Full wwPDB NMR Structure Validation Report (i)

Oct 17, 2021 – 02:05 AM EDT

PDB ID	:	1N65
Title	:	FAMILY OF NMR SOLUTION STRUCTURES OF CA CE CALBINDIN D9K IN DENATURATING CONDITIONS
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Deposited on	:	2002-11-08

This is a Full wwPDB NMR Structure Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/NMRValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (i)) were used in the production of this report:

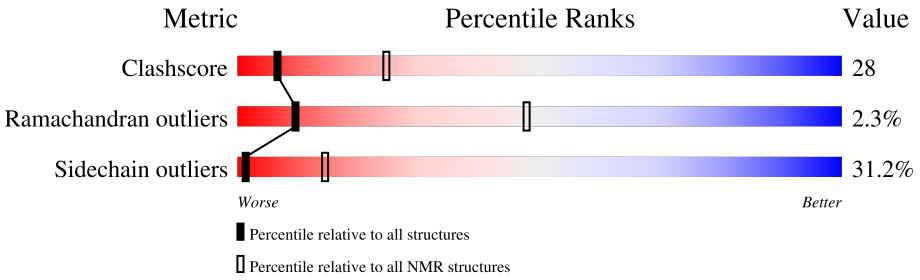
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	2.23.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.23.2

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
SOLUTION NMR

The overall completeness of chemical shifts assignment was not calculated.

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	75	35% 44% 8% 13%

2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 13 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:5-A:54, A:61-A:75 (65)	0.21	13

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

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

NmrClust was unable to cluster the ensemble.

Error message: Inconsistent models

3 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 1203 atoms, of which 602 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Vitamin D-dependent calcium-binding protein, intestinal.

Mol	Chain	Residues	Atoms						Trace
1	A	75	Total	C	H	N	O	S	0
			1202	384	602	91	124	1	

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	43	MET	PRO	engineered mutation	UNP P02633

- Molecule 2 is CERIUM (III) ION (three-letter code: CE) (formula: Ce).

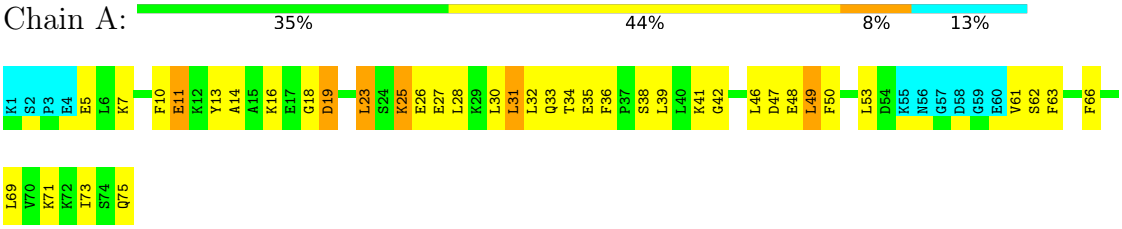
Mol	Chain	Residues	Atoms	
2	A	1	Total	Ce
			1	1

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: Vitamin D-dependent calcium-binding protein, intestinal

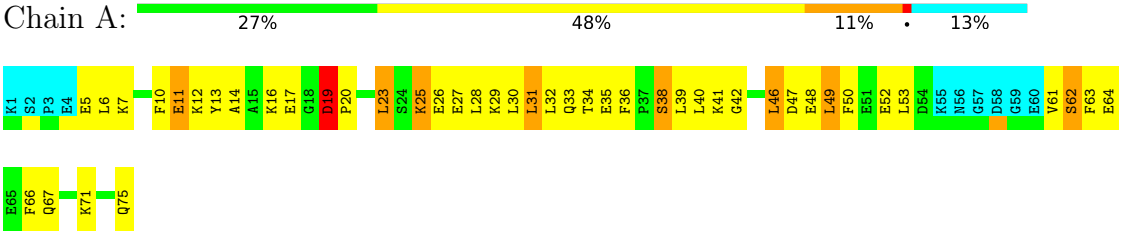


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

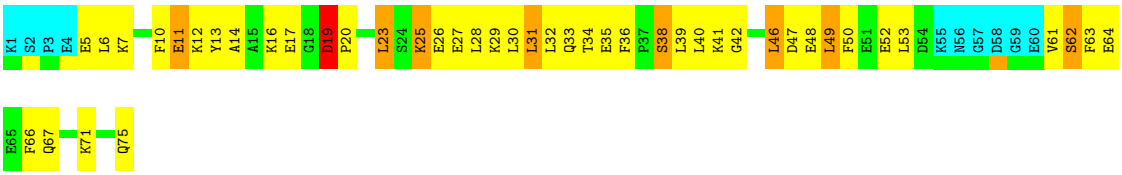
4.2.1 Score per residue for model 1

• Molecule 1: Vitamin D-dependent calcium-binding protein, intestinal



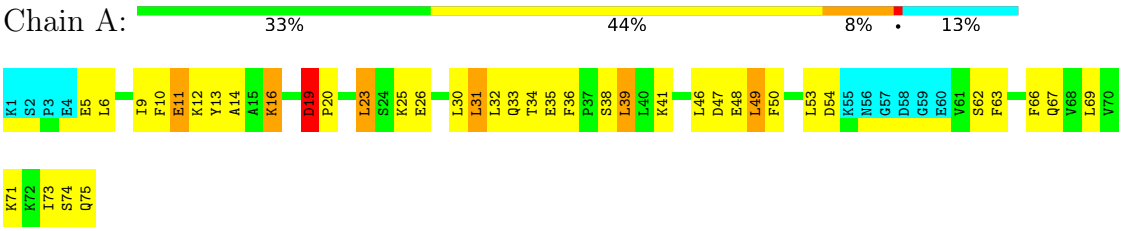
4.2.2 Score per residue for model 2

• Molecule 1: Vitamin D-dependent calcium-binding protein, intestinal



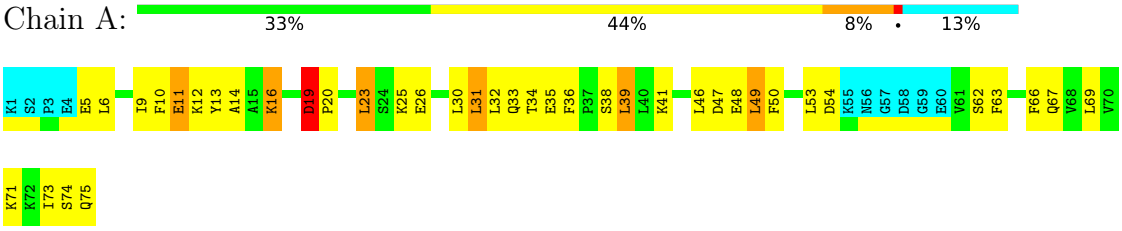
4.2.3 Score per residue for model 3

• Molecule 1: Vitamin D-dependent calcium-binding protein, intestinal



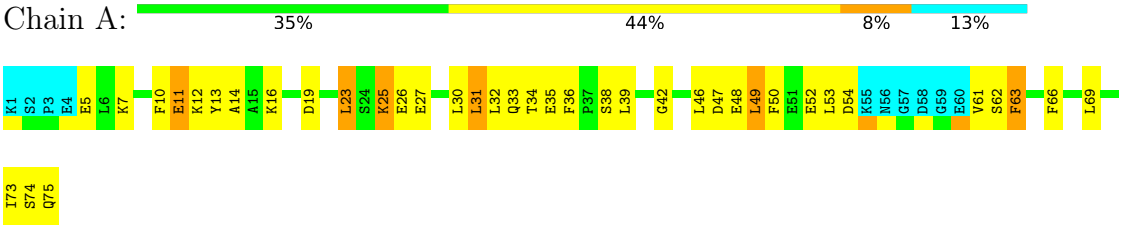
4.2.4 Score per residue for model 4

• Molecule 1: Vitamin D-dependent calcium-binding protein, intestinal



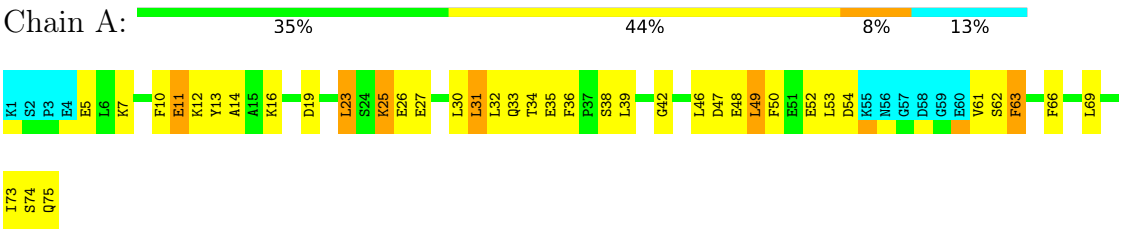
4.2.5 Score per residue for model 5

• Molecule 1: Vitamin D-dependent calcium-binding protein, intestinal



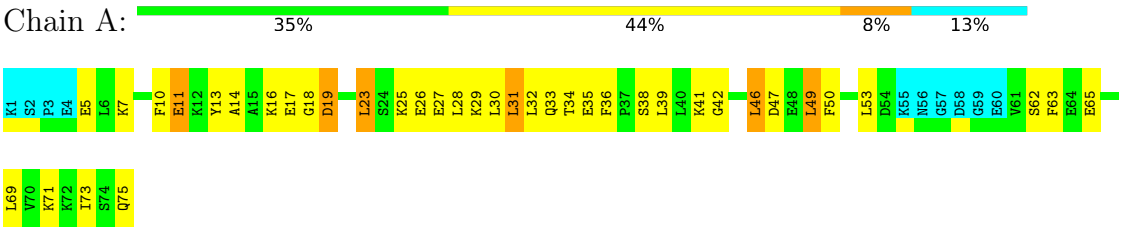
4.2.6 Score per residue for model 6

• Molecule 1: Vitamin D-dependent calcium-binding protein, intestinal



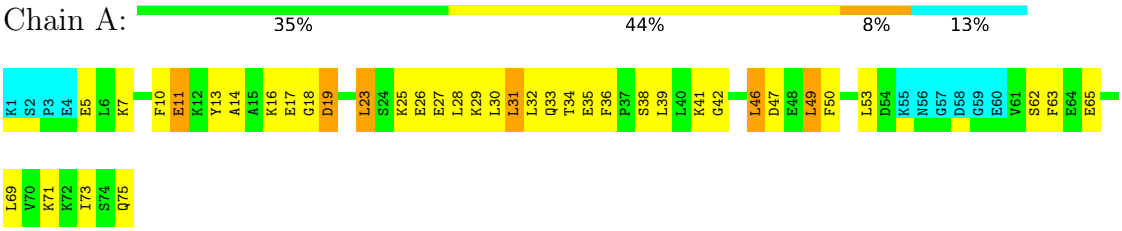
4.2.7 Score per residue for model 7

• Molecule 1: Vitamin D-dependent calcium-binding protein, intestinal



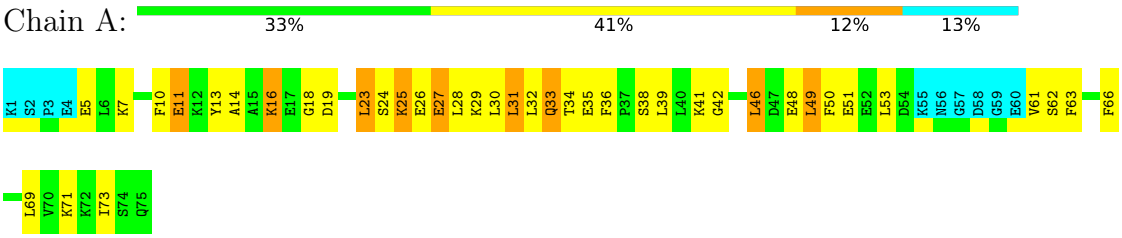
4.2.8 Score per residue for model 8

• Molecule 1: Vitamin D-dependent calcium-binding protein, intestinal



4.2.9 Score per residue for model 9

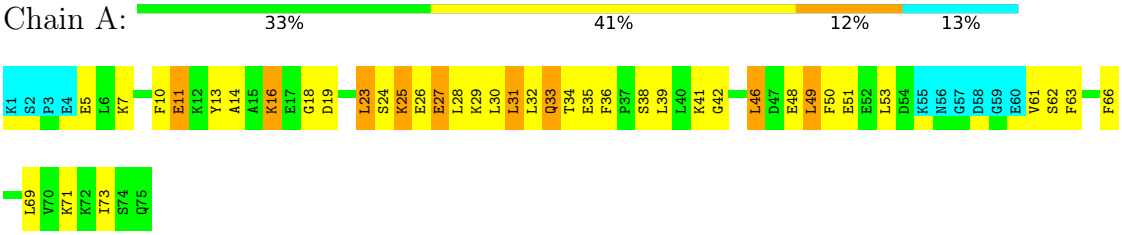
• Molecule 1: Vitamin D-dependent calcium-binding protein, intestinal



4.2.10 Score per residue for model 10

• Molecule 1: Vitamin D-dependent calcium-binding protein, intestinal

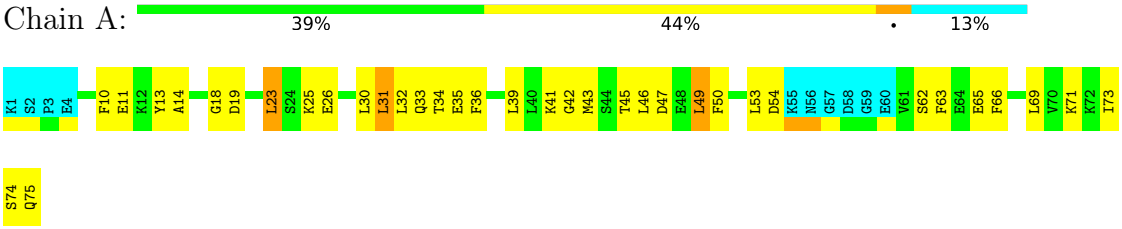
Chain A:



4.2.11 Score per residue for model 11

• Molecule 1: Vitamin D-dependent calcium-binding protein, intestinal

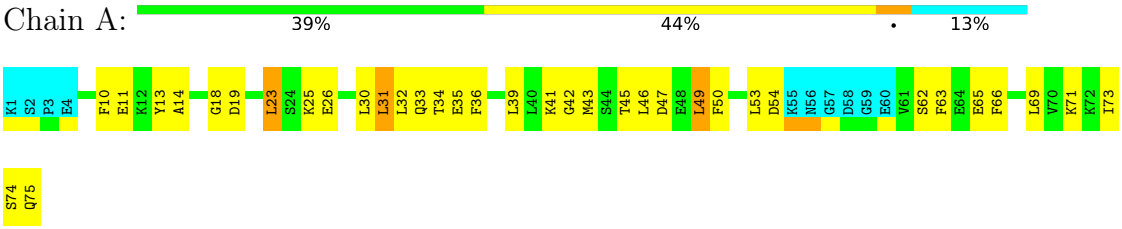
Chain A:



4.2.12 Score per residue for model 12

• Molecule 1: Vitamin D-dependent calcium-binding protein, intestinal

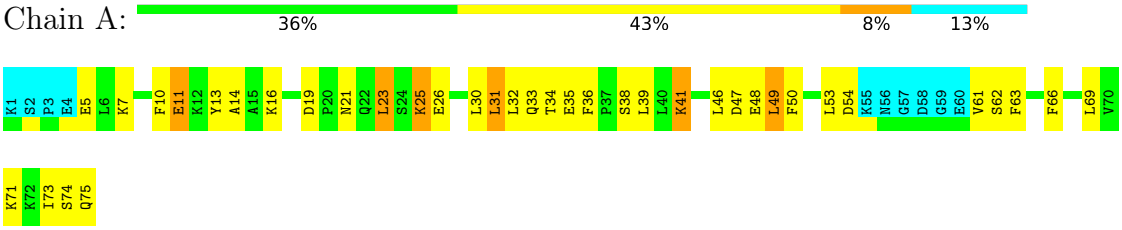
Chain A:



4.2.13 Score per residue for model 13 (medoid)

• Molecule 1: Vitamin D-dependent calcium-binding protein, intestinal

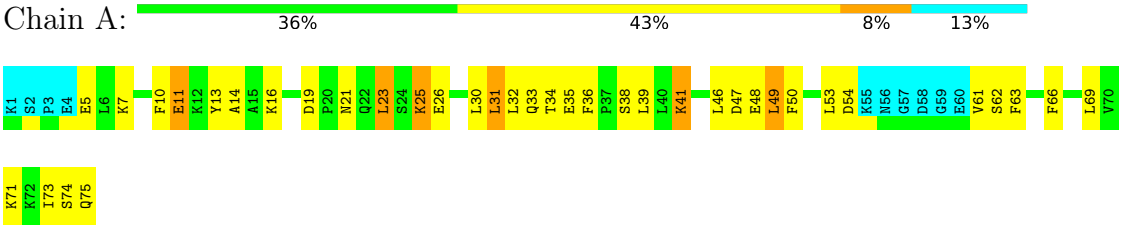
Chain A:



4.2.14 Score per residue for model 14

• Molecule 1: Vitamin D-dependent calcium-binding protein, intestinal

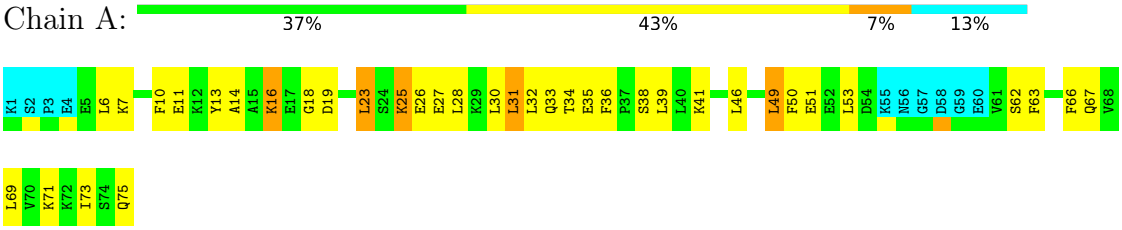
Chain A:



4.2.15 Score per residue for model 15

• Molecule 1: Vitamin D-dependent calcium-binding protein, intestinal

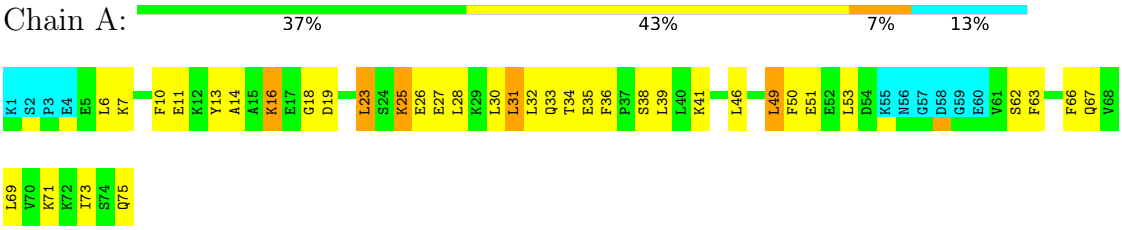
Chain A:



4.2.16 Score per residue for model 16

• Molecule 1: Vitamin D-dependent calcium-binding protein, intestinal

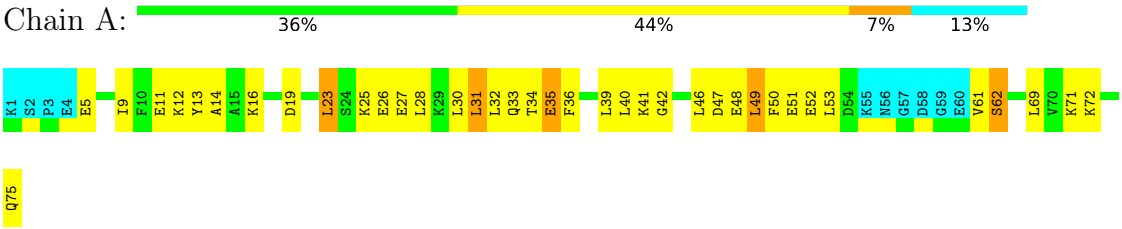
Chain A:



4.2.17 Score per residue for model 17

• Molecule 1: Vitamin D-dependent calcium-binding protein, intestinal

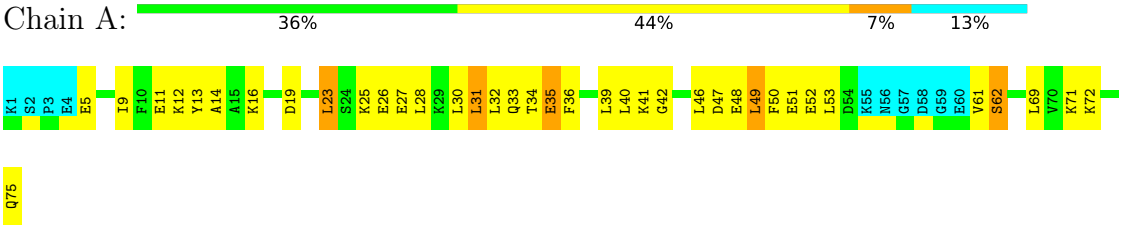
Chain A:



4.2.18 Score per residue for model 18

• Molecule 1: Vitamin D-dependent calcium-binding protein, intestinal

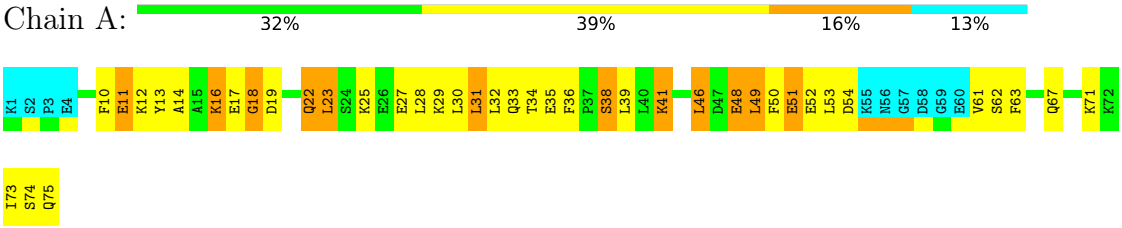
Chain A:



4.2.19 Score per residue for model 19

• Molecule 1: Vitamin D-dependent calcium-binding protein, intestinal

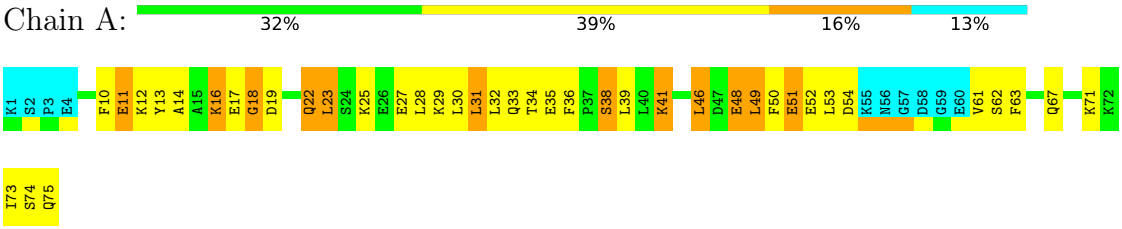
Chain A:



4.2.20 Score per residue for model 20

• Molecule 1: Vitamin D-dependent calcium-binding protein, intestinal

Chain A:



5 Refinement protocol and experimental data overview

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

Of the 200 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
PARAMAGNETIC-DYANA	structure solution	1.0
PSEUDYANA	refinement	3.1

No chemical shift data was provided.

6 Model quality

6.1 Standard geometry

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

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	527	536	536	30±4
All	All	10560	10720	10720	594

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 28.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:49:LEU:HD23	1:A:53:LEU:HD11	1.03	1.28	3	20
1:A:32:LEU:HD11	1:A:49:LEU:HD22	0.84	1.49	1	18
1:A:10:PHE:CE1	1:A:63:PHE:CD2	0.79	2.70	11	4
1:A:10:PHE:CE1	1:A:63:PHE:CE2	0.78	2.71	11	2
1:A:13:TYR:CD2	1:A:31:LEU:HD12	0.73	2.18	3	8
1:A:14:ALA:HB2	1:A:23:LEU:CD2	0.70	2.17	3	20
1:A:36:PHE:CE2	1:A:73:ILE:CG2	0.70	2.75	15	12
1:A:14:ALA:HB2	1:A:23:LEU:HD21	0.69	1.63	9	18
1:A:49:LEU:CD2	1:A:53:LEU:HD11	0.67	2.14	5	12
1:A:9:ILE:HG22	1:A:31:LEU:HD11	0.67	1.66	3	4
1:A:32:LEU:CB	1:A:40:LEU:HD21	0.63	2.23	17	4
1:A:49:LEU:HD21	1:A:69:LEU:HD13	0.63	1.69	17	8

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:10:PHE:CZ	1:A:63:PHE:CD2	0.63	2.87	11	2
1:A:32:LEU:HD12	1:A:46:LEU:CD2	0.62	2.25	17	8
1:A:6:LEU:HD22	1:A:35:GLU:OE2	0.62	1.94	3	2
1:A:49:LEU:HD11	1:A:69:LEU:CD1	0.61	2.25	17	6
1:A:32:LEU:HD12	1:A:46:LEU:HD23	0.60	1.72	17	4
1:A:32:LEU:CD1	1:A:49:LEU:HD22	0.59	2.27	13	14
1:A:63:PHE:CE2	1:A:67:GLN:NE2	0.58	2.71	3	4
1:A:36:PHE:CE2	1:A:73:ILE:HG21	0.57	2.34	11	10
1:A:32:LEU:HB3	1:A:40:LEU:HD21	0.56	1.75	17	2
1:A:13:TYR:CD2	1:A:31:LEU:CD1	0.56	2.88	3	2
1:A:31:LEU:O	1:A:35:GLU:N	0.56	2.39	3	20
1:A:49:LEU:HD21	1:A:69:LEU:HD22	0.56	1.78	15	10
1:A:61:VAL:O	1:A:62:SER:CB	0.56	2.53	17	2
1:A:36:PHE:CE2	1:A:73:ILE:HG23	0.55	2.36	3	10
1:A:49:LEU:HD21	1:A:69:LEU:CD2	0.55	2.32	11	8
1:A:53:LEU:HD13	1:A:61:VAL:HG11	0.54	1.80	19	2
1:A:29:LYS:HA	1:A:46:LEU:HD11	0.53	1.80	19	4
1:A:10:PHE:CZ	1:A:63:PHE:CD1	0.53	2.97	7	2
1:A:30:LEU:O	1:A:33:GLN:CB	0.52	2.58	5	20
1:A:49:LEU:HD11	1:A:69:LEU:HD11	0.51	1.81	5	2
1:A:10:PHE:CZ	1:A:23:LEU:HD21	0.51	2.40	19	14
1:A:10:PHE:CD2	1:A:66:PHE:CD2	0.50	2.99	3	2
1:A:10:PHE:CE2	1:A:23:LEU:HD21	0.50	2.41	19	16
1:A:51:GLU:OE1	1:A:51:GLU:CA	0.49	2.60	15	2
1:A:61:VAL:HG12	1:A:62:SER:N	0.49	2.23	1	6
1:A:10:PHE:CD2	1:A:66:PHE:CE2	0.49	3.00	11	2
1:A:10:PHE:CZ	1:A:63:PHE:HB2	0.49	2.43	19	6
1:A:63:PHE:O	1:A:67:GLN:CG	0.49	2.61	1	4
1:A:63:PHE:CZ	1:A:67:GLN:NE2	0.49	2.80	19	6
1:A:6:LEU:CD2	1:A:35:GLU:OE2	0.49	2.60	15	2
1:A:14:ALA:CB	1:A:23:LEU:CD2	0.48	2.91	9	16
1:A:25:LYS:N	1:A:50:PHE:CE1	0.48	2.81	9	6
1:A:13:TYR:CD1	1:A:31:LEU:HD12	0.48	2.43	11	4
1:A:6:LEU:CD2	1:A:35:GLU:OE1	0.48	2.62	1	2
1:A:16:LYS:CB	1:A:27:GLU:OE2	0.48	2.62	7	8
1:A:10:PHE:CD1	1:A:63:PHE:CD2	0.48	3.01	5	2
1:A:23:LEU:N	1:A:23:LEU:CD2	0.48	2.77	19	2
1:A:6:LEU:HD22	1:A:35:GLU:CD	0.47	2.30	3	2
1:A:49:LEU:HD21	1:A:69:LEU:CD1	0.47	2.39	5	8
1:A:6:LEU:CD2	1:A:35:GLU:CD	0.47	2.83	3	4
1:A:13:TYR:CE1	1:A:30:LEU:HB2	0.47	2.45	19	4

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:69:LEU:CD2	1:A:73:ILE:HD11	0.47	2.39	13	2
1:A:19:ASP:CB	1:A:20:PRO:CD	0.47	2.92	3	4
1:A:63:PHE:CE2	1:A:67:GLN:CD	0.47	2.88	19	4
1:A:25:LYS:HB2	1:A:50:PHE:CZ	0.47	2.45	7	12
1:A:39:LEU:HD12	1:A:49:LEU:HD11	0.47	1.88	3	2
1:A:25:LYS:HB2	1:A:50:PHE:CE1	0.46	2.45	3	12
1:A:32:LEU:O	1:A:36:PHE:C	0.46	2.54	1	20
1:A:10:PHE:CD1	1:A:11:GLU:N	0.46	2.84	19	8
1:A:61:VAL:CG1	1:A:62:SER:N	0.46	2.78	1	2
1:A:25:LYS:HE3	1:A:50:PHE:CE2	0.45	2.46	11	2
1:A:48:GLU:O	1:A:52:GLU:CB	0.45	2.64	19	6
1:A:6:LEU:HD22	1:A:35:GLU:OE1	0.45	2.11	1	2
1:A:17:GLU:N	1:A:27:GLU:OE2	0.45	2.49	7	2
1:A:11:GLU:C	1:A:13:TYR:N	0.44	2.70	19	12
1:A:62:SER:O	1:A:66:PHE:N	0.44	2.50	1	2
1:A:38:SER:O	1:A:41:LYS:CG	0.44	2.65	19	6
1:A:63:PHE:CD1	1:A:63:PHE:C	0.44	2.90	9	2
1:A:13:TYR:O	1:A:16:LYS:N	0.44	2.51	3	6
1:A:10:PHE:CZ	1:A:63:PHE:CB	0.44	3.01	5	2
1:A:10:PHE:CZ	1:A:63:PHE:HA	0.44	2.48	3	2
1:A:23:LEU:N	1:A:61:VAL:O	0.44	2.49	13	2
1:A:53:LEU:HD21	1:A:69:LEU:HB2	0.44	1.89	3	4
1:A:10:PHE:CE1	1:A:63:PHE:CD1	0.43	3.06	3	4
1:A:66:PHE:O	1:A:69:LEU:N	0.43	2.50	13	8
1:A:49:LEU:HD11	1:A:69:LEU:HD13	0.42	1.91	7	2
1:A:22:GLN:C	1:A:23:LEU:CD2	0.42	2.88	19	2
1:A:49:LEU:HD23	1:A:53:LEU:CD1	0.42	2.21	5	2
1:A:25:LYS:HG2	1:A:46:LEU:CD2	0.42	2.45	7	6
1:A:11:GLU:O	1:A:13:TYR:N	0.41	2.53	3	4
1:A:13:TYR:C	1:A:27:GLU:OE1	0.41	2.59	9	2
1:A:25:LYS:HG2	1:A:46:LEU:HD11	0.41	1.90	13	2
1:A:32:LEU:HD11	1:A:49:LEU:CD2	0.41	2.33	1	2
1:A:14:ALA:O	1:A:19:ASP:O	0.41	2.39	7	2
1:A:29:LYS:HD2	1:A:46:LEU:HD13	0.41	1.90	7	2
1:A:45:THR:O	1:A:46:LEU:C	0.41	2.59	11	2
1:A:23:LEU:N	1:A:23:LEU:HD23	0.41	2.30	19	2
1:A:13:TYR:O	1:A:27:GLU:OE2	0.41	2.38	19	10
1:A:31:LEU:C	1:A:33:GLN:N	0.41	2.74	7	16
1:A:14:ALA:O	1:A:17:GLU:O	0.41	2.39	1	2
1:A:32:LEU:O	1:A:36:PHE:O	0.41	2.39	3	4
1:A:25:LYS:CG	1:A:46:LEU:CD2	0.41	2.98	7	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:17:GLU:O	1:A:18:GLY:O	0.41	2.38	19	2
1:A:63:PHE:O	1:A:67:GLN:N	0.41	2.50	19	2
1:A:11:GLU:O	1:A:12:LYS:C	0.41	2.60	3	4
1:A:21:ASN:O	1:A:63:PHE:N	0.41	2.54	13	2
1:A:10:PHE:CE2	1:A:23:LEU:CD2	0.40	3.04	3	2
1:A:25:LYS:HG2	1:A:46:LEU:HD21	0.40	1.93	1	2
1:A:13:TYR:O	1:A:27:GLU:OE1	0.40	2.39	15	4
1:A:62:SER:O	1:A:66:PHE:CB	0.40	2.69	1	2

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	64/75 (85%)	50±2 (78±3%)	13±2 (20±3%)	2±1 (2±1%)	9	48
All	All	1280/1500 (85%)	992 (78%)	258 (20%)	30 (2%)	9	48

All 5 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	42	GLY	12
1	A	18	GLY	10
1	A	19	ASP	4
1	A	62	SER	2
1	A	54	ASP	2

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	60/68 (88%)	41±2 (69±3%)	19±2 (31±3%)	1 14
All	All	1200/1360 (88%)	826 (69%)	374 (31%)	1 14

All 36 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	19	ASP	20
1	A	23	LEU	20
1	A	31	LEU	20
1	A	34	THR	20
1	A	39	LEU	20
1	A	49	LEU	20
1	A	11	GLU	18
1	A	26	GLU	18
1	A	71	LYS	18
1	A	75	GLN	18
1	A	41	LYS	16
1	A	5	GLU	14
1	A	38	SER	14
1	A	47	ASP	14
1	A	62	SER	14
1	A	7	LYS	12
1	A	28	LEU	12
1	A	16	LYS	12
1	A	25	LYS	10
1	A	48	GLU	10
1	A	74	SER	10
1	A	46	LEU	8
1	A	12	LYS	6
1	A	51	GLU	6
1	A	29	LYS	2
1	A	64	GLU	2
1	A	52	GLU	2
1	A	63	PHE	2
1	A	24	SER	2
1	A	27	GLU	2
1	A	33	GLN	2
1	A	43	MET	2
1	A	54	ASP	2
1	A	35	GLU	2
1	A	72	LYS	2
1	A	22	GLN	2

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

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

6.7 Other polymers

There are no such molecules in this entry.

6.8 Polymer linkage issues

There are no chain breaks in this entry.

7 Chemical shift validation (i)

No chemical shift data were provided