



Full wwPDB NMR Structure Validation Report ⓘ

Apr 27, 2016 – 01:03 AM BST

PDB ID : 2LKG
Title : WSA major conformation
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Deposited on : 2011-10-11

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
Mogul : unknown
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
ShiftChecker : rb-20027457
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20027457

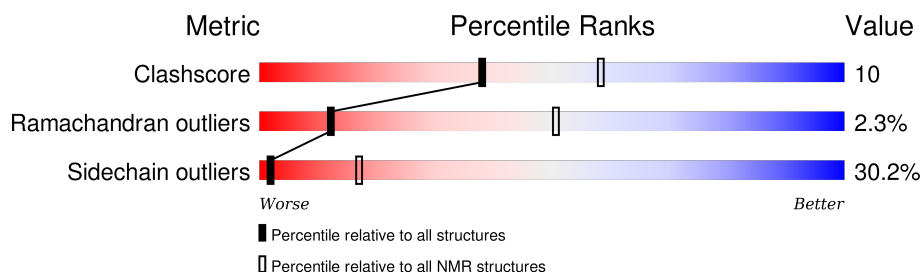
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 72%.

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	114402	11133
Ramachandran outliers	111179	9975
Sidechain outliers	111093	9958

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	140	 52% 35% • 9%

2 Ensemble composition and analysis ⓘ

This entry contains 15 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:8-A:135 (128)	0.59	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 1 single-model cluster was found.

Cluster number	Models
1	1, 4, 5, 6, 9, 10, 12, 13, 14, 15
2	3, 7
3	8, 11
Single-model clusters	2

3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 2207 atoms, of which 1118 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Acetylcholine receptor.

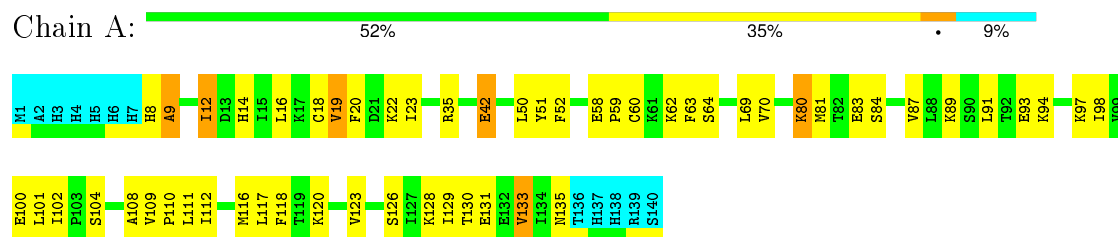
Mol	Chain	Residues	Atoms						Trace
1	A	140	Total	C	H	N	O	S	0
			2207	699	1118	181	202	7	

