



Full wwPDB NMR Structure Validation Report ⓘ

Jan 28, 2018 – 07:45 PM EST

PDB ID : 6EVI
Title : solution NMR structure of EB1 C terminus (191-260)
Authors : Barsukov, I.L.; Almeida, T.B.
Deposited on : 2017-11-01

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 : rb-20030736
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20030736

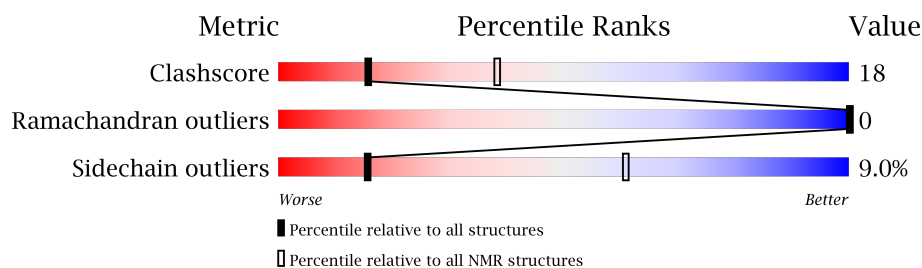
1 Overall quality at a glance

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	70	
1	B	70	

2 Ensemble composition and analysis

This entry contains 20 models. Model 6 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *closest to the average*.

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:192-A:248, B:192-B:248 (114)	0.26	6

Ill-defined regions of proteins are excluded from the global statistics.

Ligands and non-protein polymers are included in the analysis.

The models can be grouped into 3 clusters and 4 single-model clusters were found.

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

3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 2232 atoms, of which 1102 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Microtubule-associated protein RP/EB family member 1.

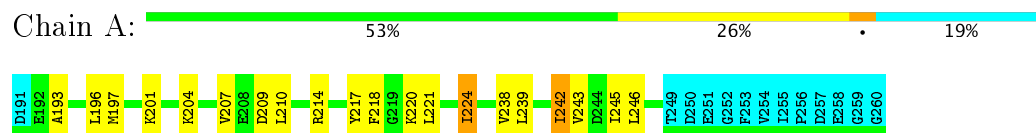
Mol	Chain	Residues	Atoms						Trace
1	A	70	Total	C	H	N	O	S	0
			1116	355	551	90	118	2	
1	B	70	Total	C	H	N	O	S	0
			1116	355	551	90	118	2	

4 Residue-property plots

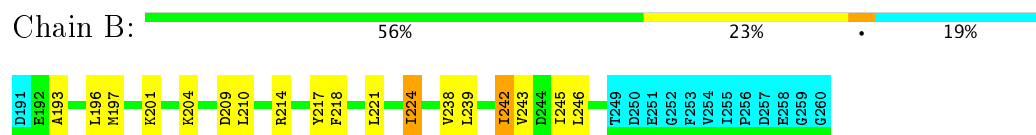
4.1 Average score per residue in the NMR ensemble

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: Microtubule-associated protein RP/EB family member 1



- Molecule 1: Microtubule-associated protein RP/EB family member 1

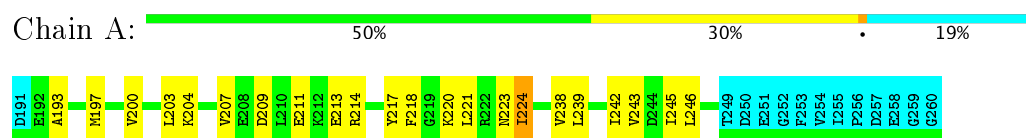


4.2 Scores per residue for each member of the ensemble

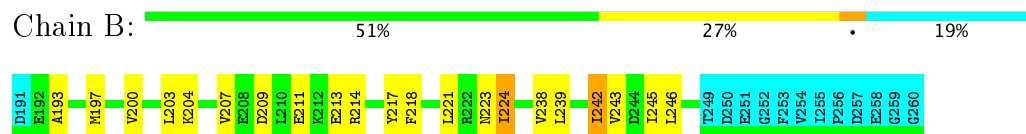
Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

