



Full wwPDB NMR Structure Validation Report ⓘ

Feb 13, 2017 – 12:15 am GMT

PDB ID : 2LNX
Title : Solution structure of Vav2 SH2 domain
Authors : Wu, B.; Zhang, J.; Wu, J.; Shi, Y.
Deposited on : 2012-01-05

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

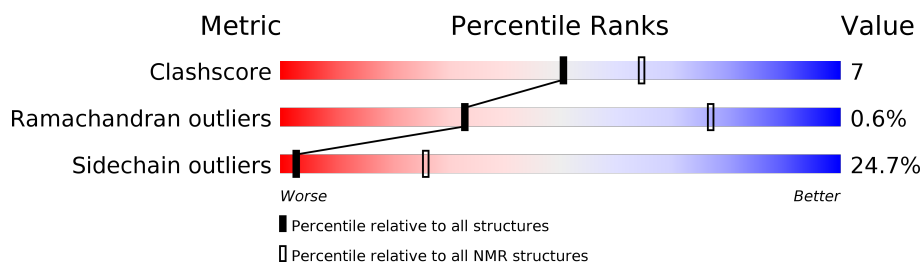
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 85%.

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	122	

2 Ensemble composition and analysis

This entry contains 20 models. Model 19 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:667-A:699, A:706-A:767 (95)	0.42	19

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. No single-model clusters were found.

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

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 1887 atoms, of which 935 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Guanine nucleotide exchange factor VAV2.

Mol	Chain	Residues	Atoms						Trace
1	A	113	Total	C	H	N	O	S	0
			1887	607	935	163	180	2	

There are 9 discrepancies between the modelled and reference sequences:

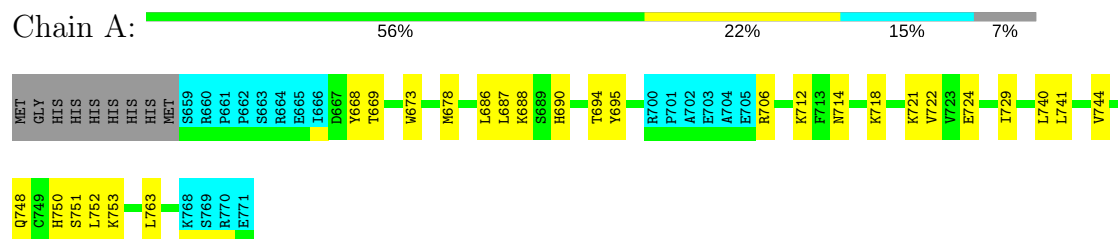
Chain	Residue	Modelled	Actual	Comment	Reference
A	650	MET	-	EXPRESSION TAG	UNP P52735
A	651	GLY	-	EXPRESSION TAG	UNP P52735
A	652	HIS	-	EXPRESSION TAG	UNP P52735
A	653	HIS	-	EXPRESSION TAG	UNP P52735
A	654	HIS	-	EXPRESSION TAG	UNP P52735
A	655	HIS	-	EXPRESSION TAG	UNP P52735
A	656	HIS	-	EXPRESSION TAG	UNP P52735
A	657	HIS	-	EXPRESSION TAG	UNP P52735
A	658	MET	-	EXPRESSION TAG	UNP P52735

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: Guanine nucleotide exchange factor VAV2

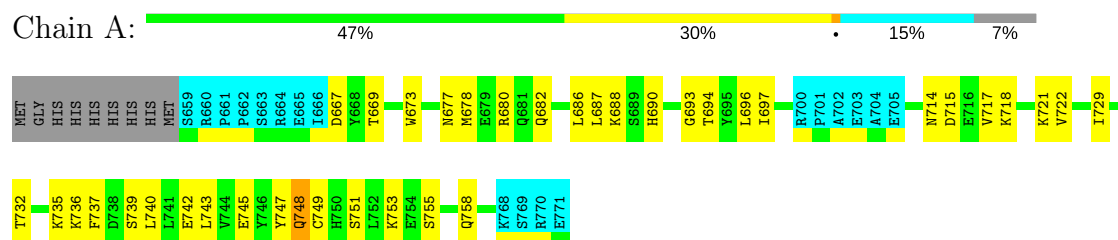


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

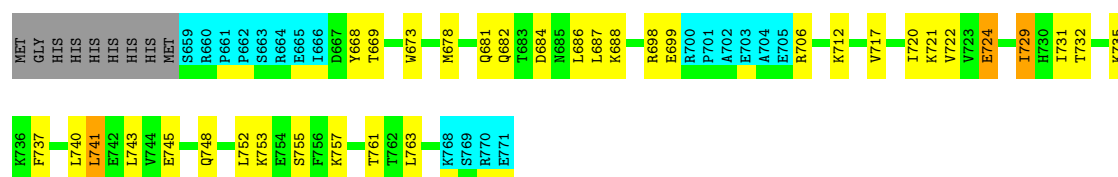
- Molecule 1: Guanine nucleotide exchange factor VAV2



4.2.2 Score per residue for model 2

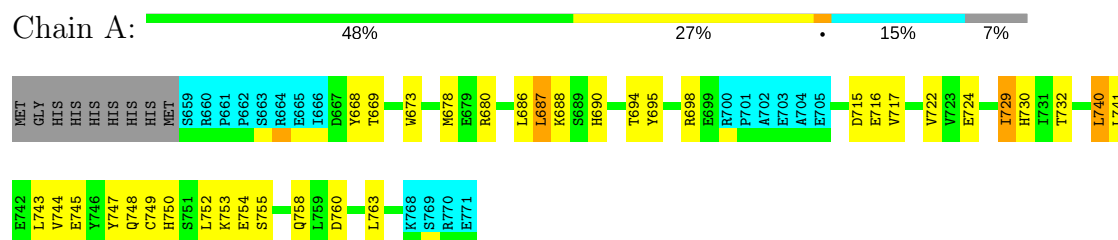
- Molecule 1: Guanine nucleotide exchange factor VAV2





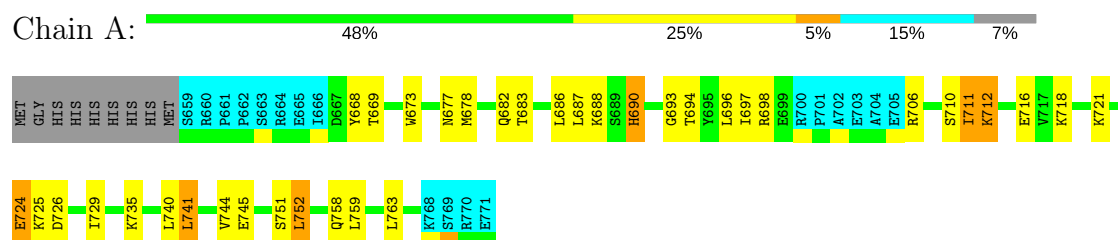
4.2.3 Score per residue for model 3

- Molecule 1: Guanine nucleotide exchange factor VAV2



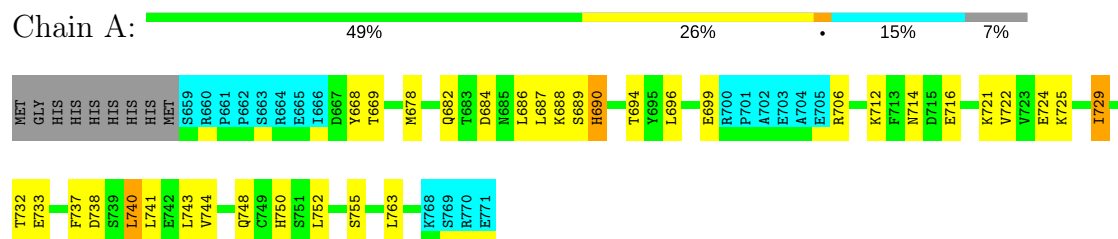
4.2.4 Score per residue for model 4

- Molecule 1: Guanine nucleotide exchange factor VAV2



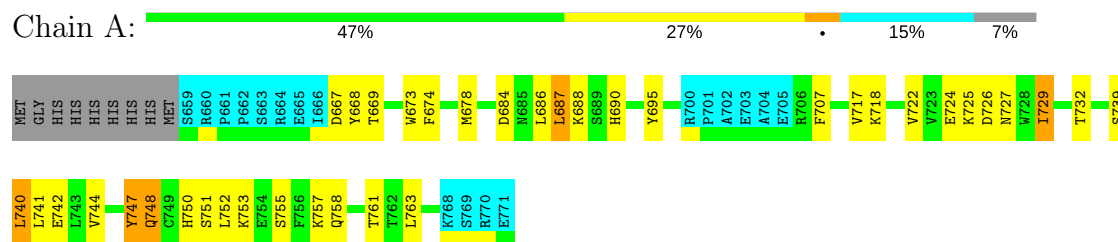
4.2.5 Score per residue for model 5

- Molecule 1: Guanine nucleotide exchange factor VAV2



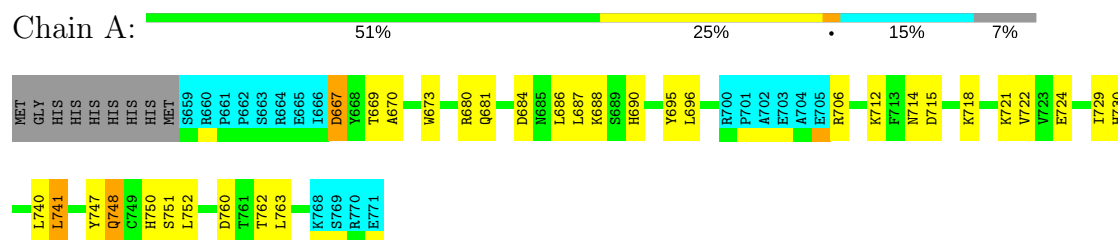
4.2.6 Score per residue for model 6

- Molecule 1: Guanine nucleotide exchange factor VAV2



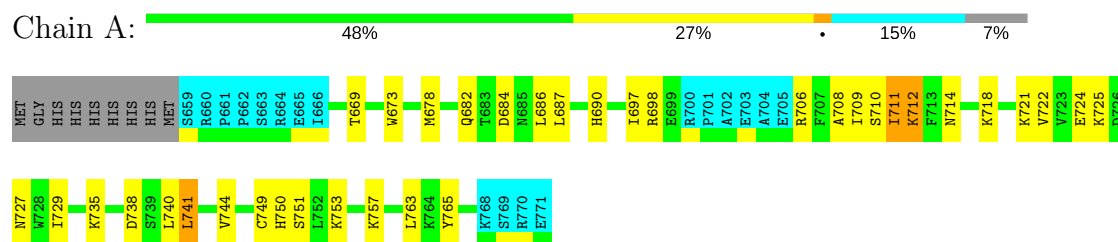
4.2.7 Score per residue for model 7

- Molecule 1: Guanine nucleotide exchange factor VAV2



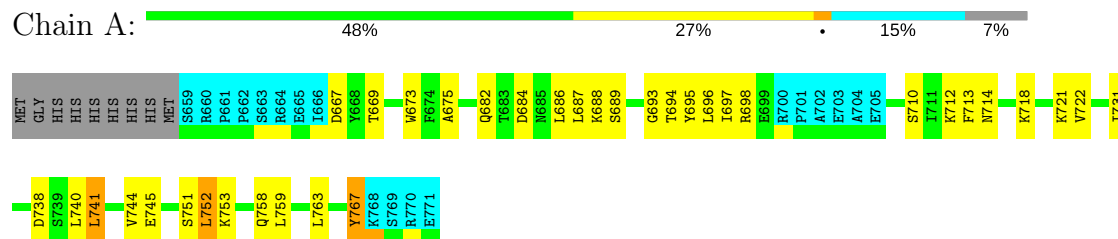
4.2.8 Score per residue for model 8

- Molecule 1: Guanine nucleotide exchange factor VAV2



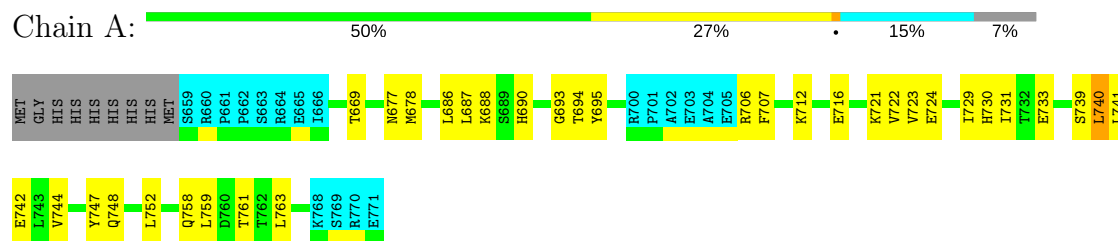
4.2.9 Score per residue for model 9

- Molecule 1: Guanine nucleotide exchange factor VAV2



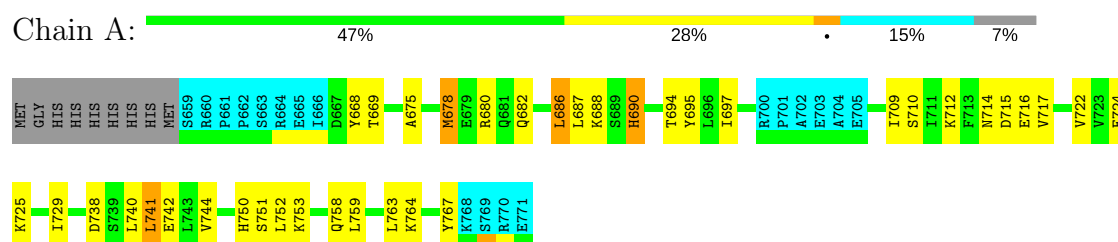
4.2.10 Score per residue for model 10

- Molecule 1: Guanine nucleotide exchange factor VAV2



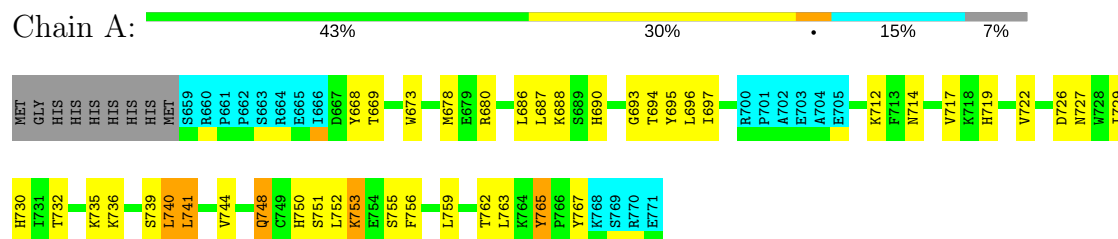
4.2.11 Score per residue for model 11

- Molecule 1: Guanine nucleotide exchange factor VAV2



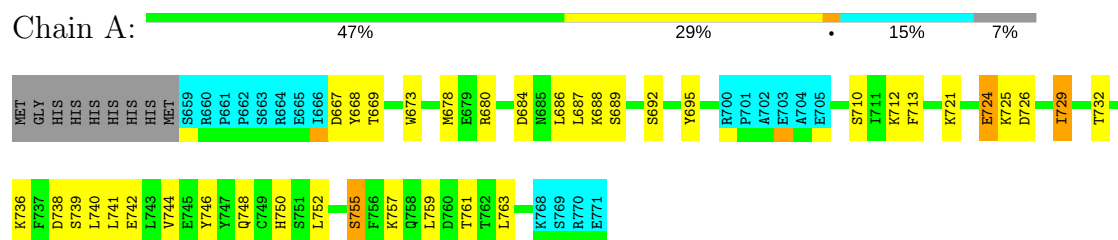
4.2.12 Score per residue for model 12

- Molecule 1: Guanine nucleotide exchange factor VAV2



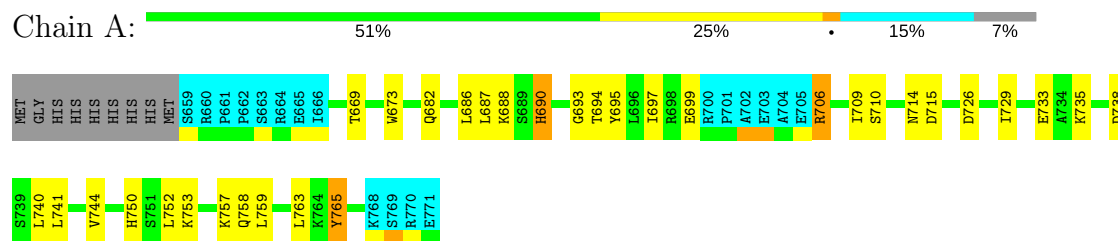
4.2.13 Score per residue for model 13

- Molecule 1: Guanine nucleotide exchange factor VAV2



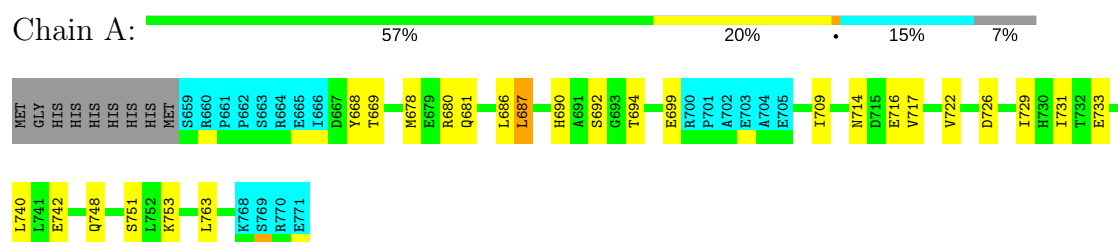
4.2.14 Score per residue for model 14

- Molecule 1: Guanine nucleotide exchange factor VAV2



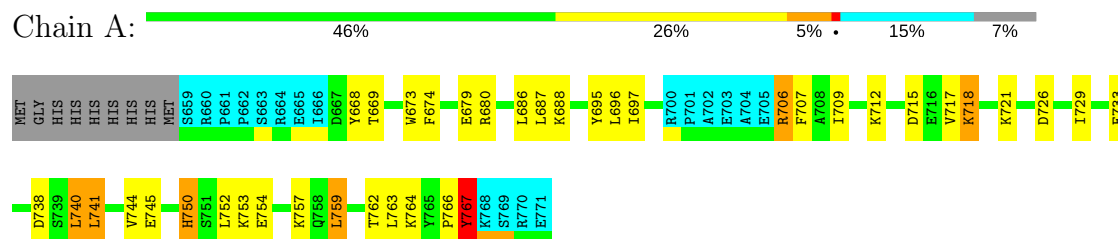
4.2.15 Score per residue for model 15

- Molecule 1: Guanine nucleotide exchange factor VAV2



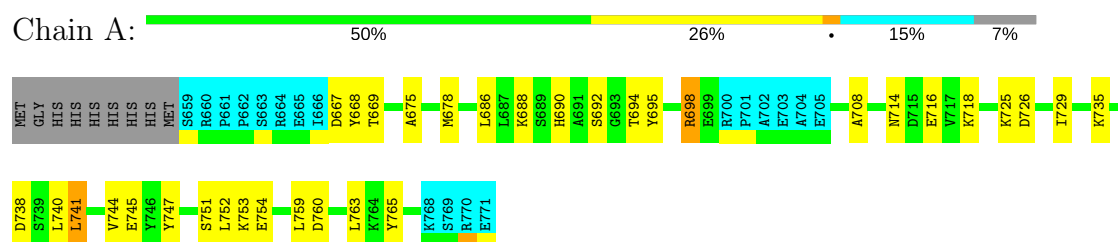
4.2.16 Score per residue for model 16

- Molecule 1: Guanine nucleotide exchange factor VAV2



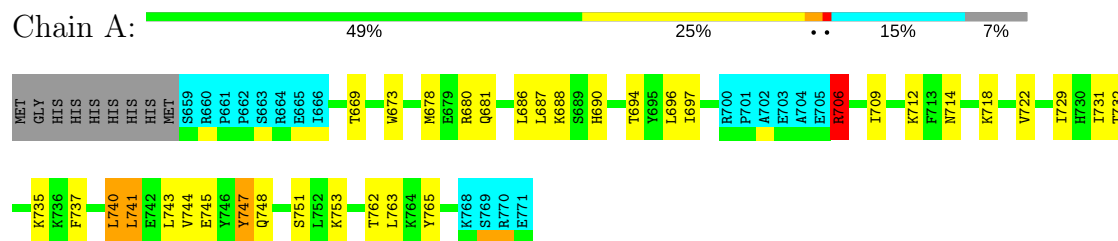
4.2.17 Score per residue for model 17

- Molecule 1: Guanine nucleotide exchange factor VAV2



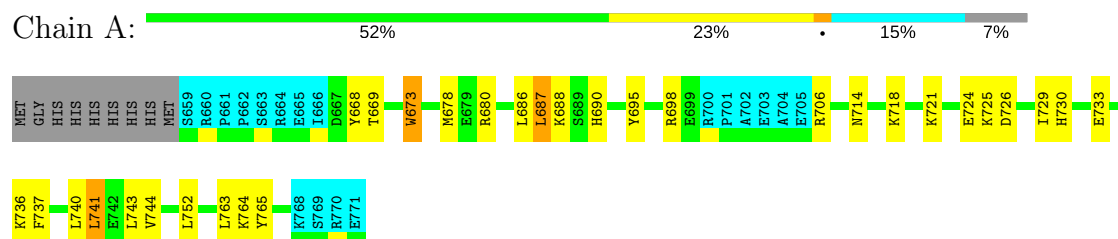
4.2.18 Score per residue for model 18

- Molecule 1: Guanine nucleotide exchange factor VAV2



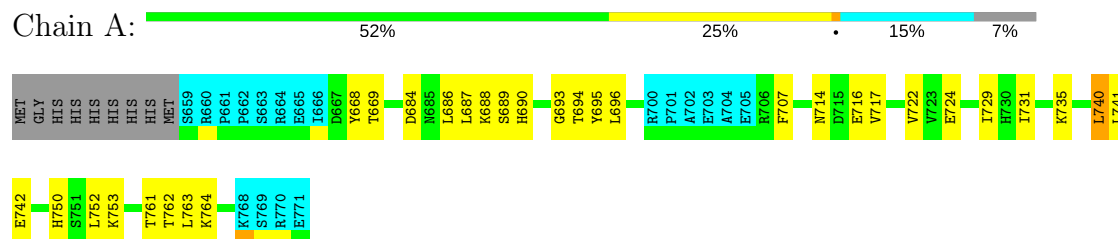
4.2.19 Score per residue for model 19 (medoid)

- Molecule 1: Guanine nucleotide exchange factor VAV2



4.2.20 Score per residue for model 20

- Molecule 1: Guanine nucleotide exchange factor VAV2



5 Refinement protocol and experimental data overview

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

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

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

Software name	Classification	Version
CNS	structure solution	
CNS	refinement	

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)	2lnx_cs.str
Number of chemical shift lists	1
Total number of shifts	1368
Number of shifts mapped to atoms	1368
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	85%

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

6 Model quality

6.1 Standard geometry

There are no covalent bond-length or bond-angle outliers.

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	805	789	785	11±3
All	All	16100	15780	15700	215

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 7.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:722:VAL:HG12	1:A:729:ILE:HD11	0.75	1.57	3	8
1:A:673:TRP:CE3	1:A:697:ILE:HD13	0.75	2.16	9	6
1:A:724:GLU:HB2	1:A:729:ILE:HD12	0.68	1.63	13	5
1:A:748:GLN:HA	1:A:763:LEU:HD13	0.68	1.65	7	1
1:A:732:THR:HG21	1:A:755:SER:HB2	0.67	1.67	2	2
1:A:748:GLN:CG	1:A:763:LEU:HD22	0.67	2.20	6	2
1:A:748:GLN:HG2	1:A:763:LEU:HD22	0.66	1.66	6	3
1:A:748:GLN:HG3	1:A:763:LEU:HD12	0.65	1.68	15	1
1:A:750:HIS:O	1:A:762:THR:HG22	0.65	1.92	7	3
1:A:687:LEU:HD12	1:A:712:LYS:HB2	0.64	1.68	18	1
1:A:675:ALA:HB1	1:A:678:MET:CE	0.63	2.24	17	1
1:A:697:ILE:CD1	1:A:709:ILE:HG23	0.63	2.24	11	2
1:A:732:THR:HG21	1:A:755:SER:OG	0.62	1.94	1	5
1:A:675:ALA:HB1	1:A:678:MET:SD	0.62	2.35	11	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:667:ASP:HB3	1:A:670:ALA:HB3	0.62	1.70	7	1
1:A:697:ILE:HD13	1:A:709:ILE:HG23	0.61	1.73	11	2
1:A:740:LEU:O	1:A:744:VAL:HG23	0.61	1.96	18	10
1:A:722:VAL:HG22	1:A:731:ILE:HG22	0.61	1.73	18	4
1:A:752:LEU:HD11	1:A:759:LEU:HD23	0.60	1.71	10	3
1:A:687:LEU:HD22	1:A:712:LYS:HB2	0.60	1.71	12	4
1:A:748:GLN:CG	1:A:763:LEU:HD12	0.59	2.28	15	2
1:A:690:HIS:CD2	1:A:694:THR:HG21	0.58	2.32	12	6
1:A:737:PHE:CD1	1:A:743:LEU:HD12	0.58	2.34	18	3
1:A:687:LEU:HD12	1:A:717:VAL:HG13	0.58	1.75	1	3
1:A:695:TYR:CD2	1:A:763:LEU:HD23	0.57	2.34	14	2
1:A:695:TYR:CG	1:A:763:LEU:HD22	0.57	2.34	3	4
1:A:697:ILE:HG13	1:A:709:ILE:HG23	0.56	1.77	14	3
1:A:695:TYR:CE1	1:A:763:LEU:HD23	0.56	2.35	6	1
1:A:695:TYR:CE2	1:A:763:LEU:HD23	0.56	2.36	20	4
1:A:696:LEU:HD22	1:A:767:TYR:CE1	0.55	2.37	16	1
1:A:748:GLN:CB	1:A:763:LEU:HD13	0.55	2.32	18	1
1:A:709:ILE:HD12	1:A:731:ILE:HG21	0.55	1.77	15	1
1:A:687:LEU:HD23	1:A:712:LYS:HB2	0.55	1.78	13	2
1:A:697:ILE:HD12	1:A:709:ILE:HG12	0.55	1.79	11	2
1:A:748:GLN:HG2	1:A:763:LEU:HD12	0.54	1.78	5	2
1:A:752:LEU:HD23	1:A:761:THR:O	0.53	2.03	10	2
1:A:673:TRP:CZ3	1:A:744:VAL:HG11	0.53	2.38	4	1
1:A:722:VAL:CG1	1:A:729:ILE:HD11	0.53	2.33	6	5
1:A:707:PHE:CD2	1:A:740:LEU:HD11	0.53	2.39	20	1
1:A:687:LEU:HD13	1:A:717:VAL:HG13	0.53	1.81	3	3
1:A:675:ALA:HB2	1:A:767:TYR:OH	0.51	2.06	9	1
1:A:722:VAL:HG22	1:A:731:ILE:CG2	0.50	2.36	20	3
1:A:744:VAL:HG13	1:A:763:LEU:CD1	0.50	2.35	16	2
1:A:687:LEU:HD23	1:A:690:HIS:CD2	0.49	2.42	15	3
1:A:722:VAL:HA	1:A:731:ILE:HG22	0.49	1.82	10	1
1:A:690:HIS:HD2	1:A:694:THR:HG21	0.49	1.67	12	1
1:A:748:GLN:CB	1:A:763:LEU:HD12	0.49	2.37	3	1
1:A:673:TRP:CE3	1:A:744:VAL:HG11	0.49	2.42	19	1
1:A:687:LEU:HD11	1:A:696:LEU:HD23	0.49	1.84	4	2
1:A:748:GLN:HB3	1:A:763:LEU:HD12	0.49	1.85	3	1
1:A:751:SER:HA	1:A:762:THR:HG22	0.48	1.85	18	1
1:A:690:HIS:CG	1:A:694:THR:HG21	0.48	2.43	10	2
1:A:744:VAL:CG1	1:A:763:LEU:HD21	0.48	2.39	13	1
1:A:687:LEU:HD21	1:A:696:LEU:HD23	0.48	1.85	1	1
1:A:687:LEU:HD13	1:A:690:HIS:CB	0.48	2.39	18	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:695:TYR:CB	1:A:763:LEU:HD22	0.48	2.39	16	1
1:A:751:SER:N	1:A:762:THR:HG22	0.48	2.23	12	1
1:A:695:TYR:CE1	1:A:763:LEU:HB3	0.47	2.45	12	2
1:A:687:LEU:HD11	1:A:696:LEU:HD21	0.47	1.86	5	1
1:A:694:THR:HA	1:A:765:TYR:O	0.47	2.10	12	3
1:A:684:ASP:HA	1:A:717:VAL:HG21	0.47	1.86	20	1
1:A:718:LYS:HE3	1:A:759:LEU:HD13	0.47	1.86	17	1
1:A:752:LEU:CD2	1:A:759:LEU:HD23	0.47	2.39	11	1
1:A:752:LEU:HD12	1:A:761:THR:O	0.47	2.10	13	2
1:A:711:ILE:HD13	1:A:712:LYS:N	0.47	2.25	8	2
1:A:687:LEU:HD22	1:A:694:THR:HB	0.47	1.85	15	3
1:A:696:LEU:HD12	1:A:697:ILE:N	0.47	2.25	4	1
1:A:744:VAL:HG13	1:A:763:LEU:CD2	0.46	2.40	14	1
1:A:673:TRP:CZ3	1:A:744:VAL:CG1	0.46	2.98	4	1
1:A:673:TRP:CH2	1:A:744:VAL:HG21	0.46	2.45	8	1
1:A:752:LEU:HD13	1:A:761:THR:O	0.46	2.11	20	1
1:A:687:LEU:HD11	1:A:694:THR:CG2	0.46	2.40	18	1
1:A:722:VAL:HG12	1:A:729:ILE:CD1	0.46	2.41	8	2
1:A:698:ARG:HG3	1:A:708:ALA:HB3	0.45	1.88	8	2
1:A:711:ILE:HD13	1:A:712:LYS:H	0.45	1.72	4	2
1:A:696:LEU:HD22	1:A:767:TYR:CZ	0.45	2.47	12	1
1:A:696:LEU:HB2	1:A:767:TYR:CE2	0.44	2.46	9	1
1:A:750:HIS:C	1:A:762:THR:HG22	0.44	2.33	12	1
1:A:747:TYR:CZ	1:A:763:LEU:HD11	0.44	2.48	6	1
1:A:687:LEU:HD12	1:A:717:VAL:CG1	0.44	2.42	1	1
1:A:695:TYR:CD2	1:A:763:LEU:HD22	0.44	2.47	3	1
1:A:763:LEU:N	1:A:763:LEU:HD12	0.44	2.27	14	1
1:A:737:PHE:CD1	1:A:743:LEU:HA	0.44	2.48	2	1
1:A:673:TRP:HE3	1:A:697:ILE:HD13	0.44	1.73	12	1
1:A:744:VAL:HG13	1:A:763:LEU:HD22	0.44	1.89	17	1
1:A:741:LEU:C	1:A:741:LEU:HD12	0.43	2.33	7	6
1:A:722:VAL:HG12	1:A:729:ILE:CG1	0.43	2.43	8	1
1:A:737:PHE:CD1	1:A:743:LEU:HG	0.43	2.48	1	1
1:A:741:LEU:HD12	1:A:741:LEU:C	0.43	2.34	17	4
1:A:747:TYR:CD1	1:A:752:LEU:HD23	0.43	2.48	17	1
1:A:717:VAL:HG12	1:A:719:HIS:CE1	0.43	2.49	12	1
1:A:763:LEU:HD22	1:A:763:LEU:N	0.43	2.28	4	1
1:A:687:LEU:HD22	1:A:712:LYS:CB	0.42	2.42	12	1
1:A:669:THR:HG22	1:A:674:PHE:CE2	0.42	2.49	16	1
1:A:687:LEU:CD1	1:A:717:VAL:HG13	0.42	2.45	2	1
1:A:709:ILE:HD12	1:A:731:ILE:CG2	0.42	2.44	15	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:696:LEU:CB	1:A:767:TYR:CE2	0.42	3.02	9	1
1:A:687:LEU:HD12	1:A:717:VAL:CG2	0.42	2.45	15	1
1:A:687:LEU:HG	1:A:696:LEU:HD21	0.42	1.91	12	1
1:A:731:ILE:HG13	1:A:732:THR:HG22	0.42	1.90	18	1
1:A:745:GLU:HA	1:A:748:GLN:HG2	0.41	1.91	1	1
1:A:673:TRP:HB3	1:A:695:TYR:CE2	0.41	2.50	14	1
1:A:707:PHE:CD2	1:A:740:LEU:HD13	0.41	2.50	6	1
1:A:720:ILE:HG21	1:A:731:ILE:HD12	0.41	1.93	2	1
1:A:752:LEU:HD12	1:A:759:LEU:CD2	0.41	2.46	16	1
1:A:763:LEU:N	1:A:763:LEU:HD22	0.41	2.31	8	1
1:A:753:LYS:HA	1:A:756:PHE:O	0.41	2.16	12	1
1:A:687:LEU:HD22	1:A:694:THR:CG2	0.41	2.46	20	1
1:A:695:TYR:CG	1:A:763:LEU:HD23	0.41	2.51	11	1
1:A:744:VAL:HA	1:A:747:TYR:CE1	0.41	2.51	18	1
1:A:751:SER:CA	1:A:762:THR:HG22	0.41	2.45	18	1
1:A:729:ILE:HG23	1:A:743:LEU:HD23	0.40	1.93	3	1
1:A:718:LYS:NZ	1:A:759:LEU:HD11	0.40	2.31	16	1
1:A:687:LEU:HD21	1:A:694:THR:HG22	0.40	1.93	9	1
1:A:686:LEU:HD12	1:A:767:TYR:HB2	0.40	1.93	11	1
1:A:752:LEU:HD22	1:A:759:LEU:HD23	0.40	1.92	4	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	95/122 (78%)	87±1 (92±2%)	7±1 (7±1%)	1±1 (1±1%)	33	77
All	All	1900/2440 (78%)	1748 (92%)	140 (7%)	12 (1%)	33	77

All 4 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	693	GLY	7
1	A	767	TYR	2

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Mol	Chain	Res	Type	Models (Total)
1	A	706	ARG	2
1	A	673	TRP	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	88/112 (79%)	66±4 (75±4%)	22±4 (25±4%)	3	26
All	All	1760/2240 (79%)	1326 (75%)	434 (25%)	3	26

All 64 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	686	LEU	20
1	A	669	THR	19
1	A	688	LYS	18
1	A	740	LEU	17
1	A	741	LEU	16
1	A	753	LYS	14
1	A	678	MET	14
1	A	714	ASN	13
1	A	729	ILE	11
1	A	721	LYS	11
1	A	680	ARG	10
1	A	690	HIS	9
1	A	706	ARG	9
1	A	751	SER	9
1	A	726	ASP	9
1	A	724	GLU	9
1	A	718	LYS	9
1	A	735	LYS	9
1	A	725	LYS	8
1	A	758	GLN	8
1	A	682	GLN	8
1	A	738	ASP	8
1	A	716	GLU	8

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Mol	Chain	Res	Type	Models (Total)
1	A	750	HIS	8
1	A	742	GLU	7
1	A	745	GLU	7
1	A	752	LEU	7
1	A	684	ASP	7
1	A	698	ARG	6
1	A	667	ASP	6
1	A	710	SER	6
1	A	715	ASP	6
1	A	747	TYR	6
1	A	733	GLU	6
1	A	757	LYS	6
1	A	765	TYR	5
1	A	673	TRP	5
1	A	748	GLN	5
1	A	712	LYS	5
1	A	739	SER	5
1	A	730	HIS	5
1	A	687	LEU	5
1	A	764	LYS	4
1	A	681	GLN	4
1	A	689	SER	4
1	A	736	LYS	4
1	A	699	GLU	4
1	A	692	SER	3
1	A	749	CYS	3
1	A	759	LEU	3
1	A	754	GLU	3
1	A	727	ASN	3
1	A	677	ASN	3
1	A	760	ASP	3
1	A	713	PHE	2
1	A	696	LEU	2
1	A	711	ILE	2
1	A	707	PHE	2
1	A	683	THR	1
1	A	679	GLU	1
1	A	674	PHE	1
1	A	767	TYR	1
1	A	755	SER	1
1	A	746	TYR	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](#)

There are no ligands in this entry.

6.7 Other polymers [i](#)

There are no such molecules in this entry.

6.8 Polymer linkage issues [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 85% for the well-defined parts and 83% for the entire structure.

7.1 Chemical shift list 1

File name: 2lnx_cs.str

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	1368
Number of shifts mapped to atoms	1368
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	105	-0.24 ± 0.18	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	103	0.23 ± 0.15	None needed (< 0.5 ppm)
$^{13}\text{C}'$	107	0.43 ± 0.11	None needed (< 0.5 ppm)
^{15}N	106	0.17 ± 0.49	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 85%, i.e. 1069 atoms were assigned a chemical shift out of a possible 1254. 0 out of 13 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	464/471 (99%)	187/188 (99%)	185/190 (97%)	92/93 (99%)
Sidechain	540/626 (86%)	346/368 (94%)	185/231 (80%)	9/27 (33%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	65/157 (41%)	64/81 (79%)	0/66 (0%)	1/10 (10%)
Overall	1069/1254 (85%)	597/637 (94%)	370/487 (76%)	102/130 (78%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 83%, i.e. 1246 atoms were assigned a chemical shift out of a possible 1500. 0 out of 13 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	537/555 (97%)	219/221 (99%)	212/226 (94%)	106/108 (98%)
Sidechain	644/788 (82%)	422/467 (90%)	213/281 (76%)	9/40 (22%)
Aromatic	65/157 (41%)	64/81 (79%)	0/66 (0%)	1/10 (10%)
Overall	1246/1500 (83%)	705/769 (92%)	425/573 (74%)	116/158 (73%)

7.1.4 Statistically unusual chemical shifts [i](#)

There are no statistically unusual chemical shifts.

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

The image below reports *random coil index* values for the protein chains in the structure. The height of each bar gives a probability of a given residue to be disordered, as predicted from the available chemical shifts and the amino acid sequence. A value above 0.2 is an indication of significant predicted disorder. The colour of the bar shows whether the residue is in the well-defined core (black) or in the ill-defined residue ranges (cyan), as described in section 2 on ensemble composition.

Random coil index (RCI) for chain A:

