Full wwPDB NMR Structure Validation Report (i)

Apr 21, 2024 – 06:46 AM EDT

PDB ID	:	2LT9
BMRB ID	:	18464
Title	:	The solution structure of Ca2+ binding domain 2B of the third isoform of the Na+/Ca2+ exchanger
Authors	:	Breukels, V.; Touw, W.G.; Vuister, G.W.
Deposited on	:	2012-05-15

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
https://www.wwpdb.org/validation/2017/NMRValidationReportHelp
with specific help available everywhere you see the (i) 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 (i)) were used in the production of this report:

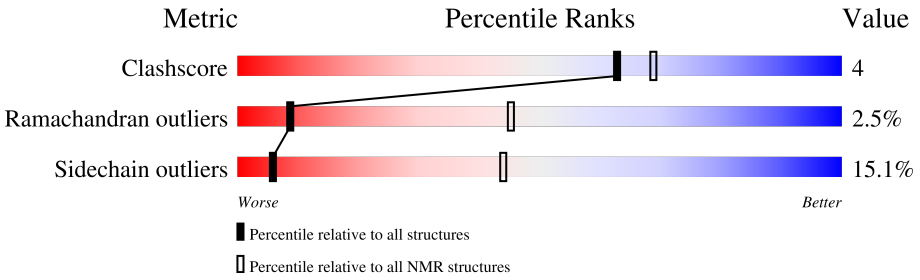
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

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 87%.

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	158937	12864
Ramachandran outliers	154571	11451
Sidechain outliers	154315	11428

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 <=5%

Mol	Chain	Length	Quality of chain
1	A	157	55% 9% • 27% 6%

2 Ensemble composition and analysis

This entry contains 20 models. Model 5 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:529-A:603, A:612-A:626, A:650-A:664 (105)	0.36	5

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 3 clusters and 2 single-model clusters were found.

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

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 2328 atoms, of which 1150 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Protein Slc8a3.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	148	2328	742	1150	193	239	4	0

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	519	MET	-	expression tag	UNP Q7TS90
A	520	ALA	-	expression tag	UNP Q7TS90
A	521	SER	-	expression tag	UNP Q7TS90
A	522	HIS	-	expression tag	UNP Q7TS90
A	523	HIS	-	expression tag	UNP Q7TS90
A	524	HIS	-	expression tag	UNP Q7TS90
A	525	HIS	-	expression tag	UNP Q7TS90
A	526	HIS	-	expression tag	UNP Q7TS90
A	527	HIS	-	expression tag	UNP Q7TS90

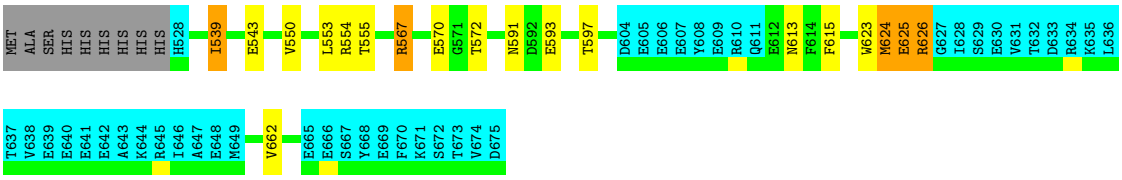
4 Residue-property plots

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: Protein Slc8a3

Chain A:



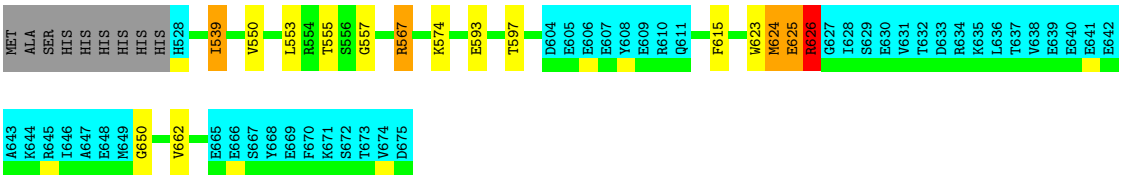
4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