- Molecule 1: Microtubule-associated protein RP/EB family member 1

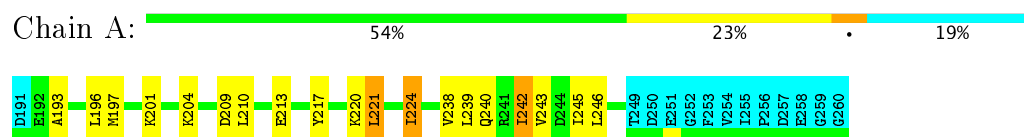


- Molecule 1: Microtubule-associated protein RP/EB family member 1

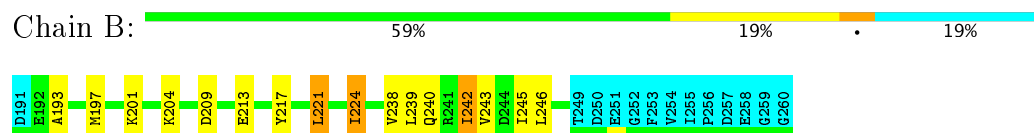


4.2.2 Score per residue for model 2

- Molecule 1: Microtubule-associated protein RP/EB family member 1

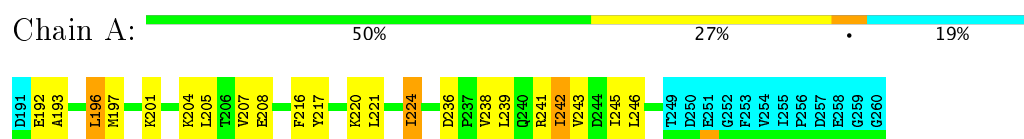


- Molecule 1: Microtubule-associated protein RP/EB family member 1

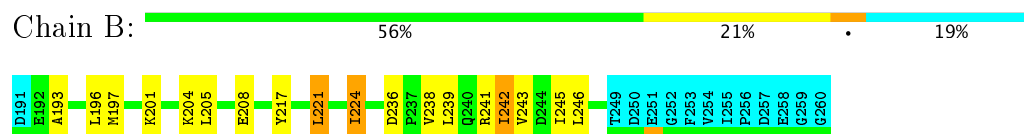


4.2.3 Score per residue for model 3

- Molecule 1: Microtubule-associated protein RP/EB family member 1

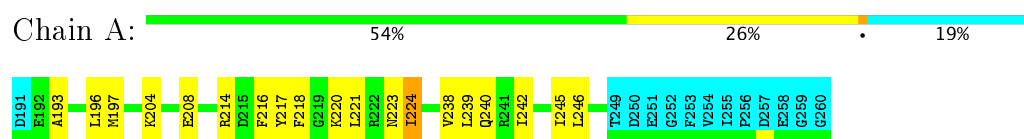


- Molecule 1: Microtubule-associated protein RP/EB family member 1

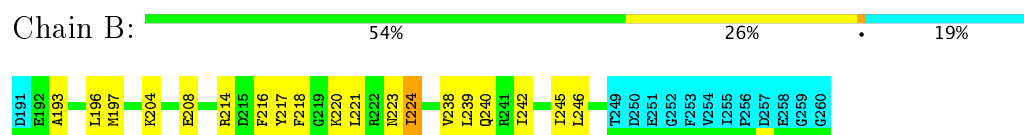


4.2.4 Score per residue for model 4

- Molecule 1: Microtubule-associated protein RP/EB family member 1

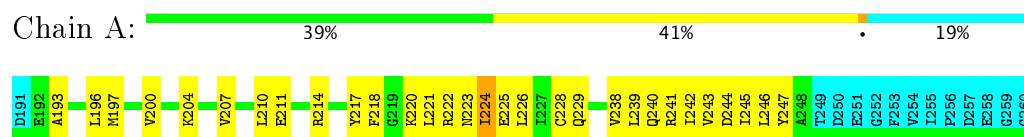


- Molecule 1: Microtubule-associated protein RP/EB family member 1

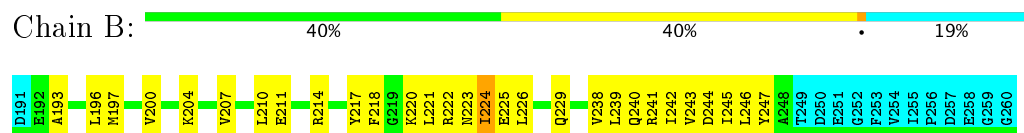


4.2.5 Score per residue for model 5

- Molecule 1: Microtubule-associated protein RP/EB family member 1

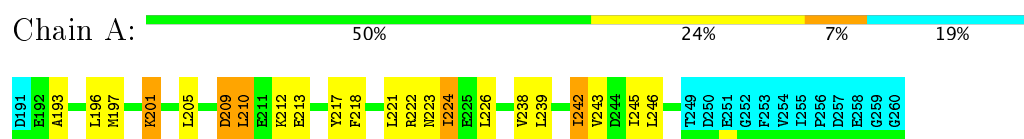


- Molecule 1: Microtubule-associated protein RP/EB family member 1

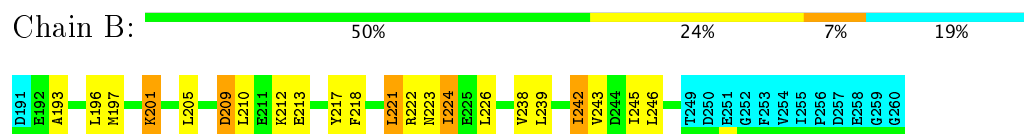


4.2.6 Score per residue for model 6 (medoid)

- Molecule 1: Microtubule-associated protein RP/EB family member 1

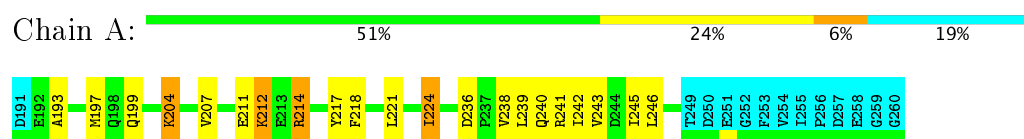


- Molecule 1: Microtubule-associated protein RP/EB family member 1

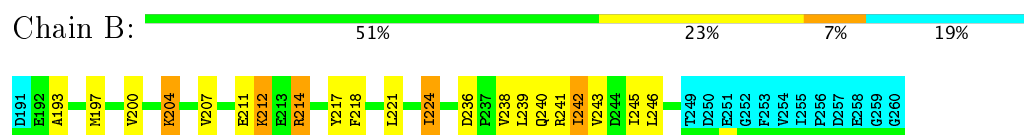


4.2.7 Score per residue for model 7

- Molecule 1: Microtubule-associated protein RP/EB family member 1

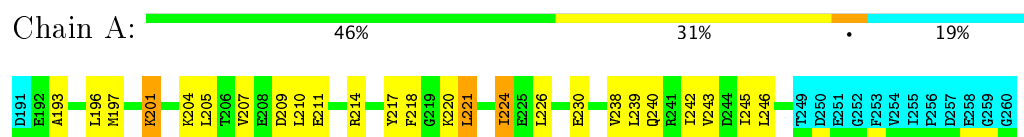


- Molecule 1: Microtubule-associated protein RP/EB family member 1

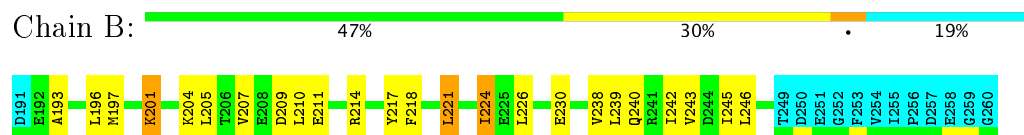


4.2.8 Score per residue for model 8

- Molecule 1: Microtubule-associated protein RP/EB family member 1

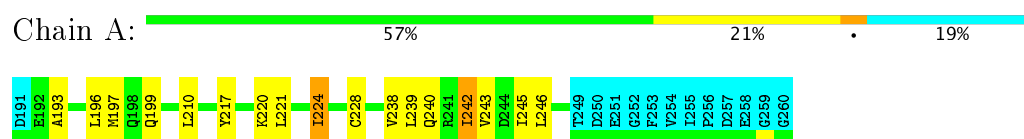


- Molecule 1: Microtubule-associated protein RP/EB family member 1

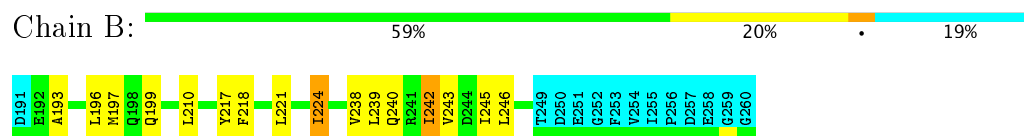


4.2.9 Score per residue for model 9

- Molecule 1: Microtubule-associated protein RP/EB family member 1

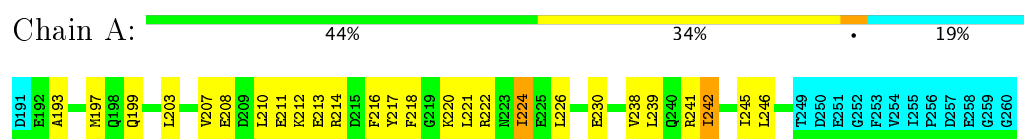


- Molecule 1: Microtubule-associated protein RP/EB family member 1

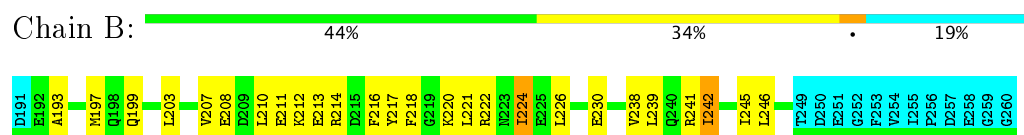


4.2.10 Score per residue for model 10

- Molecule 1: Microtubule-associated protein RP/EB family member 1

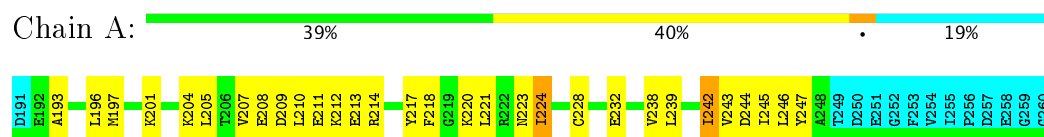


- Molecule 1: Microtubule-associated protein RP/EB family member 1

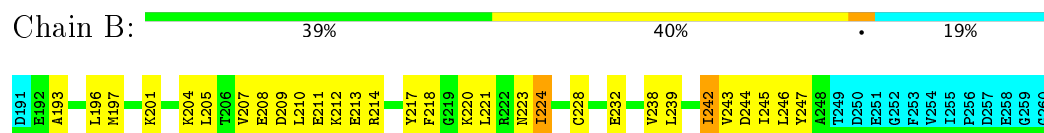


4.2.11 Score per residue for model 11

- Molecule 1: Microtubule-associated protein RP/EB family member 1

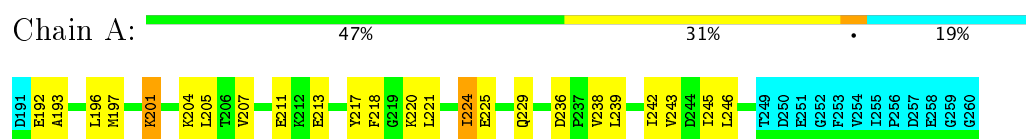


- Molecule 1: Microtubule-associated protein RP/EB family member 1

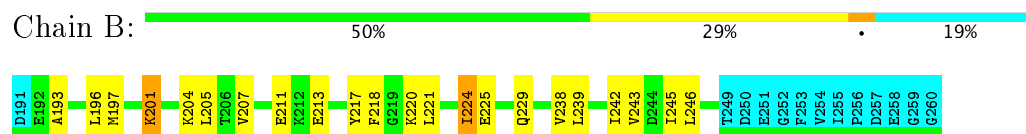


4.2.12 Score per residue for model 12

- Molecule 1: Microtubule-associated protein RP/EB family member 1

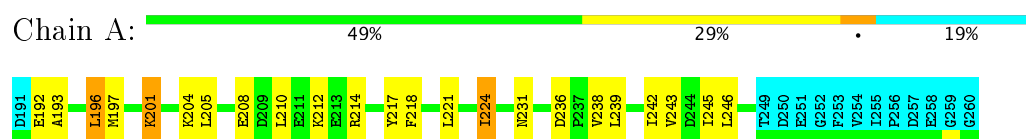


- Molecule 1: Microtubule-associated protein RP/EB family member 1

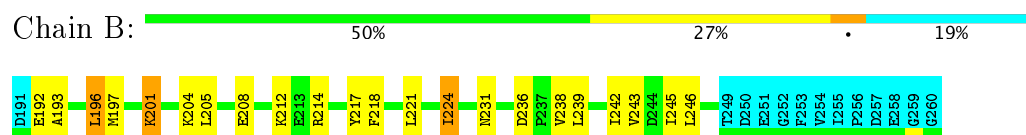


4.2.13 Score per residue for model 13

- Molecule 1: Microtubule-associated protein RP/EB family member 1

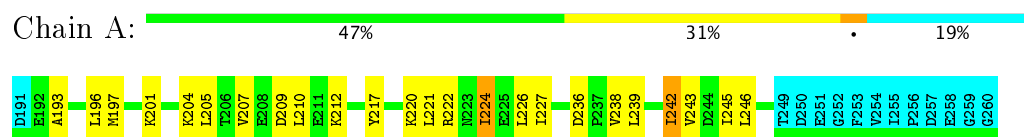


- Molecule 1: Microtubule-associated protein RP/EB family member 1

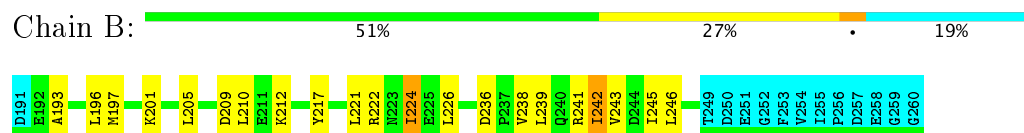


4.2.14 Score per residue for model 14

- Molecule 1: Microtubule-associated protein RP/EB family member 1

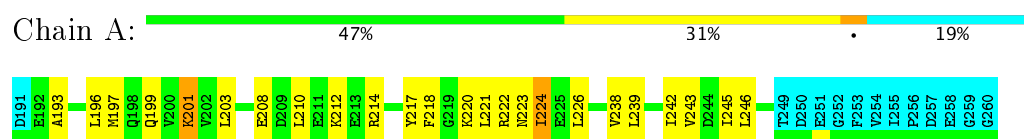


- Molecule 1: Microtubule-associated protein RP/EB family member 1

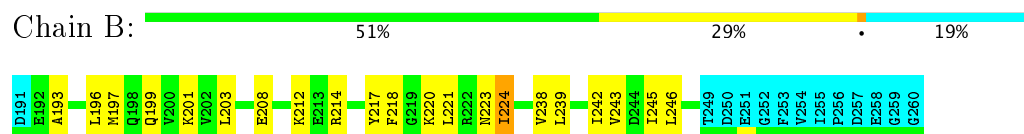


4.2.15 Score per residue for model 15

- Molecule 1: Microtubule-associated protein RP/EB family member 1

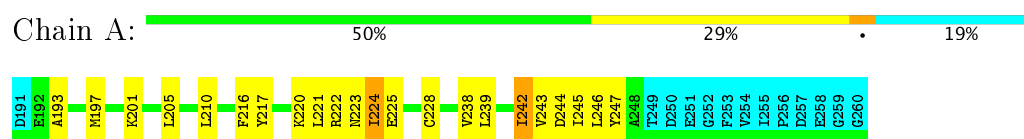


- Molecule 1: Microtubule-associated protein RP/EB family member 1

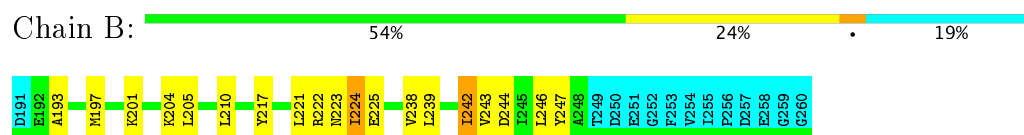


4.2.16 Score per residue for model 16

- Molecule 1: Microtubule-associated protein RP/EB family member 1

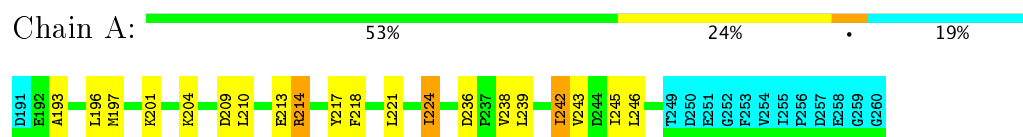


- Molecule 1: Microtubule-associated protein RP/EB family member 1

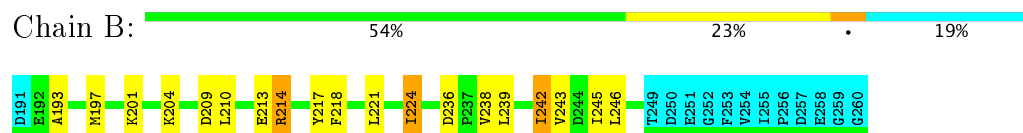


4.2.17 Score per residue for model 17

- Molecule 1: Microtubule-associated protein RP/EB family member 1

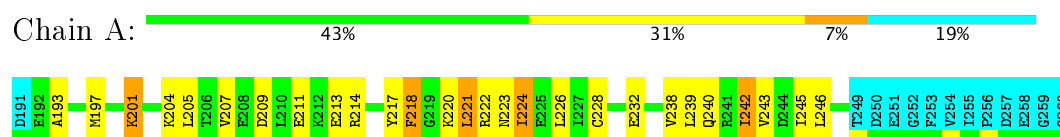


- Molecule 1: Microtubule-associated protein RP/EB family member 1

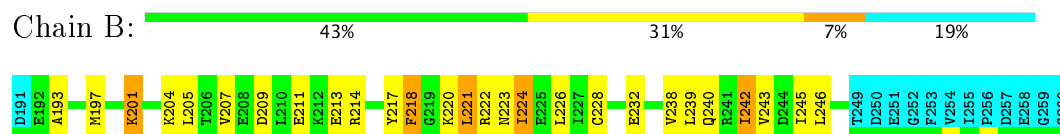


4.2.18 Score per residue for model 18

- Molecule 1: Microtubule-associated protein RP/EB family member 1

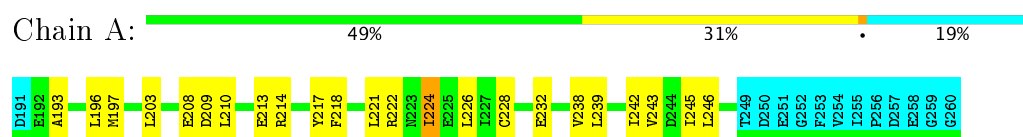


- Molecule 1: Microtubule-associated protein RP/EB family member 1

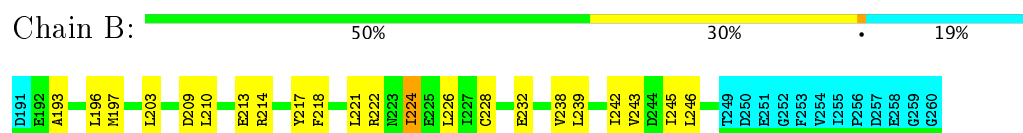


4.2.19 Score per residue for model 19

- Molecule 1: Microtubule-associated protein RP/EB family member 1

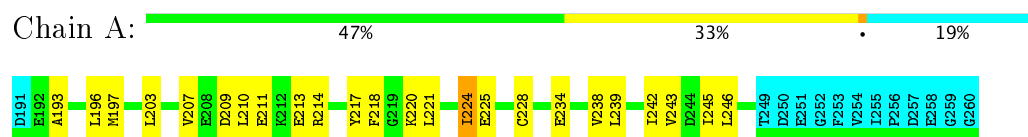


- Molecule 1: Microtubule-associated protein RP/EB family member 1

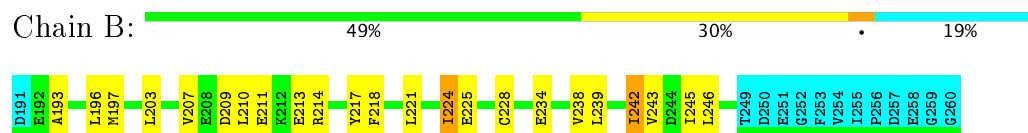


4.2.20 Score per residue for model 20

- Molecule 1: Microtubule-associated protein RP/EB family member 1



- Molecule 1: Microtubule-associated protein RP/EB family member 1



5 Refinement protocol and experimental data overview

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

Of the 20 calculated structures, 20 were deposited, based on the following criterion: *all calculated structures submitted*.

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

Software name	Classification	Version
CNS	refinement	
ARIA	structure calculation	

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)	6evi_cs.cif
Number of chemical shift lists	2
Total number of shifts	1672
Number of shifts mapped to atoms	1672
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	470	473	473	19±3
1	B	470	473	473	18±3
All	All	18800	18920	18920	692

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 18.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:239:LEU:HD13	1:A:242:ILE:HD12	0.75	1.58	4	20
1:B:239:LEU:HD13	1:B:242:ILE:HD12	0.71	1.61	4	20
1:A:224:ILE:HD13	1:A:246:LEU:HD21	0.71	1.61	10	18
1:B:224:ILE:HD13	1:B:246:LEU:HD21	0.68	1.65	10	16
1:A:224:ILE:CD1	1:A:246:LEU:HD21	0.66	2.21	8	20
1:B:238:VAL:HG23	1:B:239:LEU:HD22	0.63	1.70	19	19
1:B:221:LEU:HB3	1:B:246:LEU:HD22	0.63	1.71	1	11
1:A:217:TYR:O	1:A:221:LEU:HD22	0.62	1.94	14	20
1:A:238:VAL:HG23	1:A:239:LEU:HD22	0.62	1.69	19	19
1:B:217:TYR:O	1:B:221:LEU:HD22	0.61	1.94	14	20
1:A:220:LYS:HE2	1:B:245:ILE:O	0.60	1.97	18	1
1:B:224:ILE:CD1	1:B:246:LEU:HD21	0.60	2.27	1	20
1:A:238:VAL:HG21	1:B:238:VAL:HG21	0.59	1.74	14	17

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:221:LEU:HB3	1:A:246:LEU:HD22	0.59	1.74	1	12
1:A:221:LEU:HA	1:A:224:ILE:HG23	0.58	1.74	12	18
1:A:193:ALA:O	1:A:197:MET:HG2	0.58	1.99	20	20
1:A:209:ASP:O	1:A:213:GLU:HG2	0.58	1.99	18	8
1:A:214:ARG:HA	1:A:214:ARG:NH1	0.58	2.12	7	1
1:A:242:ILE:O	1:A:245:ILE:HB	0.57	1.99	15	20
1:A:201:LYS:O	1:A:205:LEU:HG	0.57	1.99	8	9
1:B:209:ASP:O	1:B:213:GLU:HG2	0.57	2.00	18	8
1:B:201:LYS:O	1:B:205:LEU:HG	0.57	1.99	8	9
1:B:214:ARG:NH1	1:B:214:ARG:HA	0.57	2.13	7	1
1:A:238:VAL:O	1:A:241:ARG:HG2	0.57	1.99	5	4
1:B:221:LEU:HA	1:B:224:ILE:HG23	0.57	1.76	12	17
1:A:193:ALA:HB1	1:B:196:LEU:HD13	0.56	1.77	13	2
1:B:238:VAL:O	1:B:241:ARG:HG2	0.56	2.00	5	4
1:B:193:ALA:O	1:B:197:MET:HG2	0.56	2.01	20	20
1:B:242:ILE:O	1:B:245:ILE:HB	0.55	2.01	15	19
1:A:238:VAL:O	1:A:242:ILE:HG13	0.55	2.02	13	19
1:B:244:ASP:HA	1:B:247:TYR:CE2	0.54	2.37	16	3
1:B:238:VAL:O	1:B:242:ILE:HG13	0.54	2.03	13	19
1:A:244:ASP:HA	1:A:247:TYR:CE2	0.54	2.38	16	3
1:B:214:ARG:O	1:B:218:PHE:HB2	0.53	2.03	1	12
1:A:214:ARG:O	1:A:218:PHE:HB2	0.53	2.04	19	12
1:A:245:ILE:O	1:B:220:LYS:HE2	0.53	2.04	18	1
1:A:208:GLU:O	1:A:212:LYS:HG3	0.53	2.04	10	4
1:A:213:GLU:OE2	1:B:214:ARG:HD3	0.53	2.04	10	1
1:A:196:LEU:HD13	1:B:193:ALA:HB1	0.52	1.81	13	2
1:A:216:PHE:O	1:A:220:LYS:HG2	0.52	2.05	4	3
1:B:208:GLU:O	1:B:212:LYS:HG3	0.52	2.04	10	4
1:A:228:CYS:O	1:A:232:GLU:HG2	0.51	2.05	11	2
1:B:236:ASP:OD2	1:B:238:VAL:HG22	0.51	2.05	13	1
1:A:236:ASP:OD2	1:A:238:VAL:HG22	0.51	2.05	13	1
1:A:239:LEU:CD1	1:A:242:ILE:HD12	0.51	2.34	19	2
1:A:201:LYS:O	1:A:204:LYS:HG2	0.50	2.06	11	5
1:B:201:LYS:O	1:B:204:LYS:HG2	0.50	2.06	11	6
1:B:216:PHE:O	1:B:220:LYS:HG2	0.50	2.06	4	1
1:A:239:LEU:O	1:A:243:VAL:HG23	0.50	2.06	11	18
1:B:239:LEU:O	1:B:243:VAL:HG23	0.50	2.06	11	18
1:B:204:LYS:O	1:B:208:GLU:HG2	0.49	2.08	3	2
1:B:214:ARG:HA	1:B:214:ARG:CZ	0.49	2.37	15	1
1:A:204:LYS:O	1:A:208:GLU:HG2	0.49	2.08	3	2
1:B:239:LEU:CD1	1:B:242:ILE:HD12	0.49	2.36	19	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:214:ARG:HA	1:A:214:ARG:CZ	0.49	2.38	15	1
1:B:239:LEU:HD13	1:B:242:ILE:CD1	0.48	2.38	19	6
1:A:222:ARG:O	1:A:226:LEU:HD13	0.48	2.08	10	7
1:B:228:CYS:O	1:B:232:GLU:HG2	0.48	2.09	19	2
1:A:224:ILE:HG12	1:A:246:LEU:HD11	0.48	1.85	3	2
1:A:220:LYS:HG3	1:B:245:ILE:HG23	0.47	1.85	14	3
1:B:222:ARG:O	1:B:226:LEU:HD13	0.47	2.09	10	6
1:A:199:GLN:O	1:A:203:LEU:HB2	0.47	2.09	10	2
1:A:224:ILE:HD11	1:A:246:LEU:HD21	0.47	1.85	12	3
1:B:216:PHE:O	1:B:220:LYS:HD3	0.47	2.09	10	1
1:A:236:ASP:HB3	1:A:238:VAL:HG22	0.47	1.86	3	5
1:A:200:VAL:O	1:A:204:LYS:HG2	0.47	2.09	5	2
1:B:236:ASP:HB3	1:B:238:VAL:HG22	0.47	1.87	3	4
1:B:199:GLN:O	1:B:203:LEU:HB2	0.47	2.10	10	2
1:A:217:TYR:O	1:A:220:LYS:HB2	0.47	2.10	5	7
1:B:217:TYR:O	1:B:220:LYS:HB2	0.46	2.11	5	4
1:A:214:ARG:HD3	1:B:213:GLU:OE2	0.46	2.10	10	1
1:A:204:LYS:O	1:A:207:VAL:HB	0.46	2.08	7	5
1:A:216:PHE:O	1:A:220:LYS:HD3	0.46	2.10	10	1
1:A:228:CYS:O	1:A:232:GLU:HG3	0.46	2.10	18	1
1:A:192:GLU:HG2	1:B:193:ALA:HB2	0.46	1.87	13	2
1:B:214:ARG:HA	1:B:214:ARG:NE	0.45	2.25	15	1
1:B:200:VAL:O	1:B:204:LYS:HG2	0.45	2.11	5	2
1:B:228:CYS:O	1:B:232:GLU:HG3	0.45	2.11	18	1
1:A:207:VAL:O	1:A:211:GLU:HG3	0.45	2.10	5	9
1:B:224:ILE:HG12	1:B:246:LEU:HD11	0.45	1.88	3	2
1:B:241:ARG:HA	1:B:244:ASP:OD1	0.44	2.11	5	1
1:A:214:ARG:HH11	1:A:214:ARG:HA	0.44	1.72	7	1
1:B:214:ARG:HA	1:B:214:ARG:HH11	0.44	1.72	7	1
1:B:207:VAL:O	1:B:211:GLU:HG3	0.44	2.12	5	9
1:A:220:LYS:HD2	1:B:245:ILE:HG23	0.44	1.89	11	1
1:A:239:LEU:HD13	1:A:242:ILE:CD1	0.44	2.38	19	5
1:A:225:GLU:O	1:A:229:GLN:HG2	0.44	2.13	5	2
1:A:241:ARG:HA	1:A:244:ASP:OD1	0.44	2.12	5	1
1:A:214:ARG:HA	1:A:214:ARG:NE	0.44	2.27	15	1
1:B:225:GLU:O	1:B:229:GLN:HG2	0.43	2.13	5	2
1:A:204:LYS:NZ	1:A:204:LYS:HB2	0.43	2.28	7	1
1:A:218:PHE:HA	1:A:221:LEU:CD2	0.43	2.43	10	3
1:A:210:LEU:HB3	1:B:210:LEU:HB3	0.43	1.90	16	5
1:B:222:ARG:HA	1:B:222:ARG:NE	0.43	2.29	18	1
1:B:204:LYS:O	1:B:207:VAL:HB	0.43	2.12	7	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:218:PHE:HA	1:B:221:LEU:CD2	0.43	2.44	12	3
1:A:222:ARG:HA	1:A:222:ARG:NE	0.43	2.29	18	1
1:B:204:LYS:NZ	1:B:204:LYS:HB2	0.43	2.29	7	1
1:A:193:ALA:HB2	1:B:192:GLU:HG2	0.42	1.91	13	1
1:A:228:CYS:SG	1:A:239:LEU:HD12	0.42	2.55	5	1
1:B:209:ASP:O	1:B:212:LYS:HG2	0.42	2.15	14	1
1:A:228:CYS:HA	1:A:239:LEU:HG	0.42	1.92	20	3
1:A:217:TYR:HH	1:B:218:PHE:HE1	0.42	1.55	9	1
1:B:222:ARG:O	1:B:225:GLU:HB3	0.42	2.15	16	1
1:A:231:ASN:HB3	1:A:236:ASP:HB3	0.41	1.90	13	1
1:A:209:ASP:O	1:A:212:LYS:HG2	0.41	2.16	14	1
1:A:225:GLU:HA	1:A:228:CYS:SG	0.41	2.55	20	1
1:A:220:LYS:HG3	1:B:245:ILE:CG2	0.41	2.45	5	2
1:A:204:LYS:HZ3	1:A:204:LYS:HB2	0.41	1.75	7	1
1:A:228:CYS:HA	1:A:239:LEU:HB3	0.41	1.91	19	2
1:B:226:LEU:O	1:B:230:GLU:HG3	0.41	2.14	10	2
1:A:228:CYS:HA	1:A:239:LEU:CG	0.41	2.45	11	1
1:A:222:ARG:O	1:A:225:GLU:HB3	0.41	2.16	16	1
1:A:226:LEU:O	1:A:230:GLU:HG3	0.41	2.15	8	2
1:A:227:ILE:HG12	1:B:241:ARG:NH2	0.41	2.31	14	1
1:A:197:MET:SD	1:B:196:LEU:HD21	0.41	2.56	13	1
1:A:199:GLN:HE21	1:B:200:VAL:HG11	0.41	1.76	7	1
1:B:231:ASN:HB3	1:B:236:ASP:HB3	0.41	1.90	13	1
1:A:197:MET:O	1:A:201:LYS:HE3	0.41	2.16	15	1
1:B:225:GLU:HA	1:B:228:CYS:SG	0.40	2.56	20	1
1:A:214:ARG:NH2	1:B:217:TYR:CD1	0.40	2.90	15	1
1:A:208:GLU:HG3	1:A:209:ASP:N	0.40	2.31	19	1
1:A:192:GLU:O	1:A:196:LEU:HD12	0.40	2.17	3	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	57/70 (81%)	55±1 (96±2%)	2±1 (4±2%)	0±0 (0±0%)	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	57/70 (81%)	55±1 (96±2%)	2±1 (4±2%)	0±0 (0±0%)	100	100
All	All	2280/2800 (81%)	2196 (96%)	84 (4%)	0 (0%)	100	100