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: Acetylcholine receptor

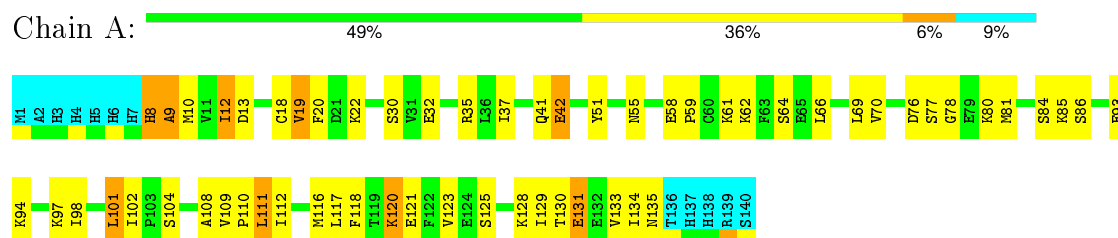


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

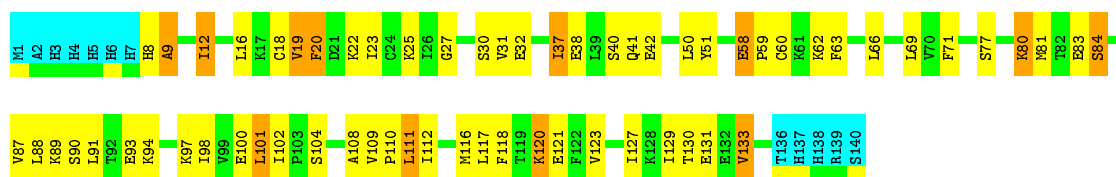
- Molecule 1: Acetylcholine receptor



4.2.2 Score per residue for model 2

- Molecule 1: Acetylcholine receptor

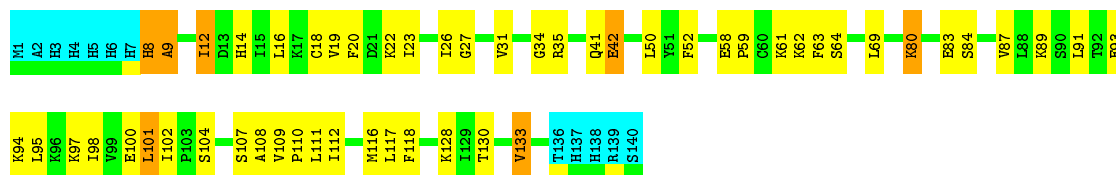




4.2.3 Score per residue for model 3

- Molecule 1: Acetylcholine receptor

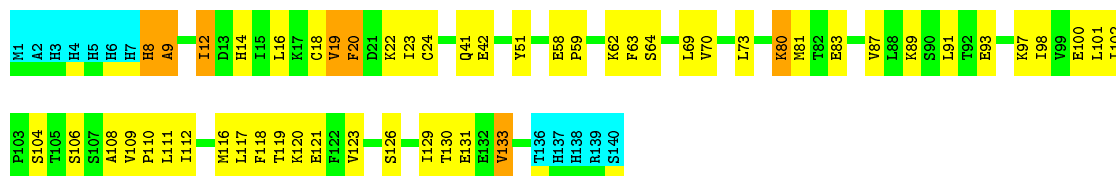
Chain A:



4.2.4 Score per residue for model 4

- Molecule 1: Acetylcholine receptor

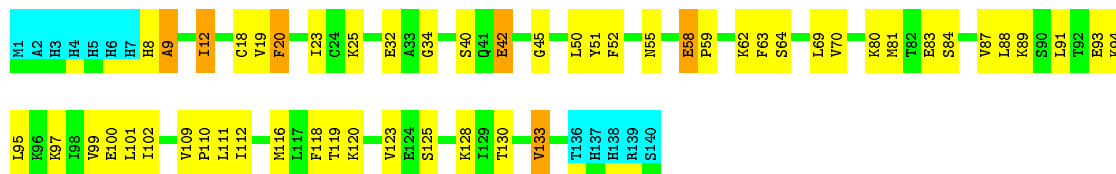
Chain A:



4.2.5 Score per residue for model 5

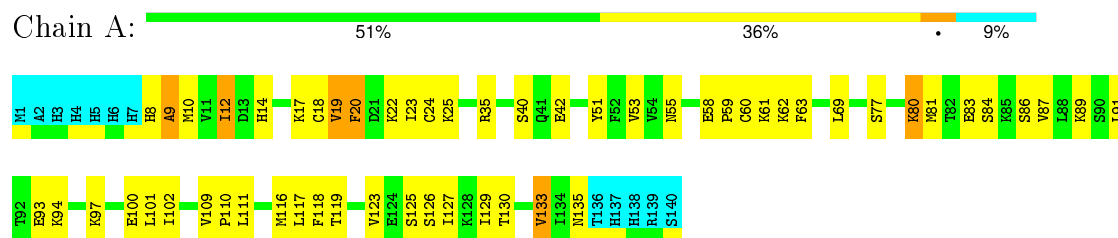
- Molecule 1: Acetylcholine receptor

Chain A:



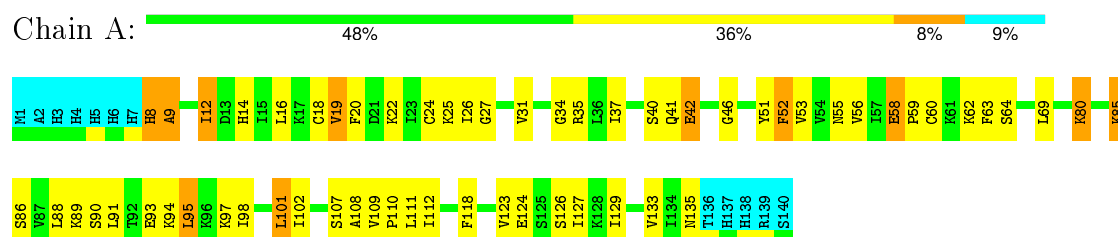
4.2.6 Score per residue for model 6 (medoid)

- Molecule 1: Acetylcholine receptor



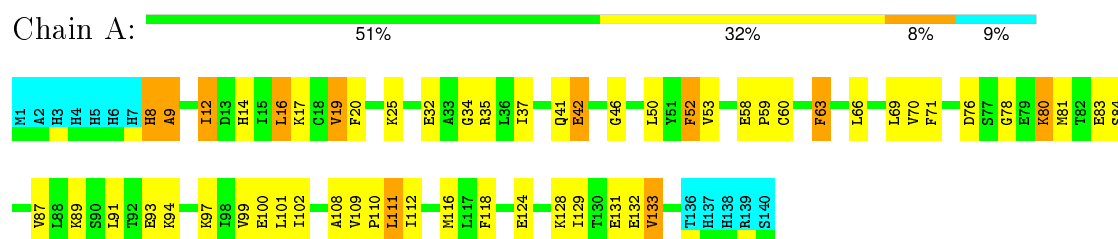
4.2.7 Score per residue for model 7

- Molecule 1: Acetylcholine receptor



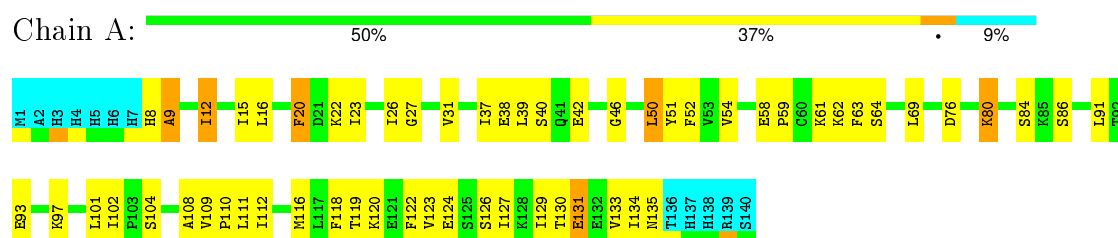
4.2.8 Score per residue for model 8

- Molecule 1: Acetylcholine receptor



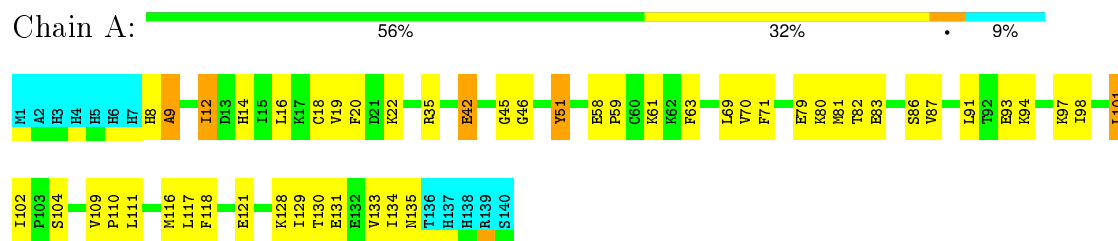
4.2.9 Score per residue for model 9

- Molecule 1: Acetylcholine receptor



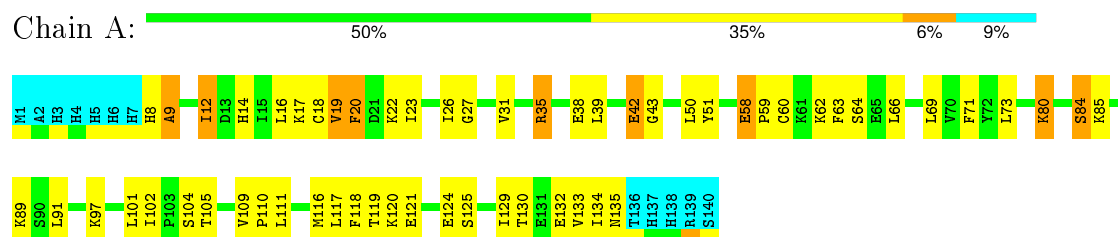
4.2.10 Score per residue for model 10

- Molecule 1: Acetylcholine receptor



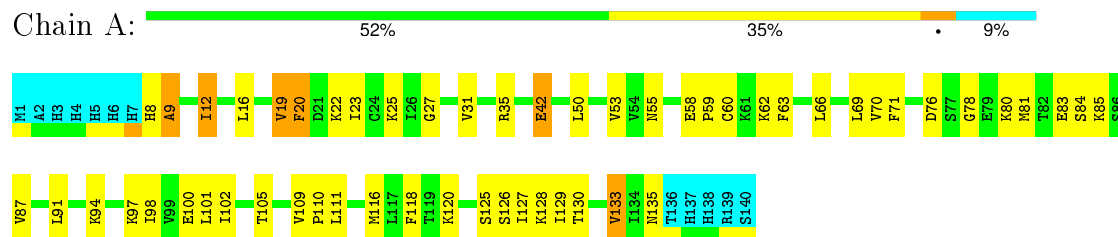
4.2.11 Score per residue for model 11

- Molecule 1: Acetylcholine receptor



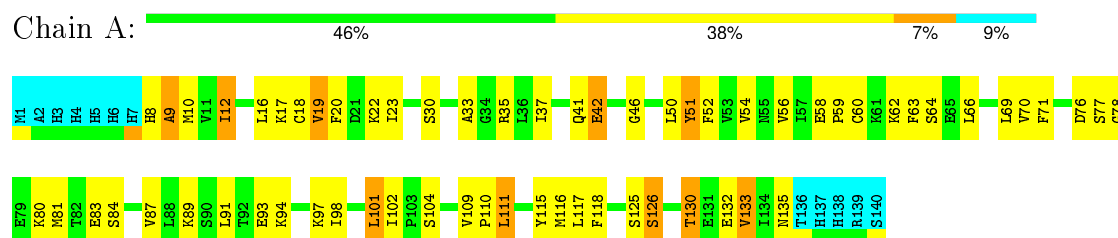
4.2.12 Score per residue for model 12

- Molecule 1: Acetylcholine receptor



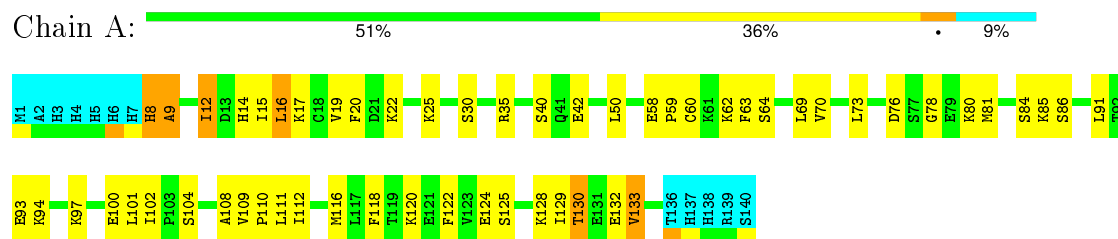
4.2.13 Score per residue for model 13

- Molecule 1: Acetylcholine receptor



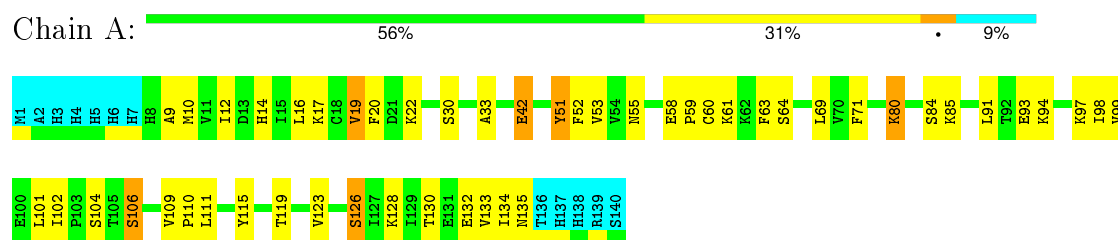
4.2.14 Score per residue for model 14

- Molecule 1: Acetylcholine receptor



4.2.15 Score per residue for model 15

- Molecule 1: Acetylcholine receptor



5 Refinement protocol and experimental data overview

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

Of the 100 calculated structures, 15 were deposited, based on the following criterion: *target function*.

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

Software name	Classification	Version
CYANA	structure solution	
CYANA	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)	2lkg_cs.str
Number of chemical shift lists	1
Total number of shifts	1306
Number of shifts mapped to atoms	1306
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	72%

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	982	1030	1030	19±4
All	All	14730	15450	15450	292

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 10.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:19:VAL:HG21	1:A:129:ILE:HD11	0.98	1.35	10	1
1:A:37:ILE:HG23	1:A:111:LEU:HD13	0.83	1.51	1	4
1:A:19:VAL:HG23	1:A:129:ILE:HD12	0.82	1.48	4	8
1:A:59:PRO:HG3	1:A:91:LEU:HD13	0.65	1.68	13	9
1:A:27:GLY:O	1:A:31:VAL:HG23	0.63	1.93	11	6
1:A:130:THR:O	1:A:134:ILE:HG23	0.63	1.94	15	1
1:A:19:VAL:CG2	1:A:129:ILE:HD12	0.63	2.24	8	4
1:A:15:ILE:HG21	1:A:129:ILE:HG21	0.62	1.71	14	1
1:A:59:PRO:HG2	1:A:91:LEU:HD22	0.62	1.72	9	5
1:A:70:VAL:CG1	1:A:130:THR:HG21	0.62	2.25	12	1
1:A:83:GLU:O	1:A:87:VAL:HG23	0.61	1.95	12	9
1:A:37:ILE:CG2	1:A:111:LEU:HD13	0.61	2.25	8	3
1:A:59:PRO:CG	1:A:91:LEU:HD13	0.60	2.25	7	2
1:A:69:LEU:HD23	1:A:80:LYS:HD2	0.60	1.73	5	11

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:119:THR:O	1:A:123:VAL:HG23	0.60	1.95	6	5
1:A:59:PRO:CG	1:A:91:LEU:HD22	0.60	2.27	4	4
1:A:88:LEU:CD1	1:A:123:VAL:HG11	0.60	2.27	2	1
1:A:88:LEU:HD13	1:A:123:VAL:HG11	0.60	1.73	2	1
1:A:41:GLN:NE2	1:A:111:LEU:HD12	0.59	2.12	13	2
1:A:124:GLU:CG	1:A:127:