GLU	14
1	A	259	ASP	13
1	A	178	GLU	11
1	A	145	HIS	9
1	A	210	LYS	9
1	A	158	GLN	8
1	A	153	LYS	8
1	A	242	ARG	8
1	A	298	ARG	7
1	A	219	GLU	7
1	A	274	LEU	7
1	A	177	LEU	6
1	A	169	CYS	6
1	A	208	ASP	6
1	A	231	ARG	6
1	A	262	ILE	6
1	A	266	LEU	6
1	A	202	SER	5
1	A	281	LYS	5
1	A	264	MET	5
1	A	195	ASP	5
1	A	224	LEU	5
1	A	283	LYS	5
1	A	261	THR	5
1	A	280	ASN	5
1	A	154	ASP	5
1	A	297	TYR	5
1	A	188	ASP	5
1	A	199	LEU	4
1	A	289	SER	4
1	A	206	GLU	4
1	A	200	PHE	4

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Mol	Chain	Res	Type	Models (Total)
1	A	166	PHE	4
1	A	143	THR	4
1	A	191	THR	4
1	A	216	TYR	4
1	A	163	TYR	3
1	A	294	MET	3
1	A	179	LYS	3
1	A	196	LEU	3
1	A	279	GLN	3
1	A	167	THR	3
1	A	285	GLU	3
1	A	230	THR	3
1	A	270	ASP	3
1	A	192	THR	3
1	A	146	THR	3
1	A	144	THR	3
1	A	171	ASP	3
1	A	140	PHE	2
1	A	260	HIS	2
1	A	239	ARG	2
1	A	185	ASP	2
1	A	272	GLU	2
1	A	142	LEU	2
1	A	276	TYR	2
1	A	168	HIS	2
1	A	265	TYR	2
1	A	176	GLU	2
1	A	243	VAL	2
1	A	277	PHE	2
1	A	173	CYS	2
1	A	175	GLU	2
1	A	232	GLU	2
1	A	221	SER	2
1	A	155	TYR	2
1	A	204	ASP	2
1	A	245	TYR	2
1	A	180	MET	2
1	A	152	ASP	2
1	A	211	GLU	1
1	A	203	ILE	1
1	A	156	LEU	1
1	A	193	LEU	1

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Mol	Chain	Res	Type	Models (Total)
1	A	181	ILE	1
1	A	162	ILE	1
1	A	246	SER	1
1	A	161	LEU	1
1	A	273	PHE	1
1	A	187	ILE	1
1	A	282	ARG	1
1	A	244	TYR	1
1	A	235	ASP	1
1	A	223	LYS	1
1	A	267	ILE	1
1	A	233	GLU	1
1	A	258	VAL	1
1	A	237	VAL	1
1	A	225	VAL	1
1	A	172	VAL	1
1	A	151	THR	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 carbohydrates in this entry.

6.6 Ligand geometry [i](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

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

No chemical shift data were provided