There are no Ramachandran outliers.

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	52/62 (84%)	47±2 (91±3%)	5±2 (9±3%)	16	61
1	B	52/62 (84%)	47±2 (91±3%)	5±2 (9±3%)	16	61
All	All	2080/2480 (84%)	1893 (91%)	187 (9%)	16	61

All 34 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	B	224	ILE	20
1	A	224	ILE	20
1	A	196	LEU	14
1	B	242	ILE	13
1	B	196	LEU	12
1	A	242	ILE	10
1	A	210	LEU	10
1	B	223	ASN	8
1	A	223	ASN	8
1	A	240	GLN	7
1	B	240	GLN	7
1	A	201	LYS	6
1	B	201	LYS	6
1	B	210	LEU	6
1	B	221	LEU	5
1	B	203	LEU	3
1	A	221	LEU	3
1	A	203	LEU	3
1	B	204	LYS	3

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Mol	Chain	Res	Type	Models (Total)
1	A	204	LYS	3
1	A	212	LYS	2
1	B	214	ARG	2
1	B	209	ASP	2
1	A	209	ASP	2
1	A	214	ARG	2
1	B	212	LYS	2
1	A	199	GLN	1
1	A	234	GLU	1
1	B	218	PHE	1
1	B	199	GLN	1
1	A	218	PHE	1
1	B	213	GLU	1
1	B	234	GLU	1
1	A	213	GLU	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 [i](#)

The completeness of assignment taking into account all chemical shift lists is 85% for the well-defined parts and 85% for the entire structure.

7.1 Chemical shift list 1

File name: 6evi_cs.cif

Chemical shift list name: *assigned_chem_shift_list_1*

7.1.1 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	871
Number of shifts mapped to atoms	871
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 [i](#)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	70	-0.48 ± 0.06	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	65	0.26 ± 0.14	None needed (< 0.5 ppm)
$^{13}\text{C}'$	67	0.47 ± 0.14	None needed (< 0.5 ppm)
^{15}N	66	-0.26 ± 0.22	None needed (< 0.5 ppm)

7.1.3 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 44%, i.e. 658 atoms were assigned a chemical shift out of a possible 1486. 13 out of 26 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	278/566 (49%)	111/226 (49%)	112/228 (49%)	55/112 (49%)
Sidechain	346/852 (41%)	207/492 (42%)	132/320 (41%)	7/40 (18%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	34/68 (50%)	18/36 (50%)	16/32 (50%)	0/0 (—%)
Overall	658/1486 (44%)	336/754 (45%)	260/580 (45%)	62/152 (41%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 44%, i.e. 773 atoms were assigned a chemical shift out of a possible 1744. 14 out of 28 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	335/692 (48%)	132/276 (48%)	137/280 (49%)	66/136 (49%)
Sidechain	395/966 (41%)	237/556 (43%)	151/370 (41%)	7/40 (18%)
Aromatic	43/86 (50%)	23/46 (50%)	20/40 (50%)	0/0 (—%)
Overall	773/1744 (44%)	392/878 (45%)	308/690 (45%)	73/176 (41%)

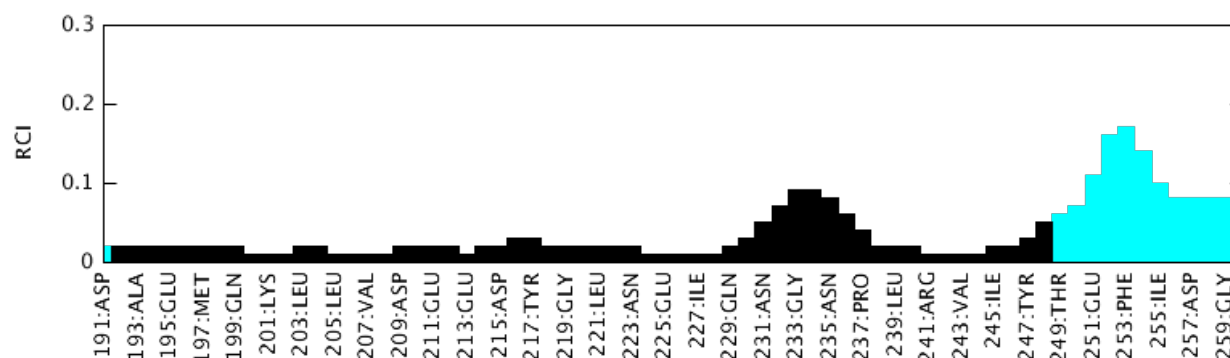
7.1.4 Statistically unusual chemical shifts [i](#)

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:



7.2 Chemical shift list 2

File name: 6evi_cs.cif

Chemical shift list name: *assigned_chem_shift_list_1_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	801
Number of shifts mapped to atoms	801
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

7.2.2 Chemical shift referencing [i](#)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	70	-0.46 ± 0.09	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	64	0.27 ± 0.18	None needed (< 0.5 ppm)
$^{13}\text{C}'$	0	—	None (insufficient data)
^{15}N	66	-0.22 ± 0.20	None needed (< 0.5 ppm)

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 40%, i.e. 601 atoms were assigned a chemical shift out of a possible 1486. 13 out of 26 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	223/566 (39%)	111/226 (49%)	57/228 (25%)	55/112 (49%)
Sidechain	344/852 (40%)	206/492 (42%)	131/320 (41%)	7/40 (18%)
Aromatic	34/68 (50%)	18/36 (50%)	16/32 (50%)	0/0 (—%)
Overall	601/1486 (40%)	335/754 (44%)	204/580 (35%)	62/152 (41%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 40%, i.e. 704 atoms were assigned a chemical shift out of a possible 1744. 14 out of 28 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	268/692 (39%)	132/276 (48%)	70/280 (25%)	66/136 (49%)

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	Total	¹H	¹³C	¹⁵N
Sidechain	393/966 (41%)	236/556 (42%)	150/370 (41%)	7/40 (18%)
Aromatic	43/86 (50%)	23/46 (50%)	20/40 (50%)	0/0 (—%)
Overall	704/1744 (40%)	391/878 (45%)	240/690 (35%)	73/176 (41%)

7.2.4 Statistically unusual chemical shifts [i](#)

There are no statistically unusual chemical shifts.

7.2.5 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 B:

