



Full wwPDB NMR Structure Validation Report ⓘ

Feb 12, 2017 – 06:58 pm GMT

PDB ID : 1MO8
Title : ATPase
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Deposited on : 2002-09-08

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	:	1.7.2 (RC1), CSD as538be (2017)
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

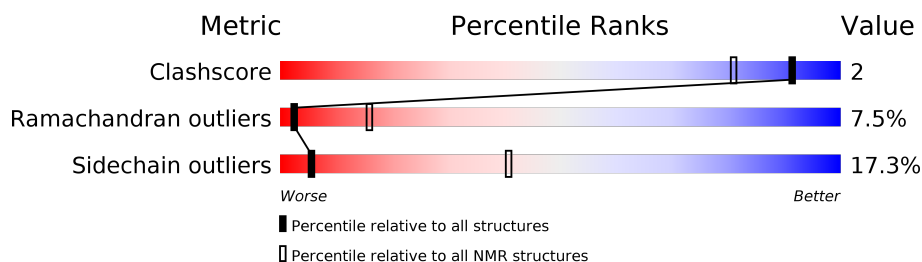
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 78%.

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	213	<div> <div style="width: 65%; background-color: green;"></div> <div style="width: 18%; background-color: yellow;"></div> <div style="width: 17%; background-color: cyan;"></div> </div> <div>65% 18% 17%</div>

2 Ensemble composition and analysis

This entry contains 20 models. Model 11 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:386-A:398, A:416-A:434, A:441-A:449, A:453-A:546, A:552-A:592 (176)	0.58	11

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 2 clusters and 4 single-model clusters were found.

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

3 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 3346 atoms, of which 1644 are hydrogens and 0 are deuteriums.

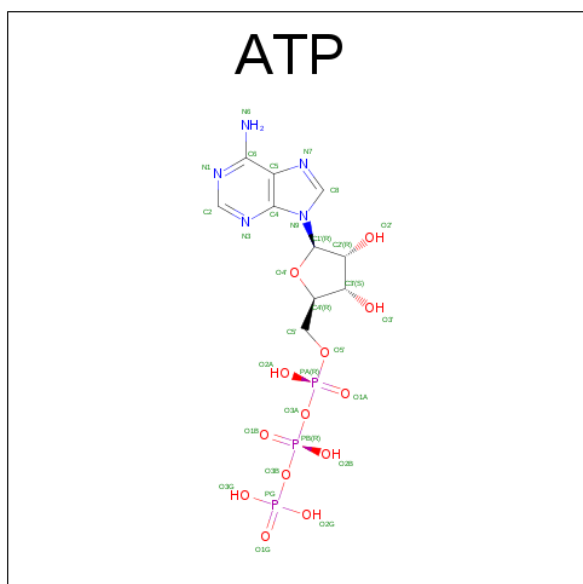
- Molecule 1 is a protein called Sodium/Potassium-Transporting ATPase alpha-1.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	213	3303	1056	1632	282	320	13	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	385	PRO	ARG	CLONING ARTIFACT	UNP P06685

- Molecule 2 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).



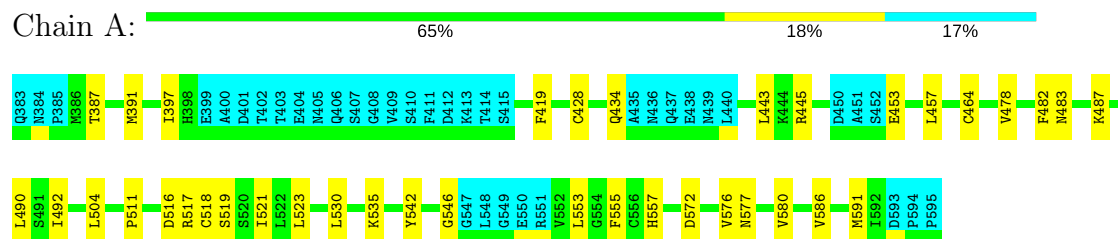
Mol	Chain	Residues	Atoms					
			Total	C	H	N	O	P
2	A	1	43	10	12	5	13	3

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: Sodium/Potassium-Transporting ATPase alpha-1

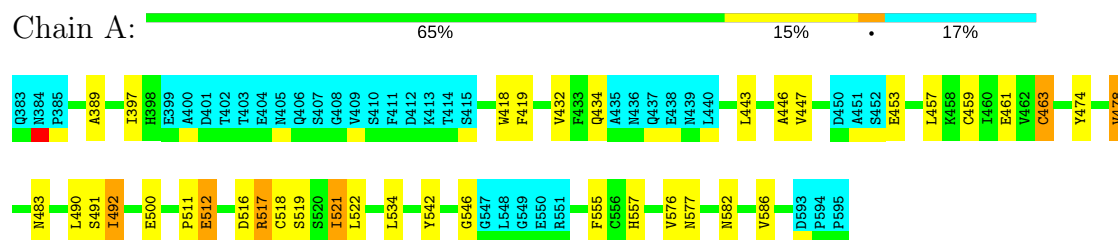


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

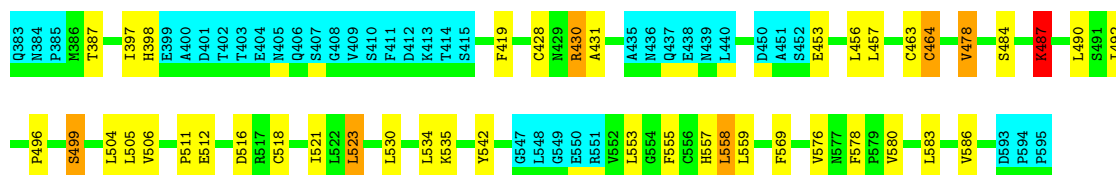
- Molecule 1: Sodium/Potassium-Transporting ATPase alpha-1



4.2.2 Score per residue for model 2

- Molecule 1: Sodium/Potassium-Transporting ATPase alpha-1

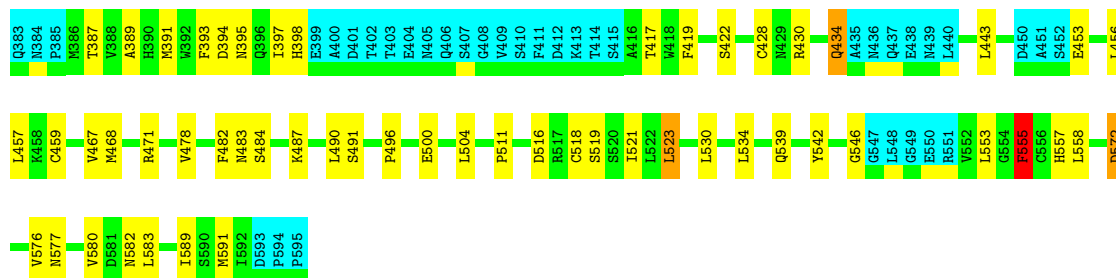




4.2.3 Score per residue for model 3

- Molecule 1: Sodium/Potassium-Transporting ATPase alpha-1

Chain A: 57% 24% 17%



4.2.4 Score per residue for model 4

- Molecule 1: Sodium/Potassium-Transporting ATPase alpha-1

Chain A: 58% 23% 17%



4.2.5 Score per residue for model 5

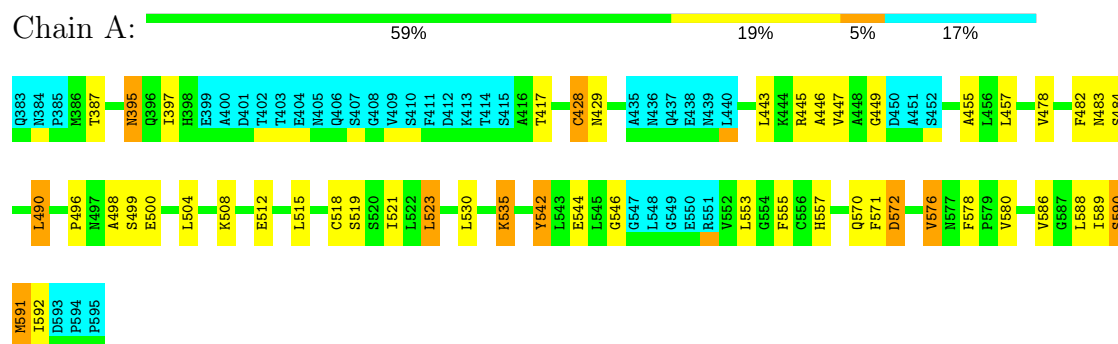
- Molecule 1: Sodium/Potassium-Transporting ATPase alpha-1

Chain A: 61% 19% 17%



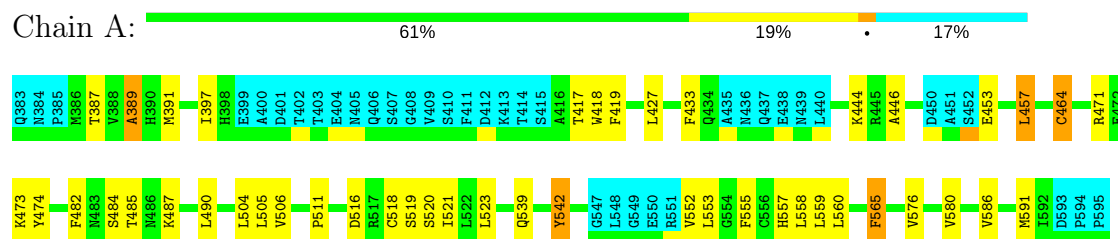
4.2.6 Score per residue for model 6

- Molecule 1: Sodium/Potassium-Transporting ATPase alpha-1



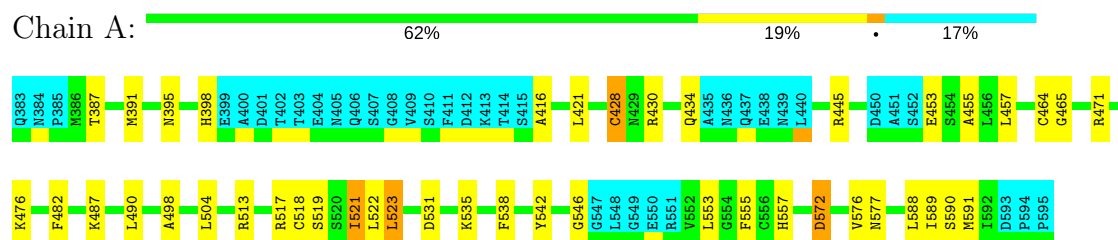
4.2.7 Score per residue for model 7

- Molecule 1: Sodium/Potassium-Transporting ATPase alpha-1



4.2.8 Score per residue for model 8

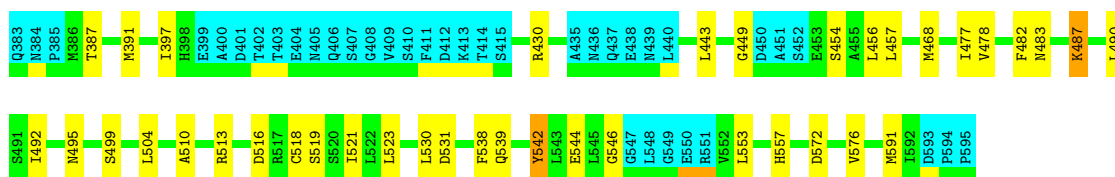
- Molecule 1: Sodium/Potassium-Transporting ATPase alpha-1



4.2.9 Score per residue for model 9

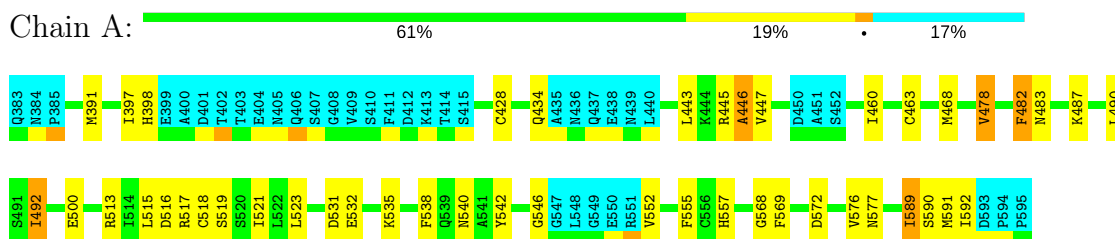
- Molecule 1: Sodium/Potassium-Transporting ATPase alpha-1





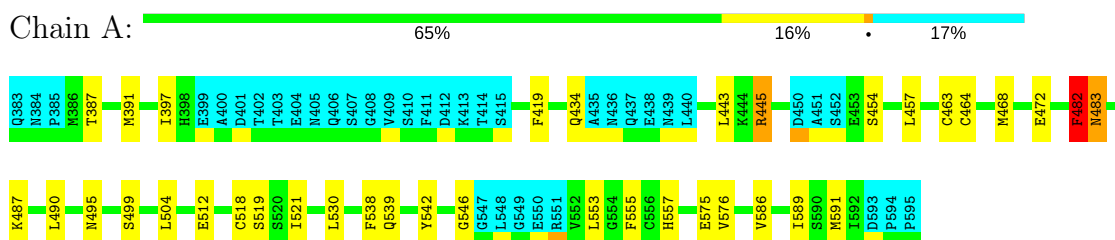
4.2.10 Score per residue for model 10

- Molecule 1: Sodium/Potassium-Transporting ATPase alpha-1



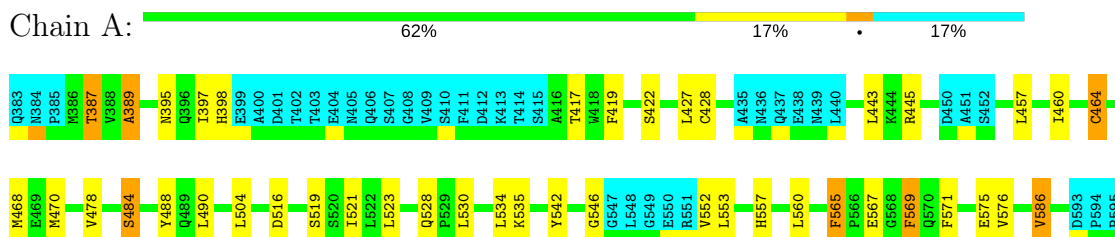
4.2.11 Score per residue for model 11 (medoid)

- Molecule 1: Sodium/Potassium-Transporting ATPase alpha-1



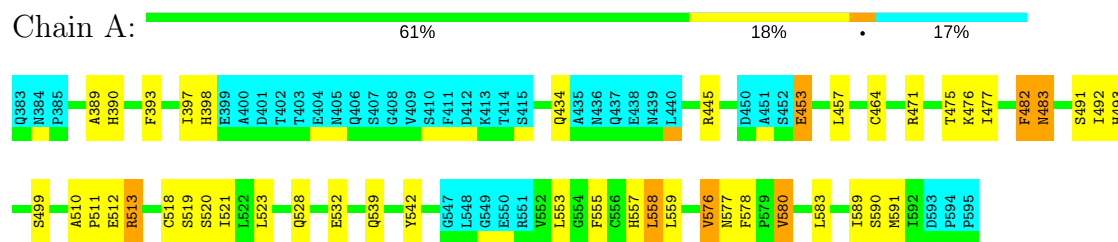
4.2.12 Score per residue for model 12

- Molecule 1: Sodium/Potassium-Transporting ATPase alpha-1



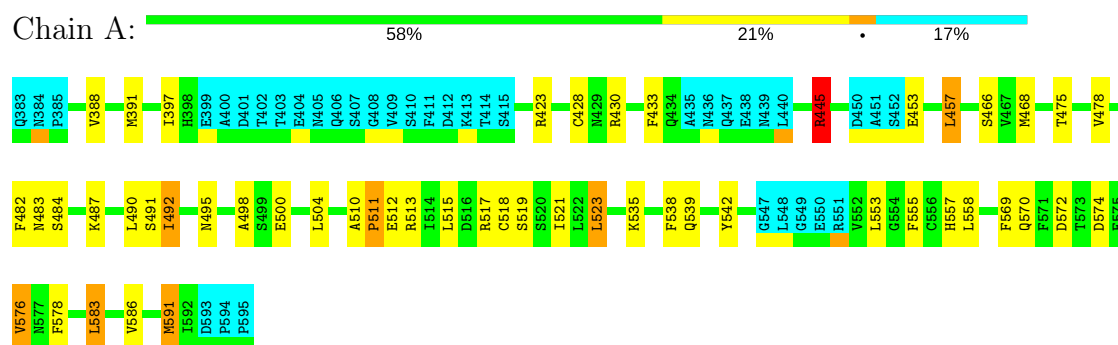
4.2.13 Score per residue for model 13

- Molecule 1: Sodium/Potassium-Transporting ATPase alpha-1



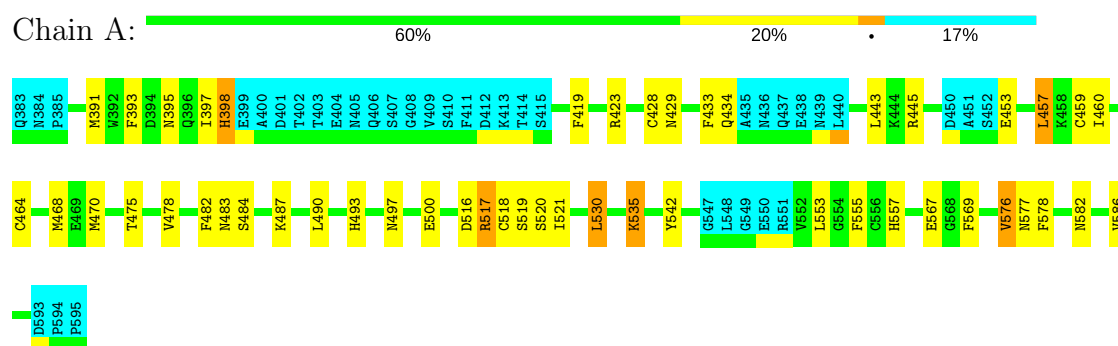
4.2.14 Score per residue for model 14

- Molecule 1: Sodium/Potassium-Transporting ATPase alpha-1



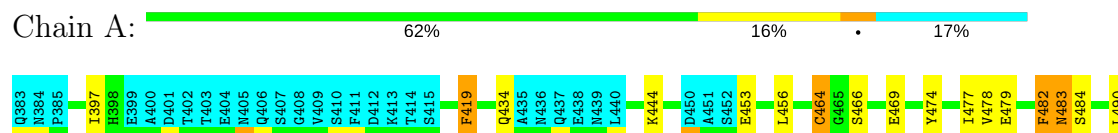
4.2.15 Score per residue for model 15

- Molecule 1: Sodium/Potassium-Transporting ATPase alpha-1



4.2.16 Score per residue for model 16

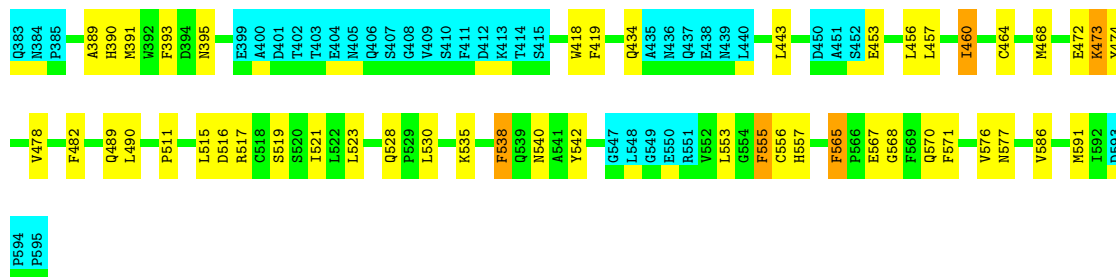
- Molecule 1: Sodium/Potassium-Transporting ATPase alpha-1





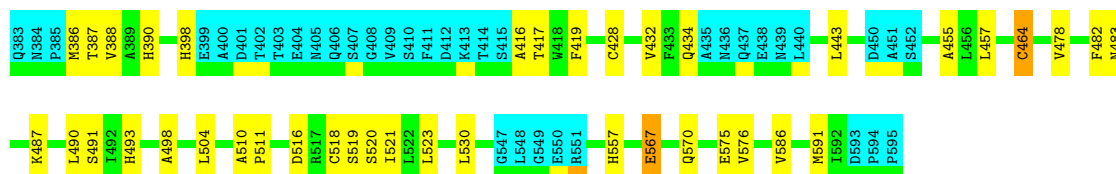
4.2.17 Score per residue for model 17

- Molecule 1: Sodium/Potassium-Transporting ATPase alpha-1



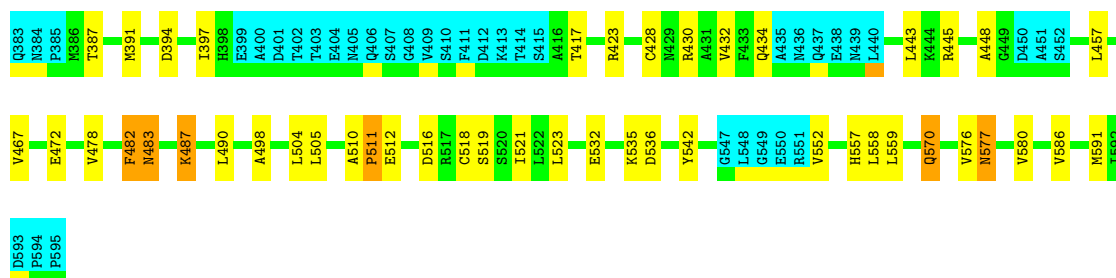
4.2.18 Score per residue for model 18

- Molecule 1: Sodium/Potassium-Transporting ATPase alpha-1



4.2.19 Score per residue for model 19

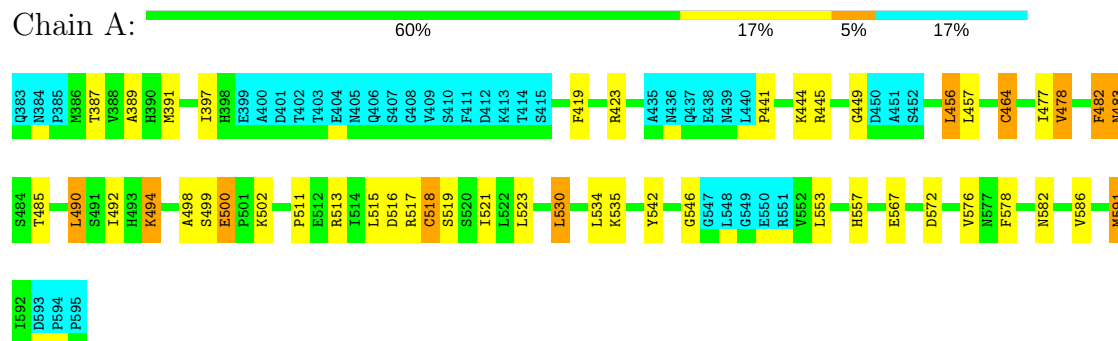
- Molecule 1: Sodium/Potassium-Transporting ATPase alpha-1



4.2.20 Score per residue for model 20

● Molecule 1: Sodium/Potassium-Transporting ATPase alpha-1

Chain A:



5 Refinement protocol and experimental data overview

The models were refined using the following method: *Automated NOESY cross peak assignment*.

Of the 200 calculated structures, 20 were deposited, based on the following criterion: *structures with the lowest energy, target function*.

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

Software name	Classification	Version
CYANA	structure solution	1.0.5
OPALp	refinement	1.0

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)	BMRB entry 5576
Number of chemical shift lists	2
Total number of shifts	2182
Number of shifts mapped to atoms	2176
Number of unparsed shifts	0
Number of shifts with mapping errors	6
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	78%

No validations of the models with respect to experimental NMR restraints is performed at this time.

6 Model quality

6.1 Standard geometry

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

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	0.59±0.01	0±0/1430 (0.0±0.0%)	1.10±0.02	1±1/1935 (0.0±0.0%)
All	All	0.59	0/28600 (0.0%)	1.10	18/38700 (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	2.0±1.0
All	All	0	40

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	555	PHE	CB-CG-CD2	-7.27	115.71	120.80	3	3
1	A	542	TYR	CB-CG-CD2	-6.29	117.22	121.00	7	2
1	A	517	ARG	NE-CZ-NH2	-6.12	117.24	120.30	15	2
1	A	513	ARG	NE-CZ-NH2	-5.90	117.35	120.30	16	1
1	A	487	LYS	CB-CA-C	5.58	121.55	110.40	10	1
1	A	445	ARG	CB-CA-C	5.46	121.32	110.40	19	1
1	A	517	ARG	NE-CZ-NH1	5.45	123.03	120.30	20	1
1	A	591	MET	CA-CB-CG	-5.35	104.21	113.30	6	1
1	A	430	ARG	NE-CZ-NH2	-5.33	117.64	120.30	2	1
1	A	419	PHE	CB-CG-CD2	-5.30	117.09	120.80	16	1
1	A	482	PHE	CB-CA-C	5.25	120.90	110.40	11	1
1	A	423	ARG	NE-CZ-NH1	5.21	122.90	120.30	4	1

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	475	THR	CA-CB-CG2	5.18	119.66	112.40	14	1
1	A	445	ARG	NE-CZ-NH2	-5.10	117.75	120.30	10	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	474	TYR	Sidechain	4
1	A	471	ARG	Sidechain	3
1	A	517	ARG	Sidechain	3
1	A	567	GLU	Peptide	3
1	A	487	LYS	Peptide	2
1	A	542	TYR	Sidechain	2
1	A	571	PHE	Peptide	2
1	A	490	LEU	Peptide	2
1	A	464	CYS	Peptide	1
1	A	418	TRP	Peptide	1
1	A	465	GLY	Peptide	1
1	A	519	SER	Peptide	1
1	A	447	VAL	Peptide	1
1	A	575	GLU	Peptide	1
1	A	580	VAL	Peptide	1
1	A	499	SER	Peptide	1
1	A	497	ASN	Peptide	1
1	A	488	TYR	Sidechain	1
1	A	513	ARG	Sidechain	1
1	A	482	PHE	Sidechain,Peptide	1
1	A	561	PRO	Peptide	1
1	A	546	GLY	Peptide	1
1	A	493	HIS	Peptide	1
1	A	445	ARG	Sidechain	1
1	A	449	GLY	Peptide	1
1	A	434	GLN	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	1397	1392	1392	5±2
All	All	28560	28080	28080	100

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
1:A:387:THR:HG23	1:A:389:ALA:H	0.68	1.47	7	2
1:A:560:LEU:HD13	1:A:565:PHE:CE2	0.64	2.27	7	1
1:A:473:LYS:HE3	1:A:474:TYR:CE2	0.63	2.29	17	1
1:A:521:ILE:HD13	1:A:522:LEU:H	0.59	1.58	1	2
1:A:558:LEU:HD22	1:A:583:LEU:HD22	0.58	1.76	16	1
1:A:515:LEU:HD11	1:A:535:LYS:HE3	0.58	1.75	4	1
1:A:478:VAL:HG11	1:A:572:ASP:HA	0.56	1.78	10	1
1:A:580:VAL:HA	1:A:583:LEU:HD11	0.55	1.78	4	3
1:A:515:LEU:HD11	1:A:535:LYS:HG3	0.54	1.78	20	1
1:A:515:LEU:HD21	1:A:535:LYS:HG3	0.54	1.80	17	3
1:A:576:VAL:HG13	1:A:578:PHE:CE1	0.54	2.38	13	3
1:A:504:LEU:HD12	1:A:505:LEU:N	0.53	2.19	2	1
1:A:455:ALA:HB3	1:A:591:MET:SD	0.52	2.45	6	2
1:A:388:VAL:HG22	1:A:591:MET:HG2	0.52	1.80	14	1
1:A:387:THR:HG23	1:A:389:ALA:N	0.52	2.20	7	1
1:A:530:LEU:HD23	1:A:535:LYS:HD2	0.52	1.80	15	1
1:A:478:VAL:CG2	1:A:492:ILE:HD12	0.51	2.35	1	5
1:A:511:PRO:HG2	1:A:542:TYR:CE1	0.51	2.40	7	3
1:A:504:LEU:CD1	1:A:506:VAL:HG13	0.51	2.35	2	1
1:A:453:GLU:OE1	1:A:456:LEU:HD11	0.50	2.06	3	1
1:A:473:LYS:HE3	1:A:474:TYR:CZ	0.50	2.42	17	1
1:A:395:ASN:HD21	1:A:534:LEU:HD22	0.49	1.67	5	1
1:A:555:PHE:CE2	1:A:589:ILE:HD13	0.49	2.43	13	2
1:A:518:CYS:SG	1:A:530:LEU:HD22	0.48	2.49	20	1
1:A:427:LEU:HD21	1:A:474:TYR:CD1	0.48	2.43	7	1
1:A:431:ALA:HB3	1:A:453:GLU:O	0.48	2.07	2	1
1:A:433:PHE:CD2	1:A:457:LEU:HD11	0.47	2.43	15	3
1:A:434:GLN:HE21	1:A:448:ALA:HB2	0.47	1.70	19	1
1:A:560:LEU:HD22	1:A:565:PHE:CE2	0.47	2.45	12	1
1:A:576:VAL:HG13	1:A:578:PHE:CZ	0.47	2.45	15	3
1:A:510:ALA:HB1	1:A:511:PRO:HD2	0.46	1.86	5	4
1:A:473:LYS:HE3	1:A:474:TYR:CE1	0.46	2.45	4	1
1:A:427:LEU:HD21	1:A:470:MET:HB3	0.46	1.86	12	1
1:A:515:LEU:HD22	1:A:538:PHE:CE1	0.46	2.45	10	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:510:ALA:HB3	1:A:513:ARG:HB2	0.46	1.88	9	3
1:A:482:PHE:CG	1:A:483:ASN:N	0.46	2.83	13	4
1:A:558:LEU:HD13	1:A:583:LEU:HD22	0.45	1.88	3	2
1:A:512:GLU:H	1:A:512:GLU:CD	0.45	2.15	1	1
1:A:456:LEU:HD23	1:A:591:MET:SD	0.45	2.52	20	1
1:A:521:ILE:HD13	1:A:522:LEU:N	0.44	2.28	1	1
1:A:558:LEU:C	1:A:558:LEU:HD12	0.44	2.33	13	1
1:A:482:PHE:CD1	1:A:483:ASN:N	0.44	2.86	20	1
1:A:511:PRO:CG	1:A:542:TYR:CE1	0.44	3.01	14	2
1:A:510:ALA:HB1	1:A:511:PRO:CD	0.44	2.42	4	1
1:A:453:GLU:HG3	1:A:455:ALA:H	0.43	1.73	8	1
1:A:393:PHE:CD2	1:A:417:THR:HG21	0.43	2.48	3	1
1:A:421:LEU:HD11	1:A:589:ILE:HD11	0.43	1.91	5	1
1:A:395:ASN:OD1	1:A:521:ILE:HD12	0.43	2.14	8	1
1:A:560:LEU:HD22	1:A:565:PHE:CZ	0.42	2.49	12	1
1:A:555:PHE:CD2	1:A:589:ILE:HD12	0.42	2.49	11	1
1:A:477:ILE:HD12	1:A:492:ILE:HG22	0.42	1.90	9	2
1:A:432:VAL:CG2	1:A:448:ALA:HB3	0.42	2.45	19	1
1:A:456:LEU:HD22	1:A:555:PHE:CE1	0.42	2.50	17	1
1:A:453:GLU:CD	1:A:454:SER:H	0.42	2.18	5	1
1:A:492:ILE:HD11	1:A:578:PHE:CE2	0.42	2.49	20	2
1:A:446:ALA:O	1:A:447:VAL:HG23	0.42	2.15	10	1
1:A:447:VAL:HG12	1:A:449:GLY:H	0.41	1.75	6	1
1:A:386:MET:CE	1:A:455:ALA:HB2	0.41	2.45	18	1
1:A:545:LEU:HD13	1:A:590:SER:HB3	0.41	1.92	4	1
1:A:487:LYS:HE2	1:A:513:ARG:CZ	0.41	2.46	8	1
1:A:505:LEU:HD23	1:A:506:VAL:N	0.41	2.31	7	1
1:A:492:ILE:HD11	1:A:578:PHE:CD2	0.41	2.51	14	1
1:A:565:PHE:CE2	1:A:571:PHE:CE1	0.41	3.09	17	1
1:A:417:THR:HG23	1:A:586:VAL:HG13	0.40	1.92	12	1
1:A:441:PRO:CG	1:A:444:LYS:HE2	0.40	2.47	20	1
1:A:558:LEU:HD13	1:A:558:LEU:C	0.40	2.36	2	1

6.3 Torsion angles ⓘ

6.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	176/213 (83%)	131±5 (75±3%)	31±4 (18±2%)	13±3 (7±2%)	2	16
All	All	3520/4260 (83%)	2628 (75%)	629 (18%)	263 (7%)	2	16

All 48 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	576	VAL	20
1	A	397	ILE	17
1	A	586	VAL	14
1	A	483	ASN	13
1	A	464	CYS	13
1	A	434	GLN	12
1	A	546	GLY	10
1	A	511	PRO	9
1	A	555	PHE	9
1	A	389	ALA	8
1	A	580	VAL	8
1	A	499	SER	7
1	A	484	SER	7
1	A	572	ASP	7
1	A	487	LYS	7
1	A	523	LEU	6
1	A	498	ALA	6
1	A	569	PHE	6
1	A	398	HIS	6
1	A	552	VAL	5
1	A	570	GLN	5
1	A	577	ASN	5
1	A	463	CYS	5
1	A	559	LEU	4
1	A	446	ALA	4
1	A	500	GLU	4
1	A	492	ILE	4
1	A	395	ASN	4
1	A	589	ILE	4
1	A	582	ASN	3
1	A	496	PRO	3
1	A	590	SER	3
1	A	477	ILE	2
1	A	493	HIS	2
1	A	460	ILE	2
1	A	416	ALA	2

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Mol	Chain	Res	Type	Models (Total)
1	A	393	PHE	2
1	A	428	CYS	2
1	A	568	GLY	2
1	A	445	ARG	2
1	A	583	LEU	2
1	A	441	PRO	1
1	A	475	THR	1
1	A	567	GLU	1
1	A	449	GLY	1
1	A	494	LYS	1
1	A	453	GLU	1
1	A	388	VAL	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	155/186 (83%)	128±3 (83±2%)	27±3 (17±2%)	5	41
All	All	3100/3720 (83%)	2564 (83%)	536 (17%)	5	41

All 100 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	557	HIS	20
1	A	521	ILE	20
1	A	490	LEU	19
1	A	457	LEU	18
1	A	519	SER	18
1	A	518	CYS	17
1	A	482	PHE	17
1	A	523	LEU	16
1	A	553	LEU	15
1	A	542	TYR	14
1	A	478	VAL	14
1	A	391	MET	13
1	A	591	MET	13

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Mol	Chain	Res	Type	Models (Total)
1	A	419	PHE	13
1	A	516	ASP	13
1	A	530	LEU	12
1	A	428	CYS	11
1	A	387	THR	11
1	A	504	LEU	11
1	A	443	LEU	11
1	A	535	LYS	9
1	A	468	MET	8
1	A	539	GLN	8
1	A	453	GLU	8
1	A	512	GLU	7
1	A	491	SER	6
1	A	517	ARG	6
1	A	534	LEU	6
1	A	430	ARG	6
1	A	464	CYS	5
1	A	577	ASN	5
1	A	500	GLU	5
1	A	528	GLN	5
1	A	538	PHE	5
1	A	423	ARG	4
1	A	531	ASP	4
1	A	558	LEU	4
1	A	445	ARG	4
1	A	487	LYS	4
1	A	417	THR	4
1	A	398	HIS	4
1	A	495	ASN	4
1	A	532	GLU	4
1	A	520	SER	4
1	A	456	LEU	4
1	A	459	CYS	4
1	A	588	LEU	3
1	A	572	ASP	3
1	A	444	LYS	3
1	A	565	PHE	3
1	A	485	THR	3
1	A	429	ASN	3
1	A	390	HIS	3
1	A	472	GLU	3
1	A	570	GLN	3

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Mol	Chain	Res	Type	Models (Total)
1	A	513	ARG	3
1	A	590	SER	3
1	A	454	SER	3
1	A	567	GLU	3
1	A	476	LYS	3
1	A	460	ILE	3
1	A	395	ASN	3
1	A	467	VAL	2
1	A	508	LYS	2
1	A	466	SER	2
1	A	575	GLU	2
1	A	569	PHE	2
1	A	556	CYS	2
1	A	484	SER	2
1	A	473	LYS	2
1	A	540	ASN	2
1	A	592	ILE	2
1	A	544	GLU	2
1	A	432	VAL	2
1	A	422	SER	2
1	A	502	LYS	2
1	A	418	TRP	2
1	A	562	ASP	2
1	A	394	ASP	2
1	A	488	TYR	1
1	A	505	LEU	1
1	A	479	GLU	1
1	A	470	MET	1
1	A	421	LEU	1
1	A	494	LYS	1
1	A	393	PHE	1
1	A	584	CYS	1
1	A	475	THR	1
1	A	471	ARG	1
1	A	580	VAL	1
1	A	574	ASP	1
1	A	483	ASN	1
1	A	582	ASN	1
1	A	469	GLU	1
1	A	497	ASN	1
1	A	461	GLU	1
1	A	536	ASP	1

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Mol	Chain	Res	Type	Models (Total)
1	A	463	CYS	1
1	A	589	ILE	1
1	A	489	GLN	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](#)

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds for which Mogul statistics could be retrieved, the number of bonds that are observed in the model and the number of bonds that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length is the number of standard deviations the observed value is removed from the expected value. A bond length with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond lengths.

Mol	Type	Chain	Res	Link	Bond lengths		
					Counts	RMSZ	#Z>2
2	ATP	A	900	-	27,33,33	0.96±0.04	0±0 (0±0%)

In the following table, the Counts columns list the number of angles for which Mogul statistics could be retrieved, the number of angles that are observed in the model and the number of angles that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond angle is the number of standard deviations the observed value is removed from the expected value. A bond angle with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond angles.

Mol	Type	Chain	Res	Link	Bond angles		
					Counts	RMSZ	#Z>2
2	ATP	A	900	-	25,52,52	1.13±0.32	0±0 (0±1%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	ATP	A	900	-	-	0±0,18,38,38	0±0,3,3,3

There are no bond-length outliers.

All unique angle outliers are listed below.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
2	A	900	ATP	C4'-O4'-C1'	8.40	100.82	109.77	1	3

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6.7 Other polymers [i](#)

There are no such molecules in this entry.

6.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

7 Chemical shift validation

The completeness of assignment taking into account all chemical shift lists is 78% for the well-defined parts and 73% for the entire structure.

7.1 Chemical shift list 1

File name: BMRB entry 5576

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	2176
Number of shifts mapped to atoms	2176
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	5

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	185	-0.06 ± 0.17	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	183	0.11 ± 0.10	None needed (< 0.5 ppm)
$^{13}\text{C}'$	0	—	None (insufficient data)
^{15}N	179	-0.24 ± 0.33	None needed (< 0.5 ppm)

7.1.3 Completeness of resonance assignments

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 78%, i.e. 1700 atoms were assigned a chemical shift out of a possible 2193. 32 out of 32 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	651/862 (76%)	331/343 (97%)	158/352 (45%)	162/167 (97%)
Sidechain	949/1142 (83%)	576/671 (86%)	360/427 (84%)	13/44 (30%)

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	Total	¹H	¹³C	¹⁵N
Aromatic	100/189 (53%)	56/103 (54%)	42/78 (54%)	2/8 (25%)
Overall	1700/2193 (78%)	963/1117 (86%)	560/857 (65%)	177/219 (81%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 73%, i.e. 1903 atoms were assigned a chemical shift out of a possible 2598. 35 out of 35 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Backbone	739/1041 (71%)	375/414 (91%)	185/426 (43%)	179/201 (89%)
Sidechain	1059/1359 (78%)	644/798 (81%)	402/506 (79%)	13/55 (24%)
Aromatic	105/198 (53%)	59/108 (55%)	44/82 (54%)	2/8 (25%)
Overall	1903/2598 (73%)	1078/1320 (82%)	631/1014 (62%)	194/264 (73%)

7.1.4 Statistically unusual chemical shifts ⓘ

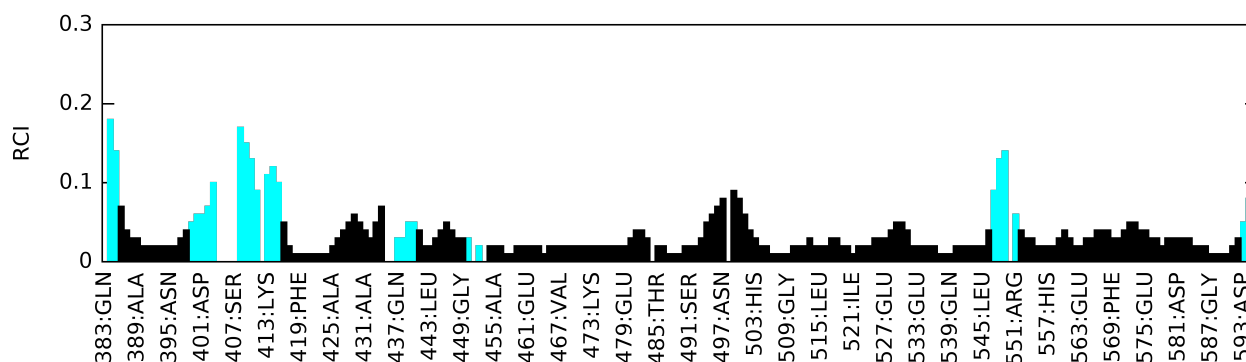
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

Mol	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	422	SER	HB2	1.83	5.18 – 2.58	-7.9
1	A	492	ILE	HD11	-0.87	2.13 – -0.77	-5.4
1	A	492	ILE	HD13	-0.87	2.13 – -0.77	-5.4
1	A	492	ILE	HD12	-0.87	2.13 – -0.77	-5.4
1	A	445	ARG	HD2	1.95	4.27 – 1.97	-5.1

7.1.5 Random Coil Index (RCI) plots ⓘ

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.

Random coil index (RCI) for chain A:



7.2 Chemical shift list 2

File name: BMRB entry 5576

Chemical shift list name: *assigned_chem_shift_list_2*

7.2.1 Bookkeeping [i](#)

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	6
Number of shifts mapped to atoms	0
Number of unparsed shifts	0
Number of shifts with mapping errors	6
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

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

- Chain not found in structure. All 6 occurrences are reported below.

Chain	Res	Type	Atom	Shift Data		
				Value	Uncertainty	Ambiguity
UNMAPPED	1	ATP	H1'	6.094	0.003	1
UNMAPPED	1	ATP	H2	8.22	0.0	1
UNMAPPED	1	ATP	H5'	4.163	0.0	1
UNMAPPED	1	ATP	H8	8.485	0.0	1
UNMAPPED	1	ATP	H3'	4.348	0.0	1
UNMAPPED	1	ATP	H4'	4.255	0.0	1

7.2.2 Chemical shift referencing [i](#)

No chemical shift referencing corrections were calculated (not enough data).

7.2.3 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 0%, i.e. 0 atoms were assigned a chemical shift out of a possible 2193. 0 out of 32 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	0/862 (0%)	0/343 (0%)	0/352 (0%)	0/167 (0%)
Sidechain	0/1142 (0%)	0/671 (0%)	0/427 (0%)	0/44 (0%)
Aromatic	0/189 (0%)	0/103 (0%)	0/78 (0%)	0/8 (0%)
Overall	0/2193 (0%)	0/1117 (0%)	0/857 (0%)	0/219 (0%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 0%, i.e. 0 atoms were assigned a chemical shift out of a possible 2598. 0 out of 35 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	0/1041 (0%)	0/414 (0%)	0/426 (0%)	0/201 (0%)
Sidechain	0/1359 (0%)	0/798 (0%)	0/506 (0%)	0/55 (0%)
Aromatic	0/198 (0%)	0/108 (0%)	0/82 (0%)	0/8 (0%)
Overall	0/2598 (0%)	0/1320 (0%)	0/1014 (0%)	0/264 (0%)

7.2.4 Statistically unusual chemical shifts [i](#)

There are no statistically unusual chemical shifts.

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

No *random coil index* (RCI) plot could be generated from the current chemical shift list (assigned_chem_shift_list_2). RCI is only applicable to proteins.