• Molecule 1: Protein Slc8a3

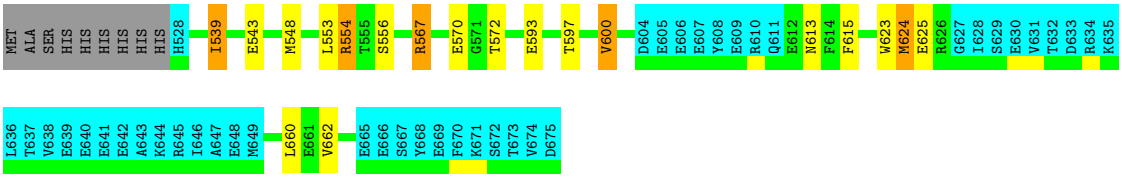
Chain A:



4.2.2 Score per residue for model 2

• Molecule 1: Protein Slc8a3

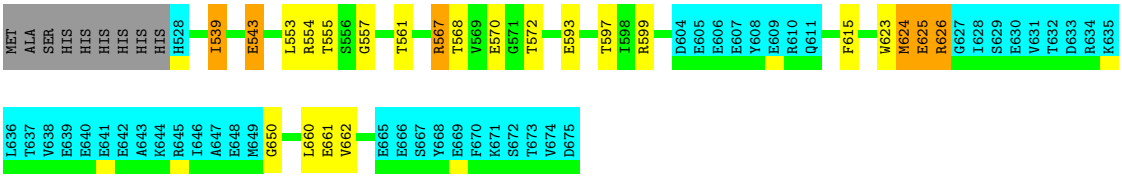
Chain A:



4.2.3 Score per residue for model 3

• Molecule 1: Protein Slc8a3

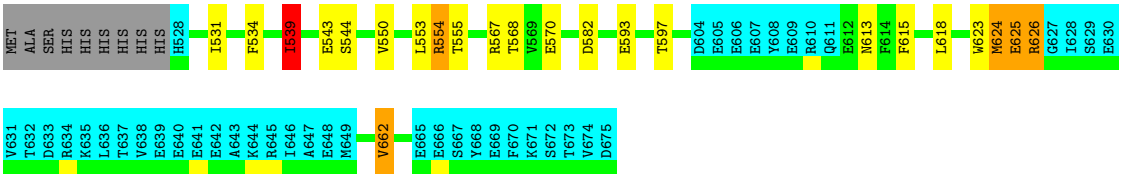
Chain A:



4.2.4 Score per residue for model 4

• Molecule 1: Protein Slc8a3

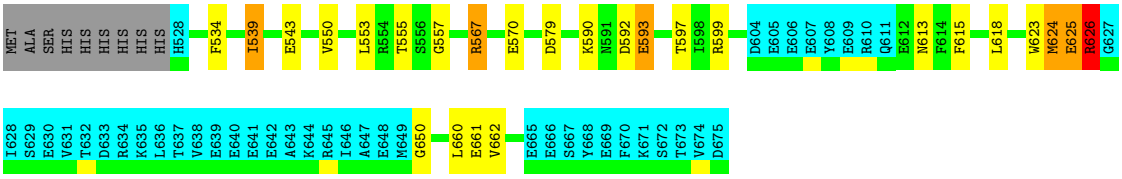
Chain A:



4.2.5 Score per residue for model 5 (medoid)

• Molecule 1: Protein Slc8a3

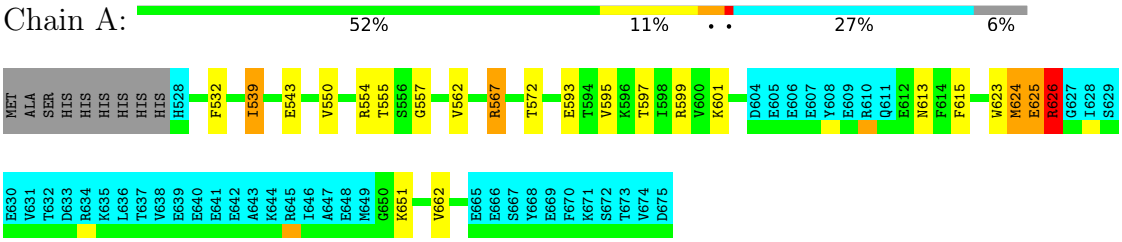
Chain A:



4.2.6 Score per residue for model 6

• Molecule 1: Protein Slc8a3

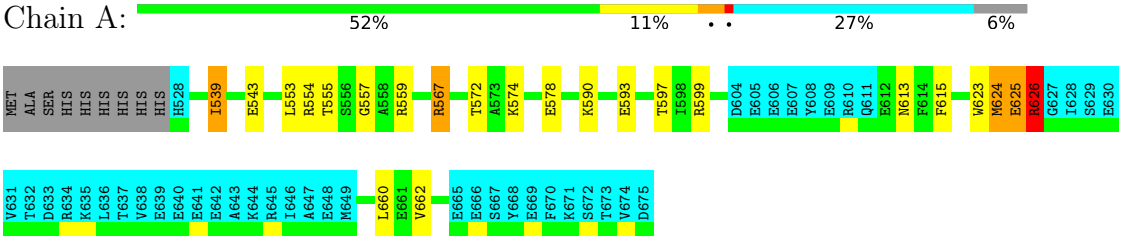
Chain A:



4.2.7 Score per residue for model 7

- Molecule 1: Protein Slc8a3

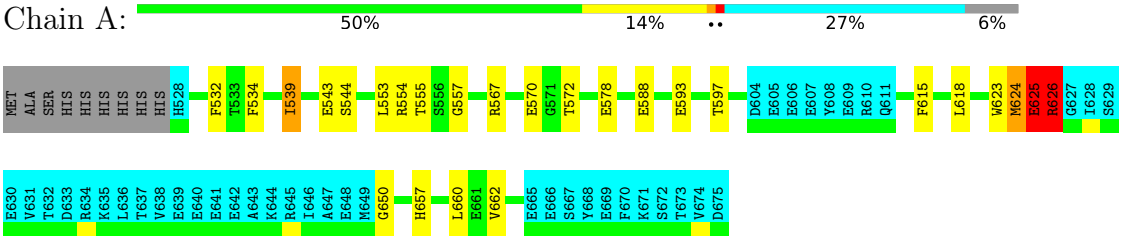
Chain A:



4.2.8 Score per residue for model 8

- Molecule 1: Protein Slc8a3

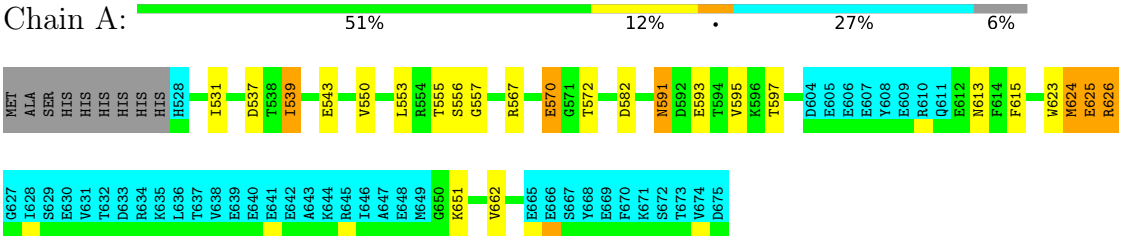
Chain A:



4.2.9 Score per residue for model 9

- Molecule 1: Protein Slc8a3

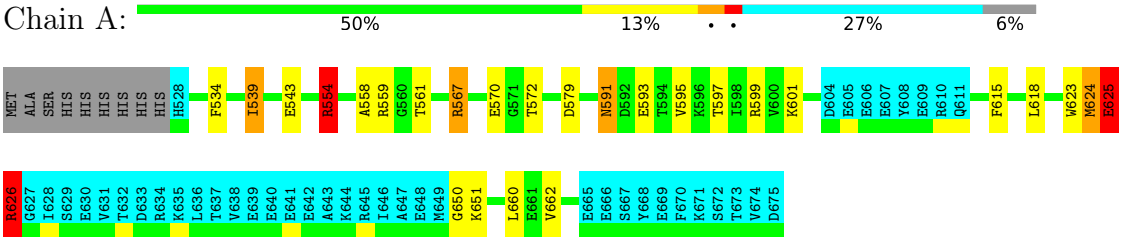
Chain A:



4.2.10 Score per residue for model 10

• Molecule 1: Protein Slc8a3

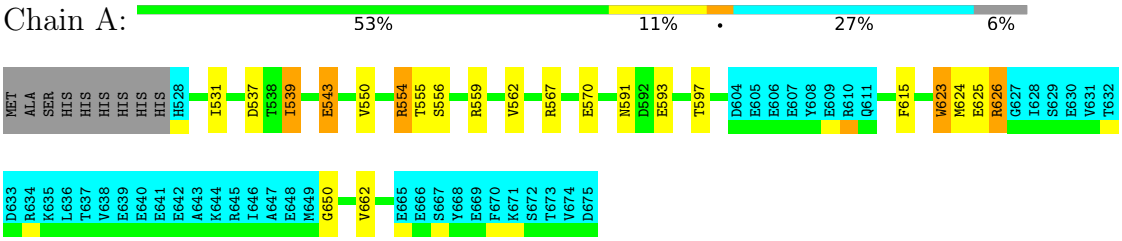
Chain A:



4.2.11 Score per residue for model 11

• Molecule 1: Protein Slc8a3

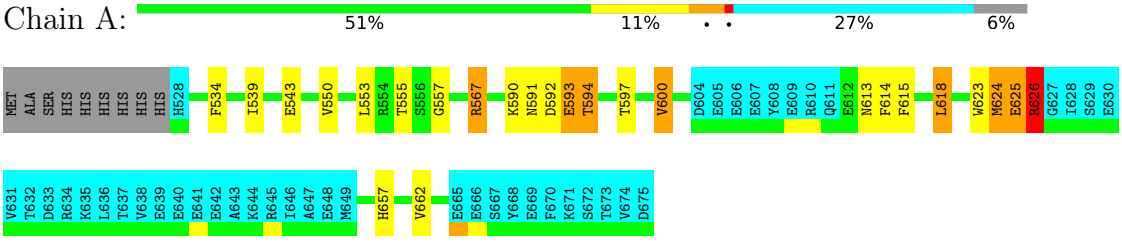
Chain A:



4.2.12 Score per residue for model 12

• Molecule 1: Protein Slc8a3

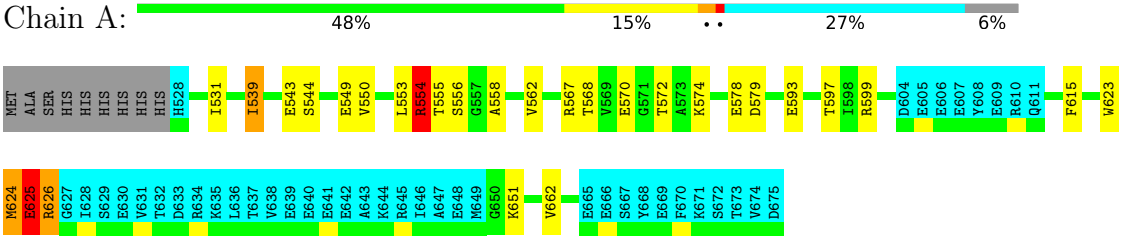
Chain A:



4.2.13 Score per residue for model 13

• Molecule 1: Protein Slc8a3

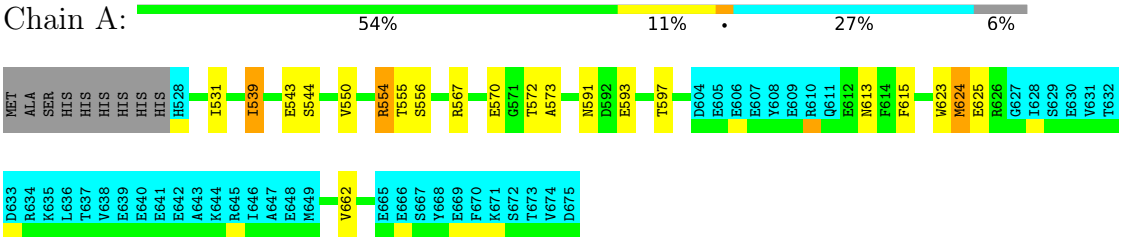
Chain A:



4.2.14 Score per residue for model 14

• Molecule 1: Protein Slc8a3

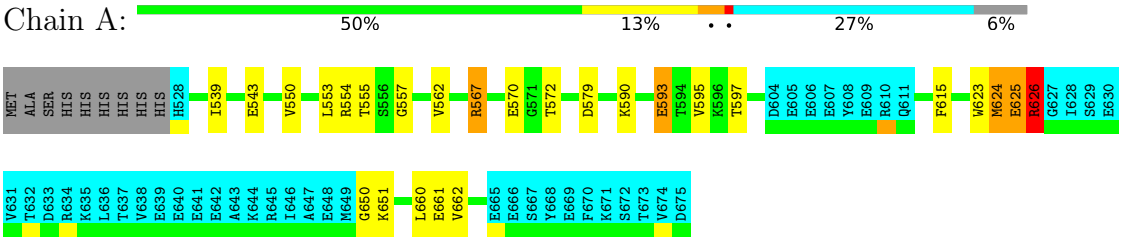
Chain A:



4.2.15 Score per residue for model 15

• Molecule 1: Protein Slc8a3

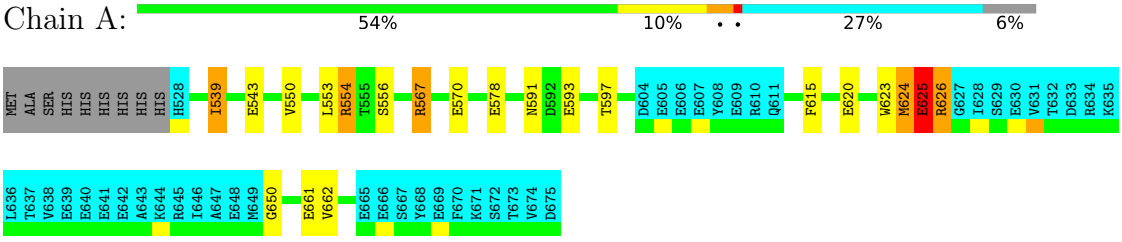
Chain A:



4.2.16 Score per residue for model 16

• Molecule 1: Protein Slc8a3

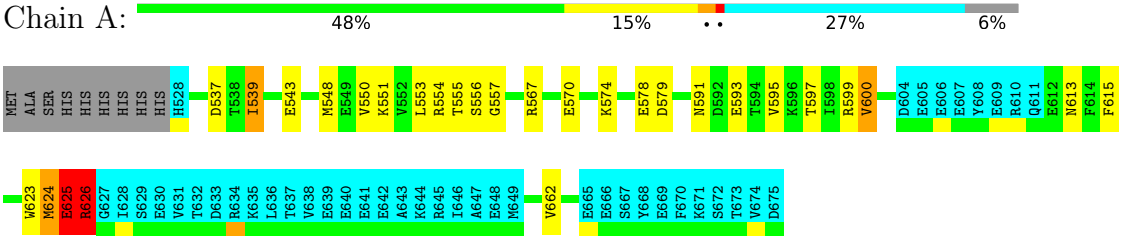
Chain A:



4.2.17 Score per residue for model 17

• Molecule 1: Protein Slc8a3

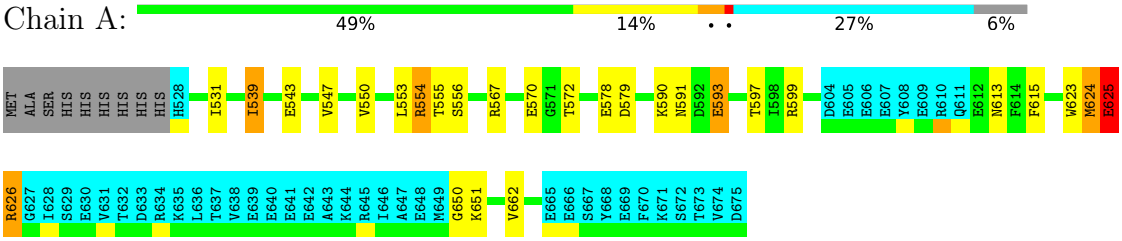
Chain A:



4.2.18 Score per residue for model 18

• Molecule 1: Protein Slc8a3

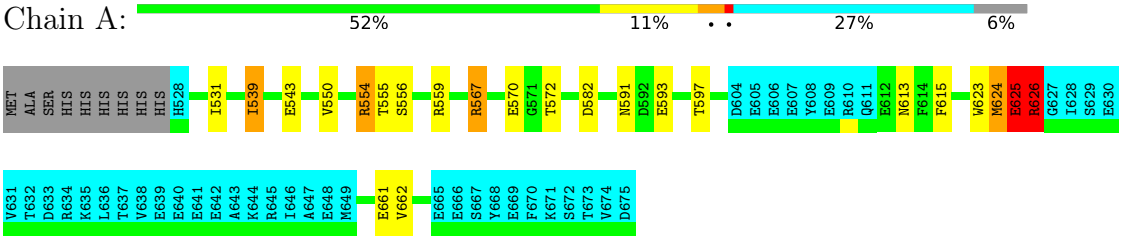
Chain A:



4.2.19 Score per residue for model 19

• Molecule 1: Protein Slc8a3

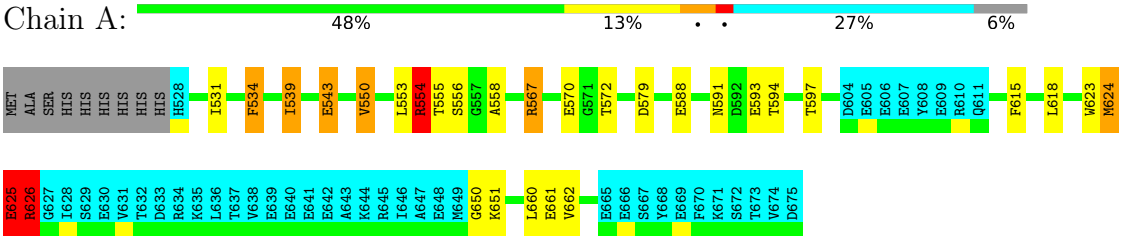
Chain A:



4.2.20 Score per residue for model 20

• Molecule 1: Protein Slc8a3

Chain A:



5 Refinement protocol and experimental data overview

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

Of the 100 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
CYANA	structure solution	3.0
YASARA	refinement	11.9.18

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	1608
Number of shifts mapped to atoms	1603
Number of unparsed shifts	0
Number of shifts with mapping errors	5
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	87%

6 Model quality

6.1 Standard geometry

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	0.79±0.02	0±0/833 (0.0± 0.1%)	0.99±0.02	5±2/1124 (0.5± 0.1%)
All	All	0.80	5/16660 (0.0%)	0.99	106/22480 (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	2.5±0.9
All	All	0	50

All unique bond 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(Å)	Ideal(Å)	Models	
								Worst	Total
1	A	625	GLU	C-O	-8.41	1.07	1.23	7	4
1	A	662	VAL	CB-CG2	-5.44	1.41	1.52	4	1

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(^{o})	Ideal(^{o})	Models	
								Worst	Total
1	A	625	GLU	N-CA-C	-6.83	92.57	111.00	11	4
1	A	567	ARG	NE-CZ-NH1	6.66	123.63	120.30	12	12
1	A	600	VAL	CG1-CB-CG2	6.60	121.46	110.90	12	3
1	A	554	ARG	NE-CZ-NH1	6.43	123.52	120.30	14	14
1	A	626	ARG	N-CA-CB	6.38	122.09	110.60	7	5
1	A	539	ILE	CG1-CB-CG2	-6.31	97.52	111.40	4	1
1	A	559	ARG	NE-CZ-NH1	5.98	123.29	120.30	11	4
1	A	625	GLU	CA-C-N	5.95	130.29	117.20	7	9

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})	Models	
								Worst	Total
1	A	626	ARG	NE-CZ-NH1	5.87	123.23	120.30	11	8
1	A	624	MET	CB-CA-C	-5.63	99.15	110.40	1	17
1	A	624	MET	CA-C-N	-5.60	104.88	117.20	2	3
1	A	625	GLU	CA-C-O	-5.54	108.46	120.10	7	2
1	A	599	ARG	NE-CZ-NH1	5.46	123.03	120.30	6	8
1	A	626	ARG	NE-CZ-NH2	-5.41	117.60	120.30	12	2
1	A	624	MET	N-CA-CB	-5.25	101.15	110.60	15	12
1	A	625	GLU	N-CA-CB	-5.21	101.22	110.60	10	1
1	A	534	PHE	CB-CG-CD2	-5.09	117.23	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	624	MET	Mainchain,Peptide	19
1	A	625	GLU	Mainchain	15

6.2 Too-close contacts (i)

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	817	822	822	7±2
All	All	16340	16440	16440	143

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:623:TRP:CZ3	1:A:626:ARG:HG3	0.60	2.32	6	18
1:A:539:ILE:HG23	1:A:662:VAL:HG13	0.57	1.76	19	17
1:A:625:GLU:O	1:A:626:ARG:HG2	0.55	2.02	7	17
1:A:623:TRP:CZ3	1:A:650:GLY:HA3	0.55	2.37	10	10
1:A:543:GLU:H	1:A:543:GLU:CD	0.55	2.05	15	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:555:THR:HG23	1:A:557:GLY:H	0.52	1.64	17	10
1:A:534:PHE:CE1	1:A:618:LEU:HD21	0.52	2.39	5	6
1:A:554:ARG:HD2	1:A:558:ALA:HB3	0.51	1.81	10	1
1:A:570:GLU:H	1:A:570:GLU:CD	0.51	2.07	16	2
1:A:531:ILE:H	1:A:555:THR:HG22	0.50	1.66	13	8
1:A:614:PHE:CE1	1:A:662:VAL:HG21	0.48	2.44	12	1
1:A:623:TRP:CH2	1:A:626:ARG:HG3	0.47	2.44	20	13
1:A:539:ILE:HG23	1:A:662:VAL:HA	0.47	1.87	4	1
1:A:625:GLU:O	1:A:626:ARG:CG	0.46	2.63	7	17
1:A:623:TRP:CE3	1:A:626:ARG:HG3	0.46	2.45	12	2
1:A:543:GLU:CD	1:A:543:GLU:H	0.45	2.15	20	3
1:A:532:PHE:CZ	1:A:554:ARG:HD3	0.45	2.46	8	2
1:A:590:LYS:H	1:A:593:GLU:HB2	0.45	1.71	5	5
1:A:534:PHE:CZ	1:A:550:VAL:HG11	0.45	2.47	5	2
1:A:554:ARG:HD2	1:A:558:ALA:HB2	0.43	1.91	20	2
1:A:561:THR:HB	1:A:625:GLU:HB2	0.43	1.91	10	2
1:A:592:ASP:C	1:A:594:THR:H	0.40	2.19	12	1
1:A:570:GLU:CD	1:A:570:GLU:H	0.40	2.19	9	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	105/157 (67%)	93±1 (89±1%)	9±2 (9±2%)	3±1 (3±1%)	9	45
All	All	2100/3140 (67%)	1859 (89%)	188 (9%)	53 (3%)	9	45

All 6 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	593	GLU	19
1	A	626	ARG	17
1	A	556	SER	8
1	A	591	ASN	6

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Mol	Chain	Res	Type	Models (Total)
1	A	582	ASP	2
1	A	573	ALA	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	88/136 (65%)	75±3 (85±3%)	13±3 (15±3%)	6 44
All	All	1760/2720 (65%)	1495 (85%)	265 (15%)	6 44

All 40 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	539	ILE	20
1	A	567	ARG	20
1	A	597	THR	20
1	A	615	PHE	20
1	A	543	GLU	17
1	A	553	LEU	15
1	A	550	VAL	14
1	A	570	GLU	14
1	A	572	THR	13
1	A	613	ASN	11
1	A	554	ARG	10
1	A	660	LEU	8
1	A	579	ASP	7
1	A	651	LYS	7
1	A	661	GLU	6
1	A	578	GLU	6
1	A	591	ASN	6
1	A	595	VAL	5
1	A	574	LYS	4
1	A	544	SER	4
1	A	562	VAL	4
1	A	600	VAL	3
1	A	623	TRP	3

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Mol	Chain	Res	Type	Models (Total)
1	A	568	THR	3
1	A	537	ASP	3
1	A	626	ARG	2
1	A	548	MET	2
1	A	601	LYS	2
1	A	588	GLU	2
1	A	657	HIS	2
1	A	556	SER	2
1	A	594	THR	2
1	A	592	ASP	1
1	A	618	LEU	1
1	A	549	GLU	1
1	A	662	VAL	1
1	A	620	GLU	1
1	A	551	LYS	1
1	A	547	VAL	1
1	A	582	ASP	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 monosaccharides 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 (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 87% for the well-defined parts and 80% 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	1608
Number of shifts mapped to atoms	1603
Number of unparsed shifts	0
Number of shifts with mapping errors	5
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	2

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

- No matching atom found in the structure. All 5 occurrences are reported below.

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	527	HIS	HA	4.662	0.000	1
1	A	527	HIS	HB2	3.112	0.000	2
1	A	527	HIS	HB3	2.994	0.000	2
1	A	527	HIS	CA	55.803	0.000	1
1	A	527	HIS	CB	30.851	0.000	1

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	138	0.03 ± 0.07	None needed (< 0.5 ppm)
$^{13}C_{\beta}$	124	-0.08 ± 0.09	None needed (< 0.5 ppm)
$^{13}C'$	116	0.04 ± 0.13	None needed (< 0.5 ppm)

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Nucleus	# values	Correction ± precision, *ppm*	Suggested action
^{15}N	131	0.05 ± 0.26	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 87%, i.e. 1245 atoms were assigned a chemical shift out of a possible 1427. 0 out of 17 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	509/529 (96%)	216/218 (99%)	193/210 (92%)	100/101 (99%)
Sidechain	668/793 (84%)	452/516 (88%)	214/252 (85%)	2/25 (8%)
Aromatic	68/105 (65%)	34/53 (64%)	33/49 (67%)	1/3 (33%)
Overall	1245/1427 (87%)	702/787 (89%)	440/511 (86%)	103/129 (80%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 80%, i.e. 1603 atoms were assigned a chemical shift out of a possible 2010. 0 out of 21 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	663/745 (89%)	279/305 (91%)	253/296 (85%)	131/144 (91%)
Sidechain	864/1125 (77%)	581/724 (80%)	280/363 (77%)	3/38 (8%)
Aromatic	76/140 (54%)	38/70 (54%)	37/66 (56%)	1/4 (25%)
Overall	1603/2010 (80%)	898/1099 (82%)	570/725 (79%)	135/186 (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.

List Id	Chain	Res	Type	Atom	Shift, *ppm*	Expected range, *ppm*	Z-score
1	A	662	VAL	HB	-0.07	0.43 – 3.54	-6.6
1	A	554	ARG	HG3	0.10	0.15 – 2.94	-5.2

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.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: