



Full wwPDB NMR Structure Validation Report ⓘ

Mar 8, 2026 – 01:09 PM UTC

PDB ID : 2KA4 / pdb_00002ka4
BMRB ID : 16014
Title : NMR structure of the CBP-TAZ1/STAT2-TAD complex
Authors : Wojciak, J.M.; Martinez-Yamout, M.A.; Dyson, H.J.; Wright, P.E.
Deposited on : 2008-10-30

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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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
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) : 2.49

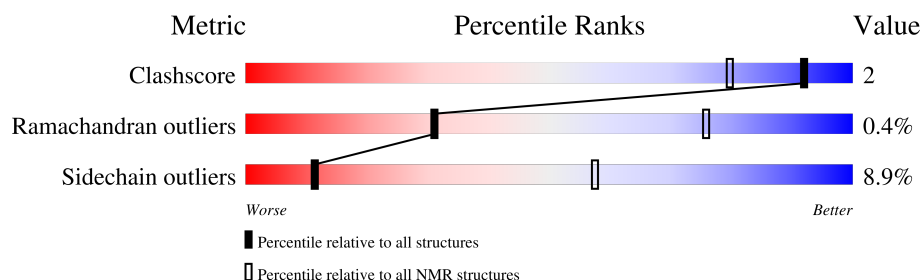
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 83%.

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	229148	14424
Ramachandran outliers	224038	12848
Sidechain outliers	223484	12823

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	100	60% 7% 32%
2	B	57	42% 9% 49%

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:346-A:367, A:381-A:395, A:405-A:435, B:788-B:816 (97)	0.28	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 10 single-model clusters were found.

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

3 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 2447 atoms, of which 1215 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Crebbp protein.

Mol	Chain	Residues	Atoms						Trace
1	A	100	Total	C	H	N	O	S	0
			1563	472	783	162	135	11	

- Molecule 2 is a protein called Signal transducer and activator of transcription 2.

Mol	Chain	Residues	Atoms						Trace
2	B	57	Total	C	H	N	O	S	0
			881	279	432	78	89	3	

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	782	GLY	-	expression tag	UNP P52630
B	783	SER	-	expression tag	UNP P52630
B	784	HIS	-	expression tag	UNP P52630
B	785	MET	-	expression tag	UNP P52630
B	793	HIS	CYS	engineered mutation	UNP P52630
B	809	SER	CYS	engineered mutation	UNP P52630

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

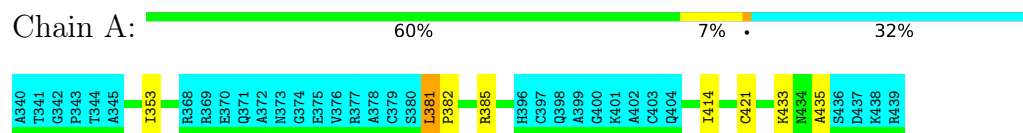
Mol	Chain	Residues	Atoms	
3	A	3	Total	Zn
			3	3

4 Residue-property plots

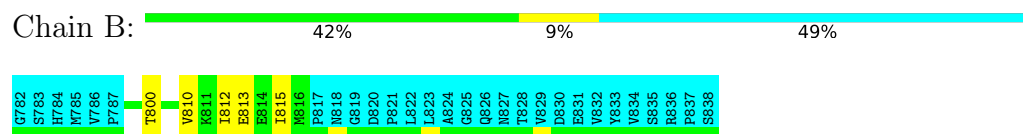
4.1 Average score per residue in the NMR ensemble

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: Crebbp protein



- Molecule 2: Signal transducer and activator of transcription 2

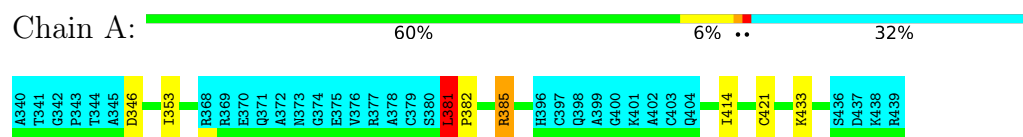


4.2 Scores per residue for each member of the ensemble

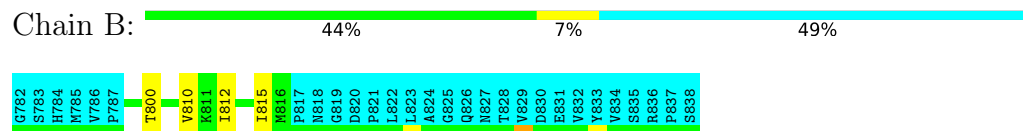
Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

- Molecule 1: Crebbp protein

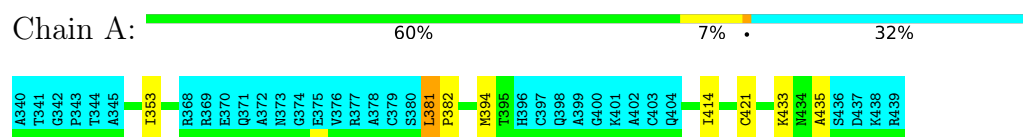


- Molecule 2: Signal transducer and activator of transcription 2

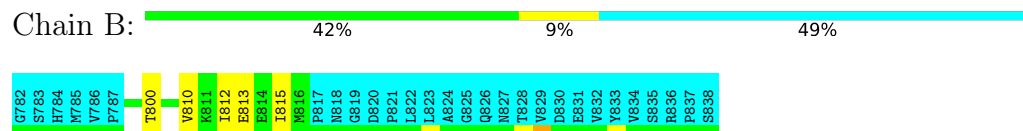


4.2.2 Score per residue for model 2

- Molecule 1: Crebbp protein

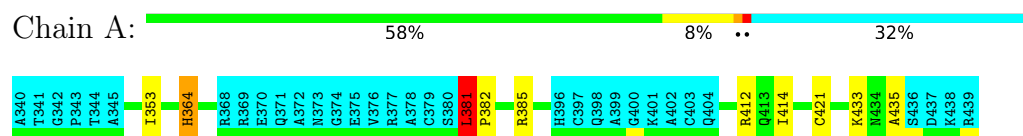


- Molecule 2: Signal transducer and activator of transcription 2

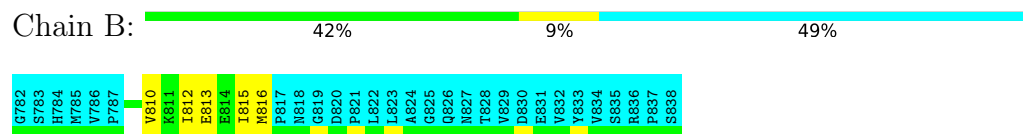


4.2.3 Score per residue for model 3

- Molecule 1: Crebbp protein

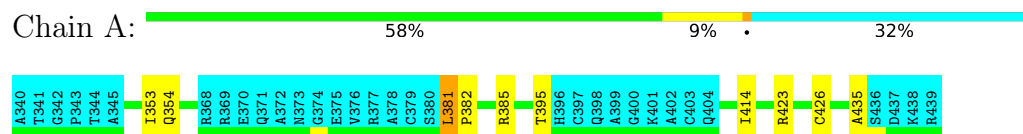


- Molecule 2: Signal transducer and activator of transcription 2

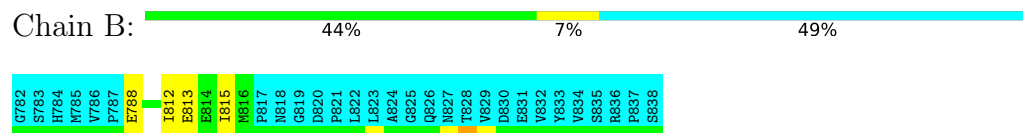


4.2.4 Score per residue for model 4

- Molecule 1: Crebbp protein

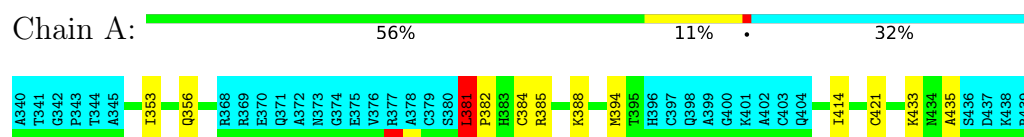


- Molecule 2: Signal transducer and activator of transcription 2

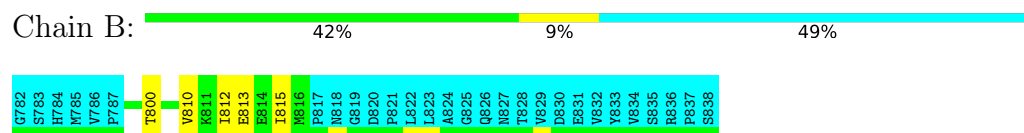


4.2.5 Score per residue for model 5

- Molecule 1: Crebbp protein

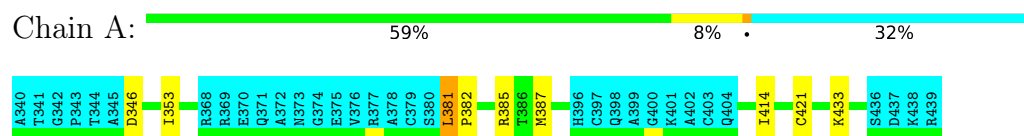


- Molecule 2: Signal transducer and activator of transcription 2

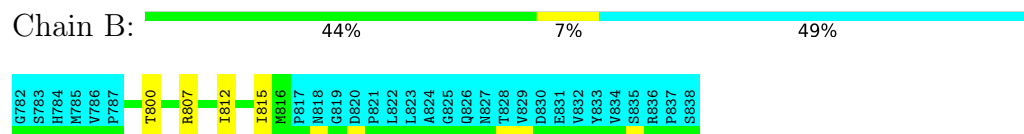


4.2.6 Score per residue for model 6 (medoid)

- Molecule 1: Crebbp protein

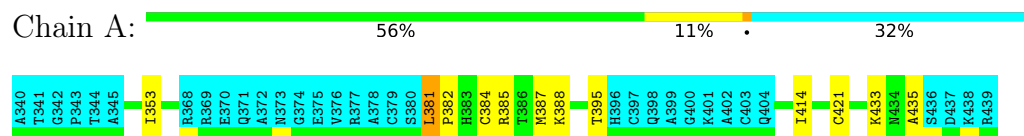


- Molecule 2: Signal transducer and activator of transcription 2

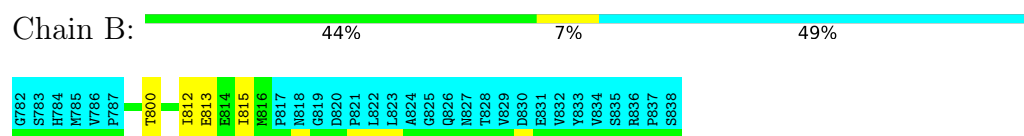


4.2.7 Score per residue for model 7

- Molecule 1: Crebbp protein

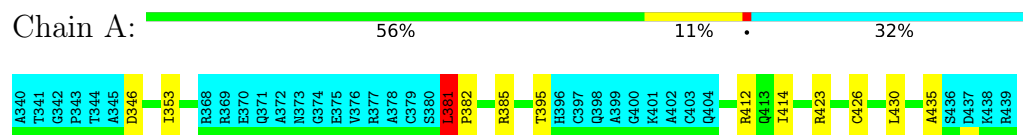


- Molecule 2: Signal transducer and activator of transcription 2

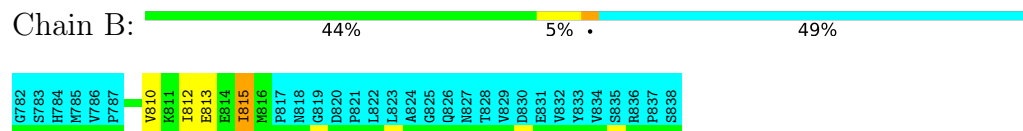


4.2.8 Score per residue for model 8

- Molecule 1: Crebbp protein

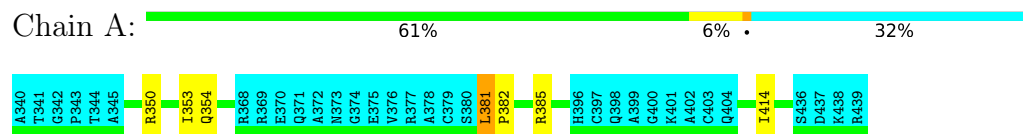


- Molecule 2: Signal transducer and activator of transcription 2

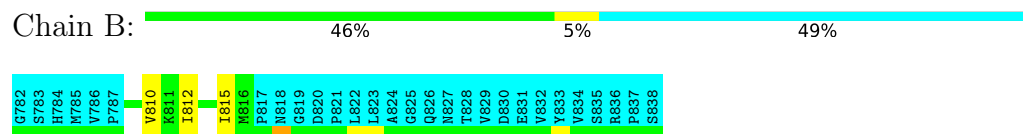


4.2.9 Score per residue for model 9

- Molecule 1: Crebbp protein

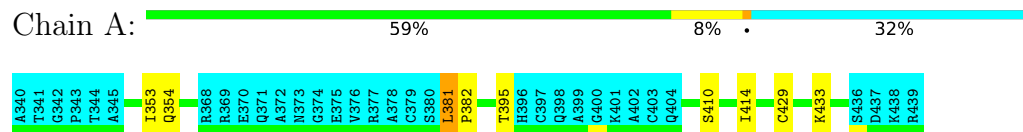


- Molecule 2: Signal transducer and activator of transcription 2

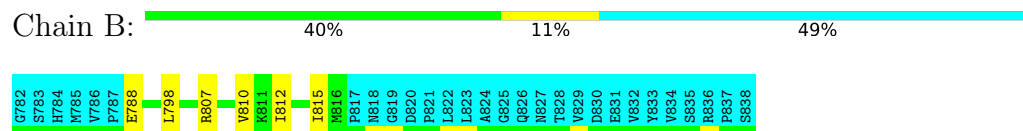


4.2.10 Score per residue for model 10

- Molecule 1: Crebbp protein

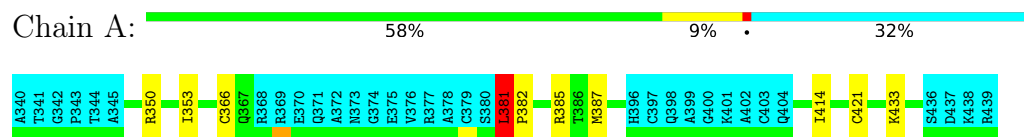


- Molecule 2: Signal transducer and activator of transcription 2

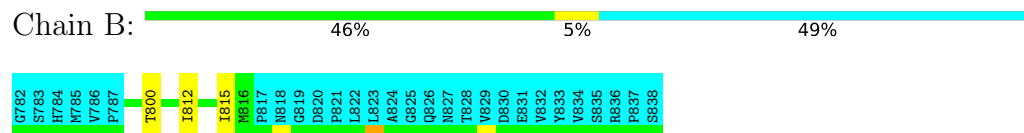


4.2.11 Score per residue for model 11

- Molecule 1: Crebbp protein

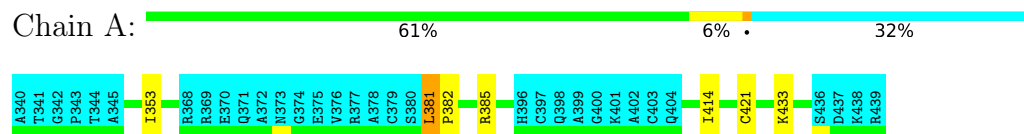


- Molecule 2: Signal transducer and activator of transcription 2

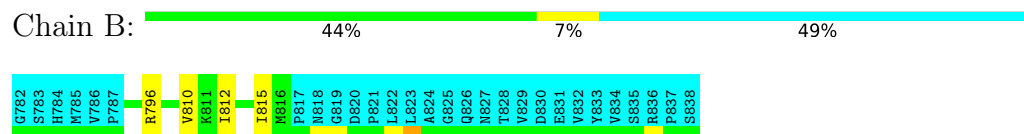


4.2.12 Score per residue for model 12

- Molecule 1: Crebbp protein

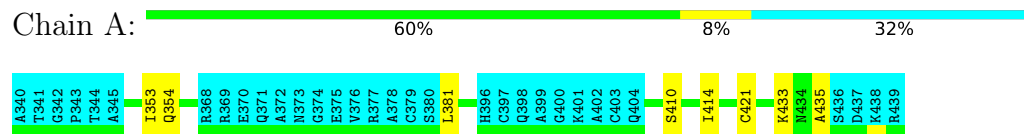


- Molecule 2: Signal transducer and activator of transcription 2

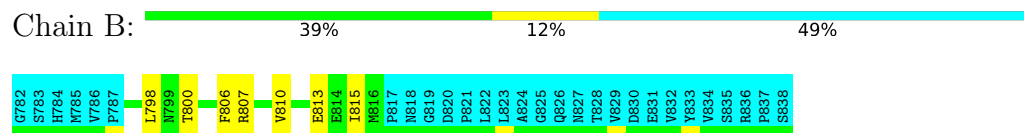


4.2.13 Score per residue for model 13

- Molecule 1: Crebbp protein

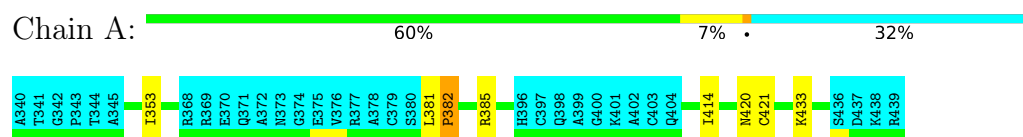


- Molecule 2: Signal transducer and activator of transcription 2

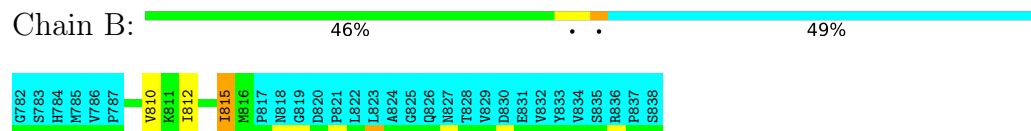


4.2.14 Score per residue for model 14

- Molecule 1: Crebbp protein

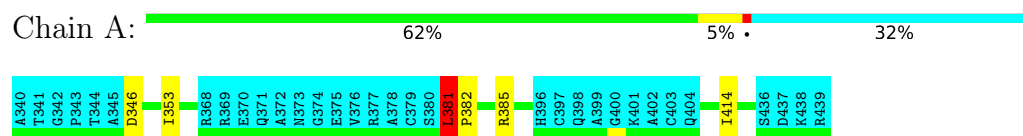


- Molecule 2: Signal transducer and activator of transcription 2

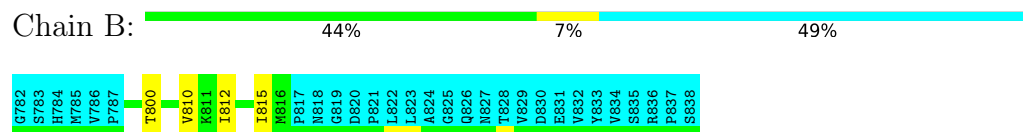


4.2.15 Score per residue for model 15

- Molecule 1: Crebbp protein

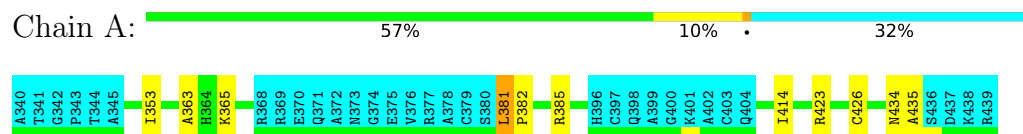


- Molecule 2: Signal transducer and activator of transcription 2

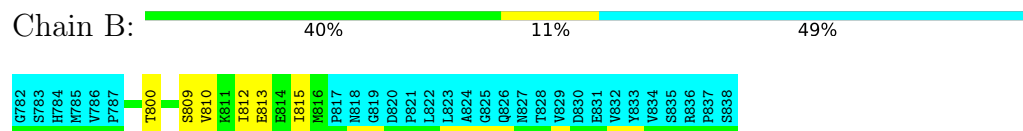


4.2.16 Score per residue for model 16

- Molecule 1: Crebbp protein

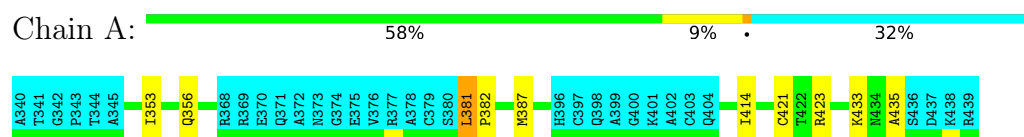


- Molecule 2: Signal transducer and activator of transcription 2

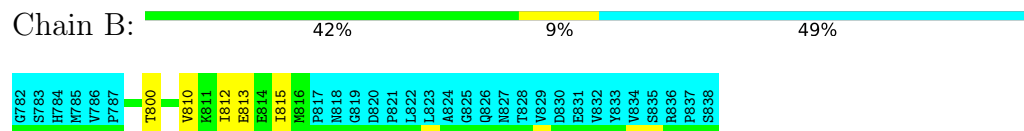


4.2.17 Score per residue for model 17

- Molecule 1: Crebbp protein

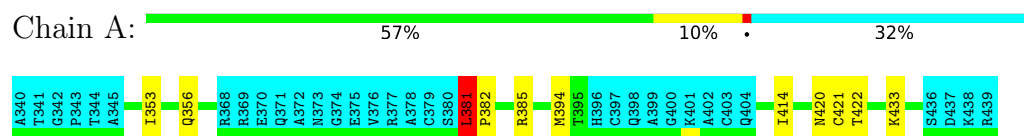


- Molecule 2: Signal transducer and activator of transcription 2

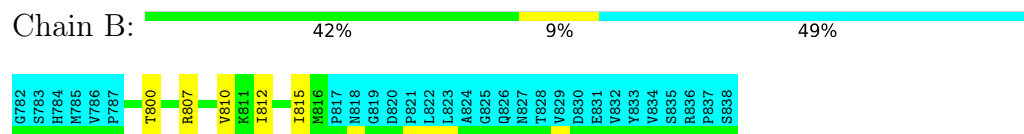


4.2.18 Score per residue for model 18

- Molecule 1: Crebbp protein

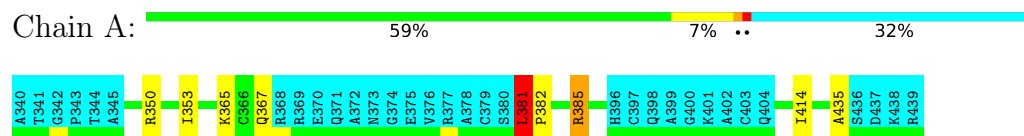


- Molecule 2: Signal transducer and activator of transcription 2

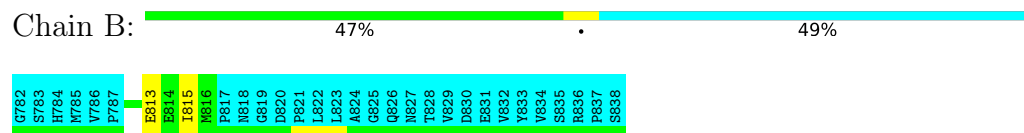


4.2.19 Score per residue for model 19

- Molecule 1: Crebbp protein

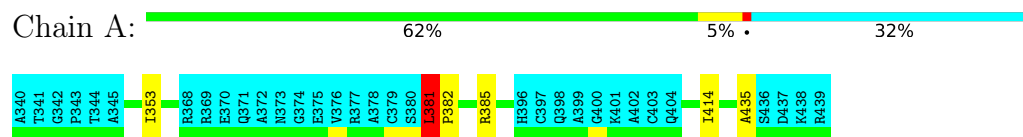


- Molecule 2: Signal transducer and activator of transcription 2

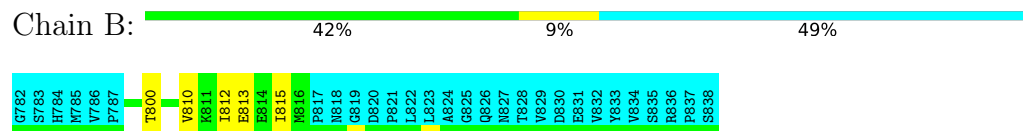


4.2.20 Score per residue for model 20

- Molecule 1: Crebbp protein



- Molecule 2: Signal transducer and activator of transcription 2



5 Refinement protocol and experimental data overview

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

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
Amber	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)	working_cs.cif
Number of chemical shift lists	1
Total number of shifts	1719
Number of shifts mapped to atoms	1719
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	83%

6 Model quality i

6.1 Standard geometry i

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

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	0.93±0.01	0±0/560 (0.0± 0.0%)	1.65±0.02	2±1/758 (0.2± 0.1%)
2	B	0.96±0.02	0±0/250 (0.0± 0.0%)	1.53±0.05	0±1/340 (0.1± 0.3%)
All	All	0.94	0/16200 (0.0%)	1.61	44/21960 (0.2%)

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	0.3±0.6
2	B	0.0±0.0	0.1±0.4
All	All	0	9

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	364	HIS	CB-CG-CD2	-6.16	123.19	131.20	3	1
1	A	381	LEU	CA-C-N	5.86	126.26	119.47	19	12
1	A	381	LEU	C-N-CA	5.86	126.26	119.47	19	12
1	A	354	GLN	OE1-CD-NE2	-5.71	116.89	122.60	13	4
1	A	356	GLN	OE1-CD-NE2	-5.45	117.15	122.60	17	3
2	B	806	PHE	CA-C-N	5.12	128.88	120.63	13	1
2	B	806	PHE	C-N-CA	5.12	128.88	120.63	13	1
2	B	815	ILE	CA-C-N	5.12	129.21	121.03	8	2
2	B	815	ILE	C-N-CA	5.12	129.21	121.03	8	2
2	B	816	MET	N-CA-C	5.11	116.95	109.84	3	1

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	363	ALA	N-CA-C	5.09	117.49	111.33	16	1
2	B	816	MET	CA-C-N	5.06	124.72	119.56	3	1
2	B	816	MET	C-N-CA	5.06	124.72	119.56	3	1
1	A	434	ASN	CA-CB-CG	5.05	117.65	112.60	16	1
2	B	796	ARG	CD-NE-CZ	5.01	131.41	124.40	12	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)
2	B	807	ARG	Sidechain	3
1	A	350	ARG	Sidechain	3
1	A	385	ARG	Sidechain	2
1	A	412	ARG	Sidechain	1

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	547	561	561	2±1
2	B	244	238	238	1±1
All	All	15880	15980	15980	48

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:429:CYS:CB	1:A:433:LYS:HZ3	0.61	2.08	10	1
1:A:381:LEU:HD13	1:A:382:PRO:HD2	0.54	1.79	4	16
1:A:435:ALA:HB2	2:B:813:GLU:HA	0.49	1.85	7	11
1:A:384:CYS:SG	1:A:388:LYS:NZ	0.46	2.89	5	2
1:A:421:CYS:SG	1:A:433:LYS:NZ	0.44	2.91	13	12
1:A:410:SER:HA	2:B:798:LEU:HD22	0.42	1.92	13	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:421:CYS:SG	1:A:423:ARG:NH1	0.42	2.93	17	1
1:A:423:ARG:NH2	1:A:426:CYS:SG	0.41	2.93	16	3

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	68/100 (68%)	64±1 (95±2%)	3±1 (5±2%)	0±0 (0±1%)	31	76
2	B	29/57 (51%)	26±1 (91±3%)	3±1 (9±3%)	0±0 (0±1%)	44	80
All	All	1940/3140 (62%)	1817 (94%)	116 (6%)	7 (0%)	31	76

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	346	ASP	4
2	B	807	ARG	1
1	A	382	PRO	1
1	A	422	THR	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	64/87 (74%)	59±1 (92±1%)	5±1 (8±1%)	14	62
2	B	29/53 (55%)	26±1 (88±3%)	3±1 (12±3%)	7	50
All	All	1860/2800 (66%)	1695 (91%)	165 (9%)	11	57

All 20 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	353	ILE	20
1	A	414	ILE	20
2	B	815	ILE	20
1	A	381	LEU	19
2	B	812	ILE	18
1	A	385	ARG	16
2	B	810	VAL	15
2	B	800	THR	12
1	A	395	THR	4
1	A	387	MET	4
1	A	394	MET	3
1	A	382	PRO	3
2	B	788	GLU	2
1	A	420	ASN	2
1	A	365	LYS	2
1	A	364	HIS	1
1	A	412	ARG	1
1	A	430	LEU	1
2	B	809	SER	1
1	A	367	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 oligosaccharides in this entry.

6.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

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 83% for the well-defined parts and 81% 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 [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	1719
Number of shifts mapped to atoms	1719
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
$^{13}\text{C}_\alpha$	156	-0.41 ± 0.19	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	150	0.37 ± 0.12	None needed (< 0.5 ppm)
$^{13}\text{C}'$	0	—	None (insufficient data)
^{15}N	130	0.02 ± 0.23	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 83%, i.e. 1155 atoms were assigned a chemical shift out of a possible 1395. 0 out of 17 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	363/471 (77%)	182/187 (97%)	96/194 (49%)	85/90 (94%)
Sidechain	738/839 (88%)	502/545 (92%)	225/258 (87%)	11/36 (31%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	54/85 (64%)	28/47 (60%)	25/28 (89%)	1/10 (10%)
Overall	1155/1395 (83%)	712/779 (91%)	346/480 (72%)	97/136 (71%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 81%, i.e. 1718 atoms were assigned a chemical shift out of a possible 2134. 0 out of 24 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	579/767 (75%)	293/308 (95%)	156/314 (50%)	130/145 (90%)
Sidechain	1071/1259 (85%)	729/815 (89%)	328/384 (85%)	14/60 (23%)
Aromatic	68/108 (63%)	36/59 (61%)	31/37 (84%)	1/12 (8%)
Overall	1718/2134 (81%)	1058/1182 (90%)	515/735 (70%)	145/217 (67%)

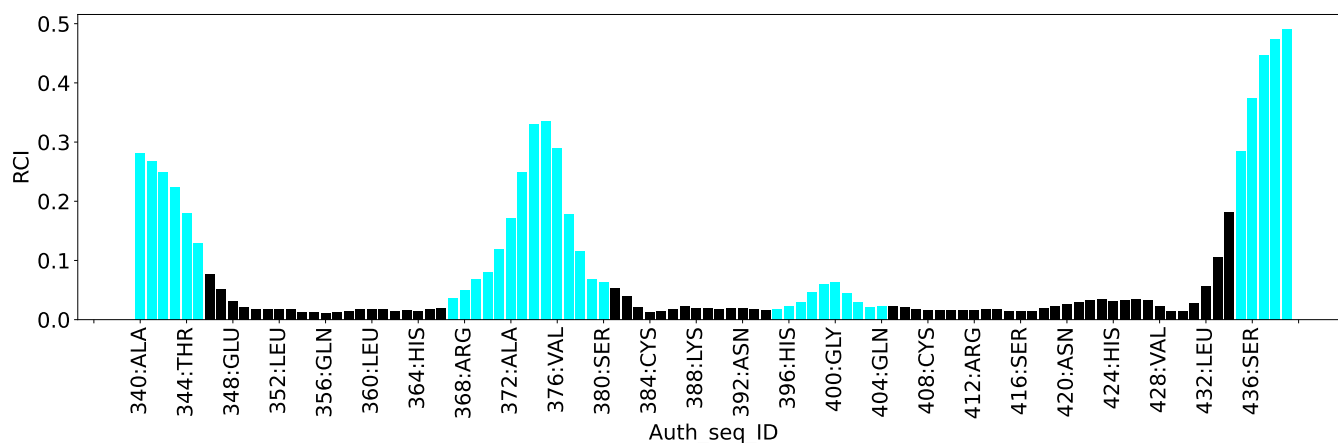
7.1.4 Statistically unusual chemical shifts [i](#)

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. 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:



Random coil index (RCI) for chain B:

