



Full wwPDB NMR Structure Validation Report ⓘ

Apr 26, 2016 – 08:30 PM BST

PDB ID : 2EW9
Title : Solution structure of apoWLN5-6
Authors : Ciofi-Baffoni, S.; Structural Proteomics in Europe (SPINE)
Deposited on : 2005-11-02

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
Mogul : unknown
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
ShiftChecker : rb-20027457
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20027457

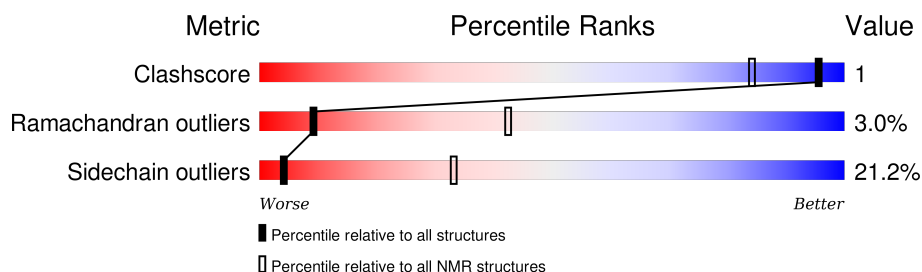
1 Overall quality at a glance

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	114402	11133
Ramachandran outliers	111179	9975
Sidechain outliers	111093	9958

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	149	 80% 13% 7%

2 Ensemble composition and analysis

This entry contains 31 models. Model 1 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:4-A:72, A:80-A:149 (139)	0.60	1

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. No single-model clusters were found.

Cluster number	Models
1	1, 2, 4, 6, 7, 8, 9, 11, 19, 21, 24, 26, 30, 31
2	3, 5, 12, 14, 16, 20, 25, 27, 28
3	13, 15, 18, 23, 29
4	10, 17, 22

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 2267 atoms, of which 1147 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Copper-transporting ATPase 2.

Mol	Chain	Residues	Atoms						Trace
1	A	149	Total	C	H	N	O	S	0
			2267	709	1147	183	218	10	

There is a discrepancy between the modelled and reference sequences:

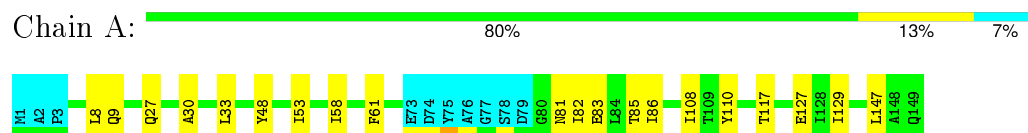
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	INITIATING METHIONINE	UNP P35670

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: Copper-transporting ATPase 2

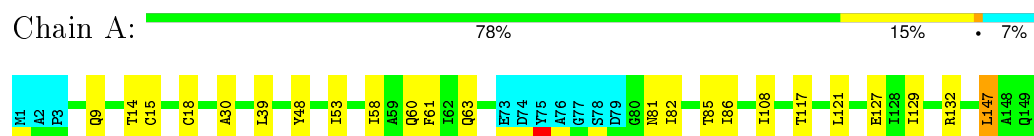


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

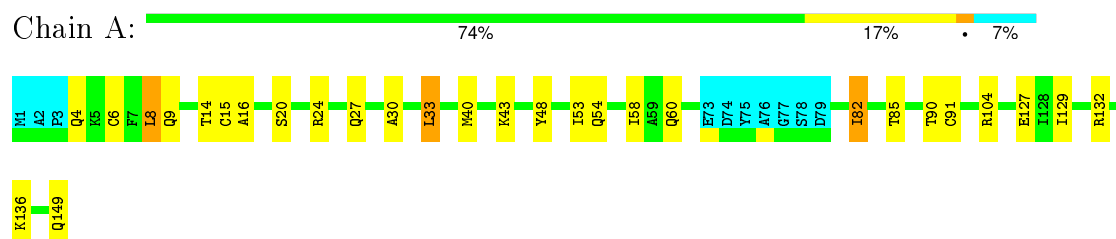
4.2.1 Score per residue for model 1 (medoid)

- Molecule 1: Copper-transporting ATPase 2



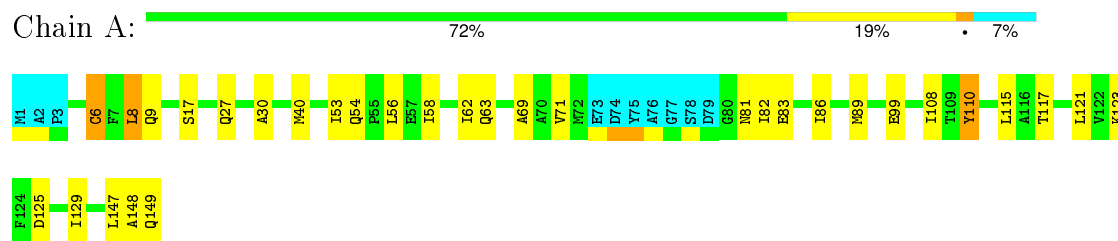
4.2.2 Score per residue for model 2

- Molecule 1: Copper-transporting ATPase 2



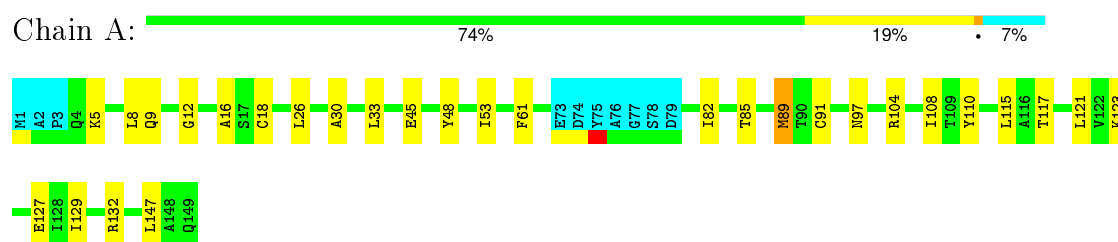
4.2.3 Score per residue for model 3

- Molecule 1: Copper-transporting ATPase 2



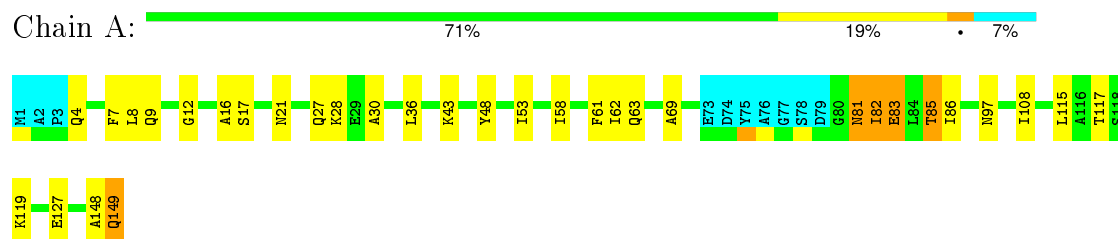
4.2.4 Score per residue for model 4

- Molecule 1: Copper-transporting ATPase 2



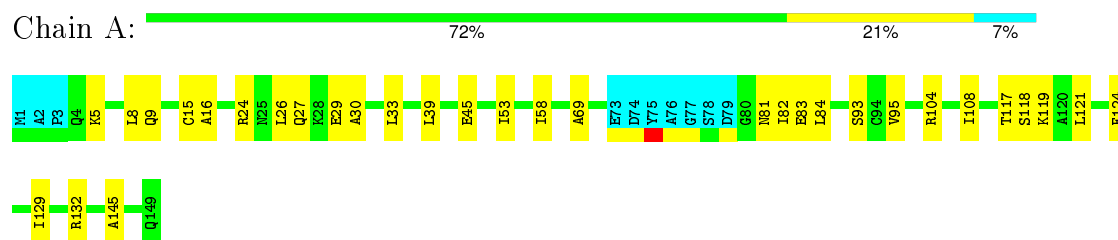
4.2.5 Score per residue for model 5

- Molecule 1: Copper-transporting ATPase 2



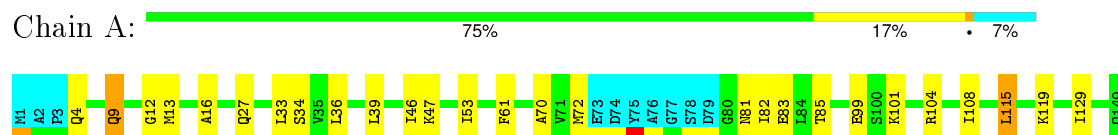
4.2.6 Score per residue for model 6

- Molecule 1: Copper-transporting ATPase 2



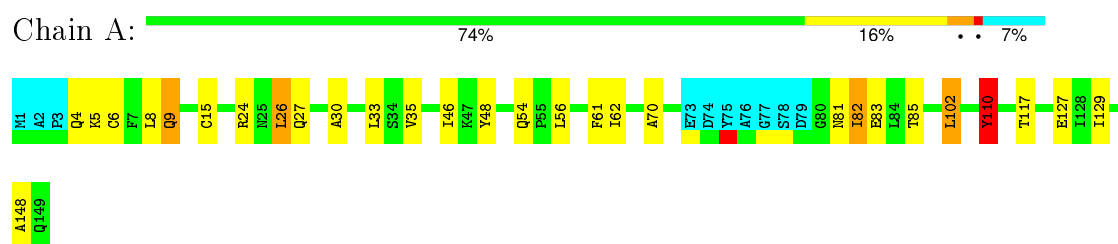
4.2.7 Score per residue for model 7

- Molecule 1: Copper-transporting ATPase 2



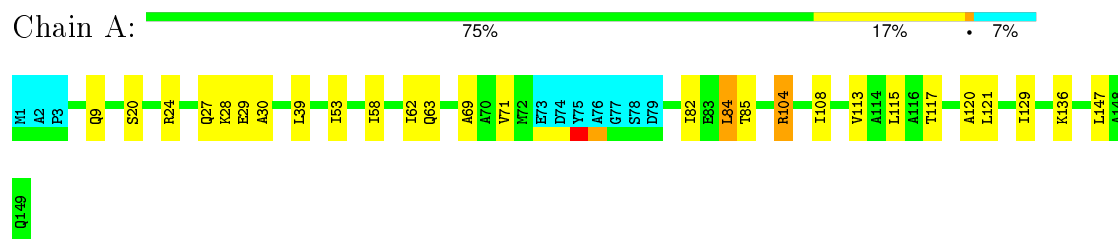
4.2.8 Score per residue for model 8

- Molecule 1: Copper-transporting ATPase 2



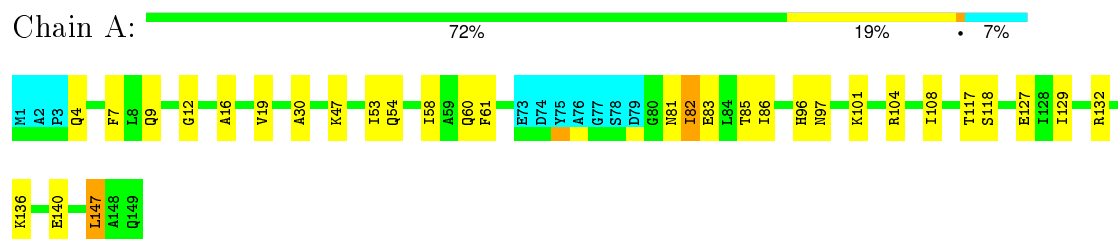
4.2.9 Score per residue for model 9

- Molecule 1: Copper-transporting ATPase 2



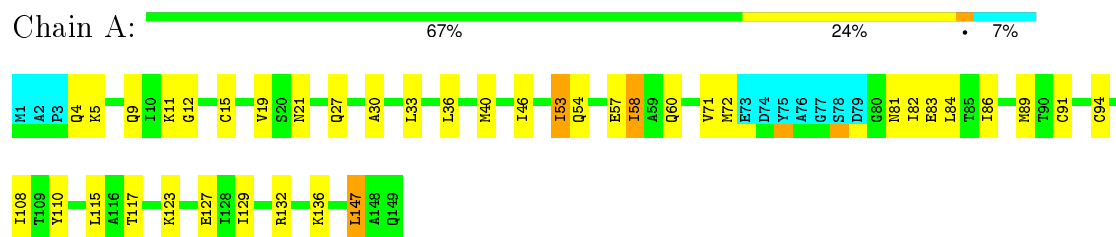
4.2.10 Score per residue for model 10

- Molecule 1: Copper-transporting ATPase 2



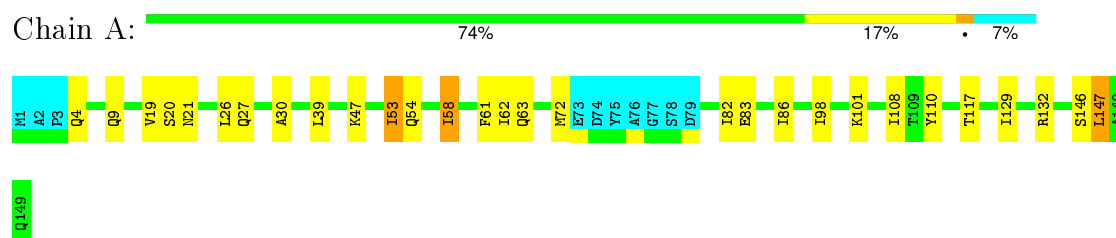
4.2.11 Score per residue for model 11

- Molecule 1: Copper-transporting ATPase 2



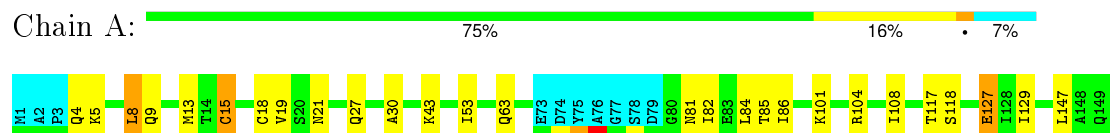
4.2.12 Score per residue for model 12

- Molecule 1: Copper-transporting ATPase 2



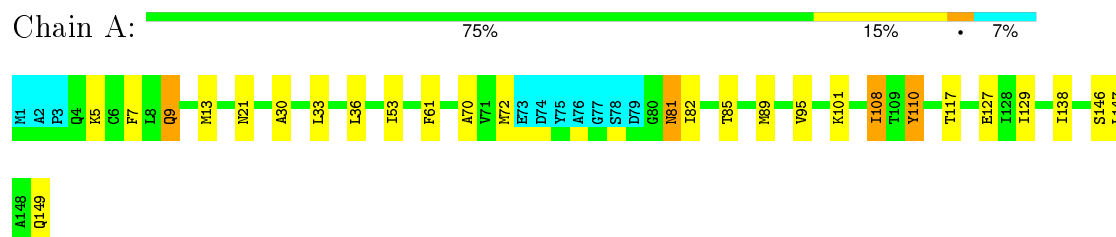
4.2.13 Score per residue for model 13

- Molecule 1: Copper-transporting ATPase 2



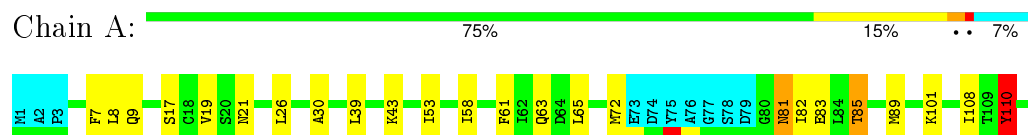
4.2.14 Score per residue for model 14

- Molecule 1: Copper-transporting ATPase 2



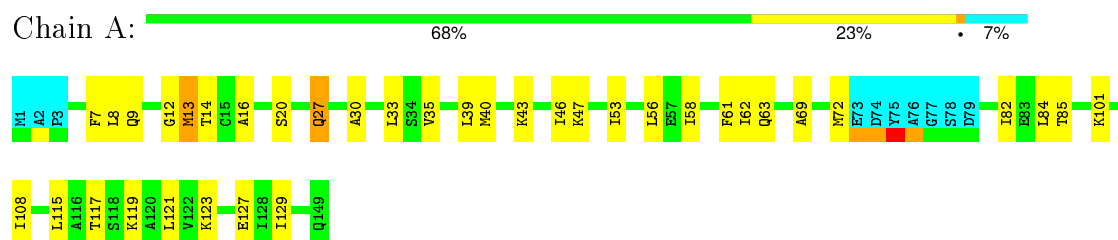
4.2.15 Score per residue for model 15

- Molecule 1: Copper-transporting ATPase 2



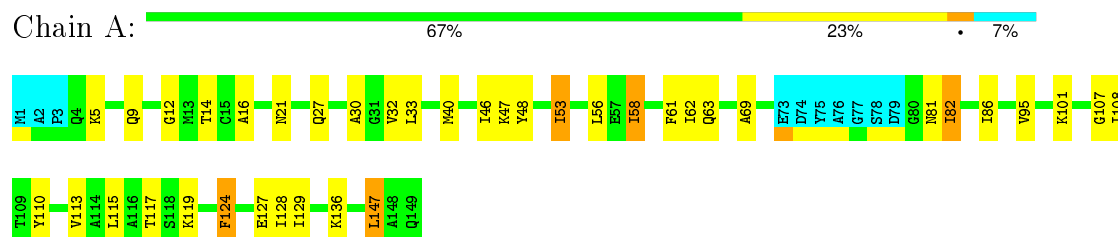
4.2.16 Score per residue for model 16

- Molecule 1: Copper-transporting ATPase 2



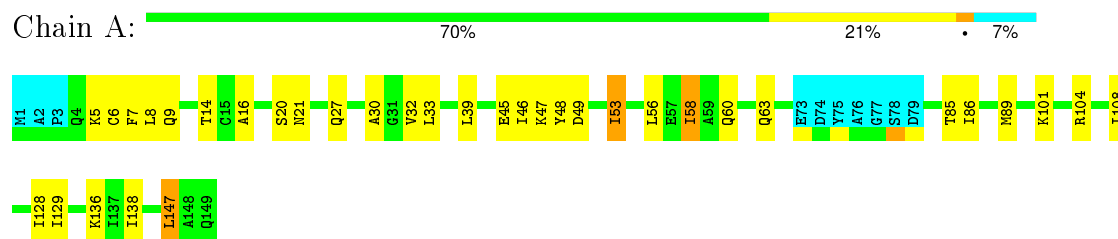
4.2.17 Score per residue for model 17

- Molecule 1: Copper-transporting ATPase 2



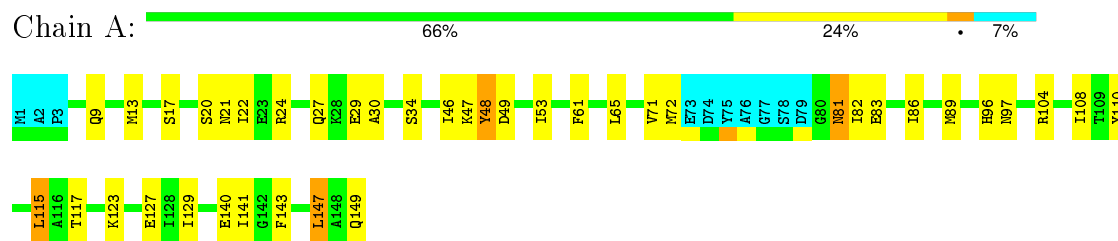
4.2.18 Score per residue for model 18

- Molecule 1: Copper-transporting ATPase 2



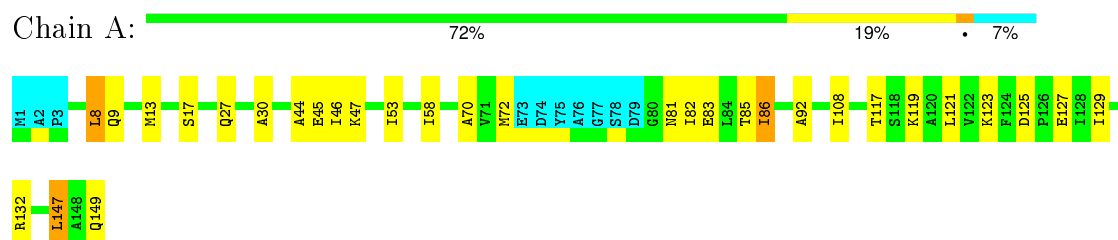
4.2.19 Score per residue for model 19

- Molecule 1: Copper-transporting ATPase 2



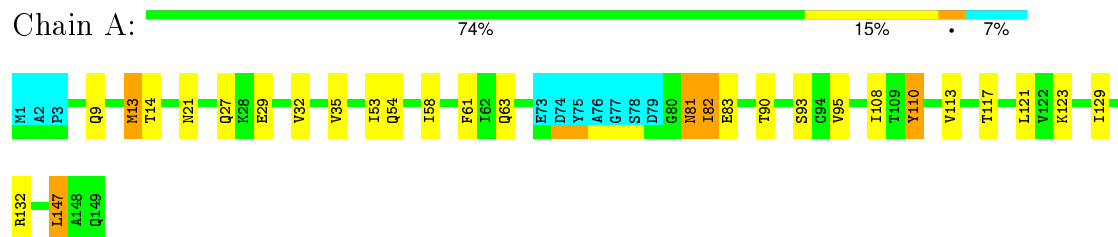
4.2.20 Score per residue for model 20

- Molecule 1: Copper-transporting ATPase 2



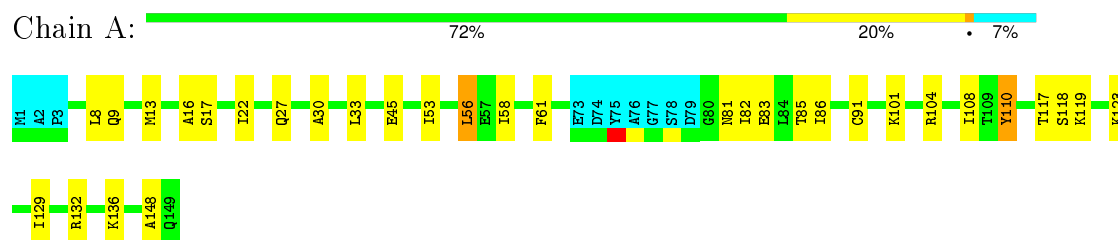
4.2.21 Score per residue for model 21

- Molecule 1: Copper-transporting ATPase 2



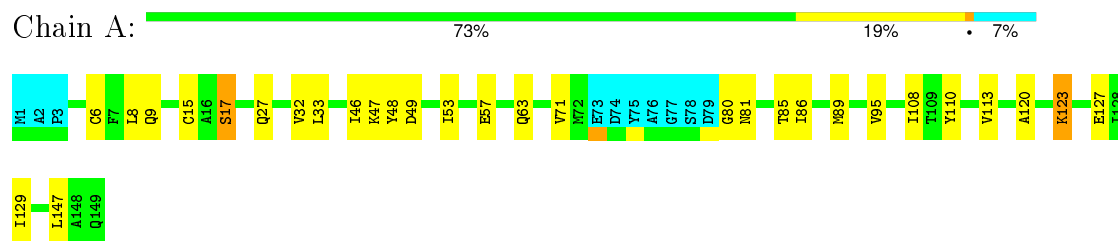
4.2.22 Score per residue for model 22

- Molecule 1: Copper-transporting ATPase 2



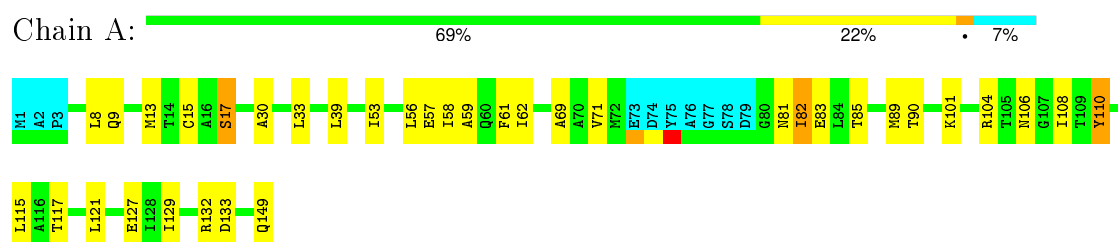
4.2.23 Score per residue for model 23

- Molecule 1: Copper-transporting ATPase 2



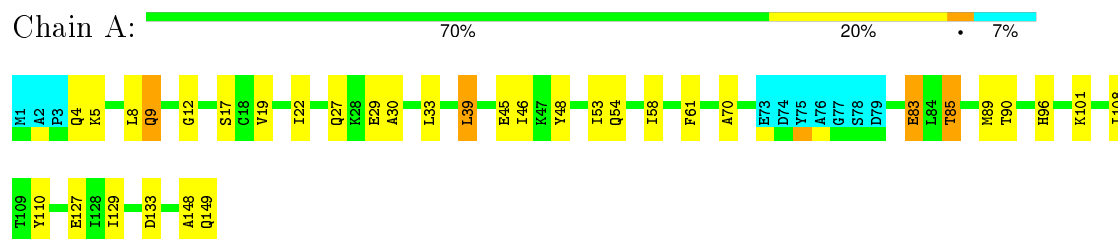
4.2.24 Score per residue for model 24

- Molecule 1: Copper-transporting ATPase 2



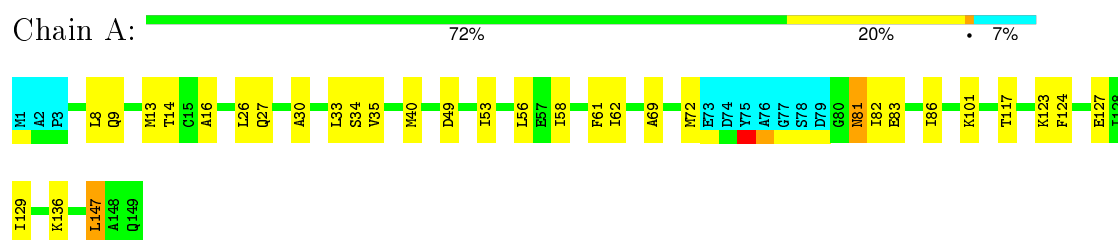
4.2.25 Score per residue for model 25

- Molecule 1: Copper-transporting ATPase 2



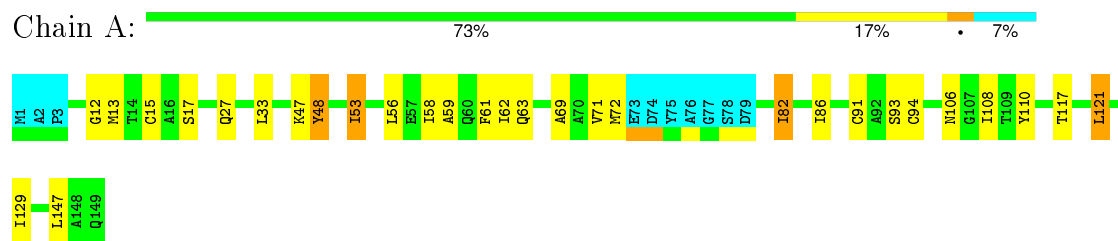
4.2.26 Score per residue for model 26

- Molecule 1: Copper-transporting ATPase 2



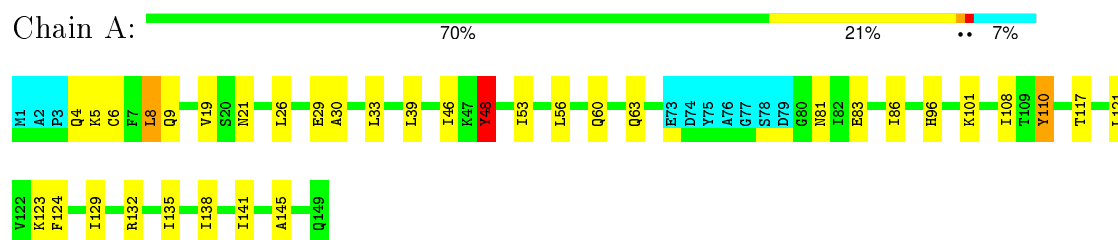
4.2.27 Score per residue for model 27

- Molecule 1: Copper-transporting ATPase 2



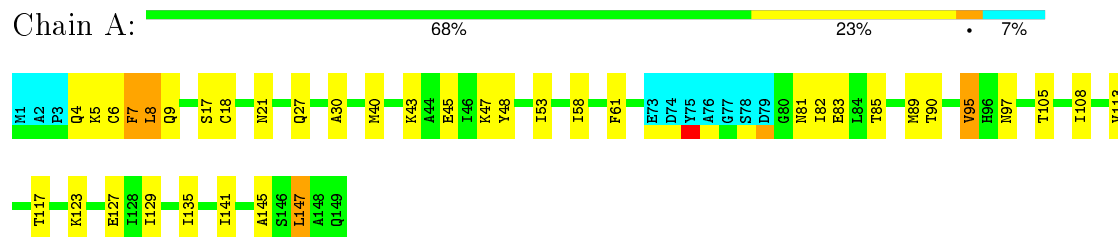
4.2.28 Score per residue for model 28

- Molecule 1: Copper-transporting ATPase 2



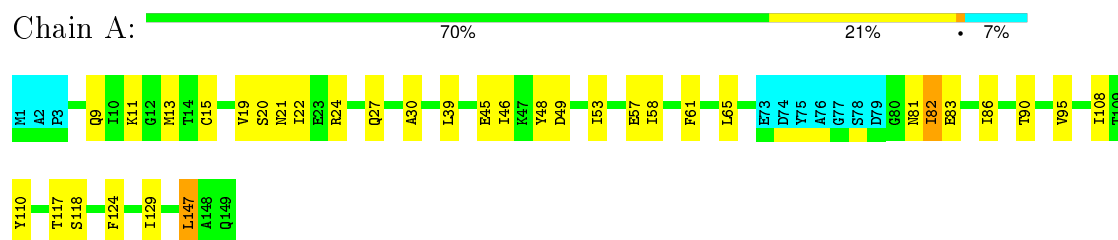
4.2.29 Score per residue for model 29

- Molecule 1: Copper-transporting ATPase 2



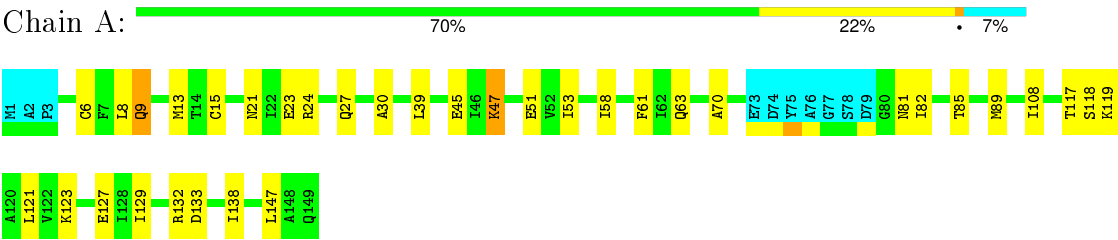
4.2.30 Score per residue for model 30

- Molecule 1: Copper-transporting ATPase 2



4.2.31 Score per residue for model 31

● Molecule 1: Copper-transporting ATPase 2



5 Refinement protocol and experimental data overview ⓘ

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

Of the 300 calculated structures, 31 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	
AMBER	refinement	5.0

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

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	0.51±0.01	0±0/1060 (0.0±0.0%)	0.91±0.02	0±0/1430 (0.0±0.0%)
All	All	0.51	0/32860 (0.0%)	0.91	6/44330 (0.0%)

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	1.2±0.7
All	All	0	36

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	102	LEU	CB-CG-CD1	5.64	120.59	111.00	8	1
1	A	110	TYR	CB-CG-CD2	-5.54	117.68	121.00	15	2
1	A	48	TYR	CB-CG-CD2	-5.13	117.92	121.00	28	1
1	A	148	ALA	CB-CA-C	5.03	117.64	110.10	22	1
1	A	72	MET	C-N-CA	5.01	134.24	121.70	7	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	110	TYR	Sidechain	14
1	A	48	TYR	Sidechain	12
1	A	7	PHE	Sidechain	5

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Mol	Chain	Res	Type	Group	Models (Total)
1	A	80	GLY	Peptide	1
1	A	132	ARG	Sidechain	1
1	A	124	PHE	Sidechain	1
1	A	104	ARG	Sidechain	1
1	A	33	LEU	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	1048	1088	1088	3±2
All	All	32488	33728	33728	86

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:82:ILE:HD12	1:A:82:ILE:N	0.65	2.06	8	1
1:A:83:GLU:OE1	1:A:148:ALA:HB3	0.62	1.94	8	2
1:A:9:GLN:HE22	1:A:70:ALA:HB3	0.58	1.58	8	1
1:A:81:ASN:O	1:A:82:ILE:HD13	0.57	1.98	14	1
1:A:135:ILE:HG22	1:A:145:ALA:HB3	0.56	1.77	28	2
1:A:86:ILE:H	1:A:86:ILE:HD12	0.55	1.60	20	1
1:A:115:LEU:H	1:A:115:LEU:HD13	0.55	1.61	19	2
1:A:107:GLY:HA3	1:A:128:ILE:HD11	0.55	1.78	17	1
1:A:32:VAL:C	1:A:33:LEU:HD12	0.55	2.22	17	1
1:A:95:VAL:HG13	1:A:113:VAL:HG13	0.53	1.80	17	2
1:A:53:ILE:HD11	1:A:58:ILE:HD12	0.53	1.81	17	4
1:A:19:VAL:HB	1:A:39:LEU:HD21	0.53	1.81	25	3
1:A:9:GLN:NE2	1:A:70:ALA:HB3	0.53	2.19	25	5
1:A:8:LEU:HD22	1:A:44:ALA:O	0.52	2.03	20	1
1:A:62:ILE:HD13	1:A:69:ALA:H	0.52	1.64	24	2
1:A:81:ASN:C	1:A:82:ILE:HD13	0.52	2.25	5	5
1:A:6:CYS:SG	1:A:8:LEU:HD11	0.52	2.45	29	2
1:A:6:CYS:SG	1:A:8:LEU:HD21	0.51	2.45	2	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:62:ILE:HG12	1:A:69:ALA:HB2	0.51	1.81	26	1
1:A:56:LEU:C	1:A:56:LEU:HD22	0.51	2.26	22	1
1:A:82:ILE:N	1:A:82:ILE:HD13	0.49	2.23	2	1
1:A:128:ILE:HD12	1:A:129:ILE:HB	0.49	1.85	17	1
1:A:113:VAL:HG23	1:A:120:ALA:HB2	0.48	1.85	23	1
1:A:62:ILE:HD13	1:A:69:ALA:N	0.48	2.24	17	7
1:A:84:LEU:HD13	1:A:145:ALA:HB1	0.47	1.86	6	1
1:A:46:ILE:C	1:A:46:ILE:HD12	0.47	2.29	19	1
1:A:121:LEU:H	1:A:121:LEU:HD22	0.46	1.70	27	1
1:A:45:GLU:OE2	1:A:47:LYS:NZ	0.46	2.45	31	1
1:A:48:TYR:CD2	1:A:53:ILE:HD11	0.46	2.46	19	1
1:A:97:ASN:HD21	1:A:141:ILE:HD13	0.46	1.70	29	1
1:A:85:THR:HB	1:A:148:ALA:HB2	0.45	1.86	5	3
1:A:101:LYS:HG3	1:A:141:ILE:HD11	0.45	1.88	28	1
1:A:48:TYR:HB2	1:A:53:ILE:HD12	0.44	1.90	27	1
1:A:115:LEU:HD23	1:A:115:LEU:H	0.44	1.72	17	1
1:A:82:ILE:H	1:A:82:ILE:HD13	0.44	1.72	30	2
1:A:86:ILE:HD13	1:A:98:ILE:HD13	0.43	1.90	12	1
1:A:113:VAL:HG12	1:A:120:ALA:HB1	0.43	1.89	9	1
1:A:101:LYS:CE	1:A:138:ILE:HG22	0.43	2.44	14	1
1:A:82:ILE:CD1	1:A:82:ILE:N	0.43	2.82	30	1
1:A:26:LEU:HD11	1:A:62:ILE:HD11	0.43	1.91	8	2
1:A:84:LEU:N	1:A:84:LEU:HD13	0.42	2.29	9	1
1:A:110:TYR:CE2	1:A:123:LYS:HD3	0.42	2.50	23	1
1:A:82:ILE:HD12	1:A:82:ILE:C	0.42	2.34	3	1
1:A:141:ILE:HG21	1:A:143:PHE:CE2	0.42	2.49	19	1
1:A:81:ASN:HB2	1:A:123:LYS:CD	0.42	2.45	26	2
1:A:95:VAL:HG13	1:A:113:VAL:CG2	0.41	2.45	29	1
1:A:8:LEU:HD12	1:A:69:ALA:HB1	0.41	1.92	6	1
1:A:8:LEU:N	1:A:8:LEU:HD13	0.41	2.30	28	1
1:A:5:LYS:NZ	1:A:149:GLN:O	0.41	2.53	14	1
1:A:8:LEU:HD22	1:A:8:LEU:N	0.40	2.31	13	1
1:A:119:LYS:NZ	1:A:149:GLN:O	0.40	2.54	5	1
1:A:56:LEU:O	1:A:59:ALA:HB3	0.40	2.17	24	2
1:A:8:LEU:HD12	1:A:71:VAL:HB	0.40	1.93	3	1
1:A:27:GLN:HE22	1:A:35:VAL:HG11	0.40	1.77	16	1
1:A:82:ILE:HD11	1:A:124:PHE:CE1	0.40	2.51	17	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	138/149 (93%)	120±3 (87±2%)	14±3 (10±2%)	4±1 (3±1%)	9	42
All	All	4278/4619 (93%)	3728 (87%)	422 (10%)	128 (3%)	9	42

All 18 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	30	ALA	27
1	A	127	GLU	19
1	A	147	LEU	15
1	A	13	MET	11
1	A	16	ALA	11
1	A	17	SER	10
1	A	12	GLY	9
1	A	15	CYS	9
1	A	90	THR	5
1	A	29	GLU	3
1	A	118	SER	2
1	A	95	VAL	1
1	A	148	ALA	1
1	A	89	MET	1
1	A	92	ALA	1
1	A	108	ILE	1
1	A	91	CYS	1
1	A	32	VAL	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	115/122 (94%)	91±4 (79±3%)	24±4 (21±3%)	4	33
All	All	3565/3782 (94%)	2809 (79%)	756 (21%)	4	33

All 88 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	9	GLN	29
1	A	53	ILE	29
1	A	129	ILE	28
1	A	108	ILE	28
1	A	117	THR	25
1	A	82	ILE	24
1	A	27	GLN	24
1	A	58	ILE	23
1	A	61	PHE	21
1	A	85	THR	20
1	A	147	LEU	19
1	A	83	GLU	18
1	A	81	ASN	18
1	A	8	LEU	18
1	A	86	ILE	16
1	A	33	LEU	15
1	A	63	GLN	15
1	A	21	ASN	14
1	A	132	ARG	12
1	A	47	LYS	12
1	A	89	MET	12
1	A	101	LYS	12
1	A	104	ARG	11
1	A	46	ILE	11
1	A	123	LYS	11
1	A	4	GLN	11
1	A	39	LEU	11
1	A	5	LYS	10
1	A	121	LEU	10
1	A	110	TYR	10
1	A	72	MET	9
1	A	115	LEU	9
1	A	45	GLU	8
1	A	54	GLN	8
1	A	136	LYS	8
1	A	56	LEU	8

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Mol	Chain	Res	Type	Models (Total)
1	A	14	THR	7
1	A	24	ARG	7
1	A	149	GLN	7
1	A	119	LYS	7
1	A	40	MET	7
1	A	20	SER	7
1	A	6	CYS	6
1	A	60	GLN	6
1	A	71	VAL	6
1	A	26	LEU	6
1	A	43	LYS	6
1	A	19	VAL	5
1	A	49	ASP	5
1	A	13	MET	4
1	A	124	PHE	4
1	A	57	GLU	4
1	A	18	CYS	4
1	A	95	VAL	4
1	A	97	ASN	4
1	A	96	HIS	4
1	A	36	LEU	4
1	A	118	SER	4
1	A	84	LEU	4
1	A	22	ILE	4
1	A	91	CYS	4
1	A	35	VAL	3
1	A	34	SER	3
1	A	15	CYS	3
1	A	29	GLU	3
1	A	93	SER	3
1	A	65	LEU	3
1	A	133	ASP	3
1	A	48	TYR	3
1	A	17	SER	3
1	A	138	ILE	3
1	A	7	PHE	3
1	A	125	ASP	2
1	A	140	GLU	2
1	A	94	CYS	2
1	A	32	VAL	2
1	A	99	GLU	2
1	A	106	ASN	2

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Mol	Chain	Res	Type	Models (Total)
1	A	28	LYS	2
1	A	146	SER	2
1	A	11	LYS	2
1	A	128	ILE	2
1	A	102	LEU	1
1	A	105	THR	1
1	A	127	GLU	1
1	A	23	GLU	1
1	A	51	GLU	1
1	A	90	THR	1

6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

6.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.6 Ligand geometry ⓘ

There are no ligands in this entry.

6.7 Other polymers ⓘ

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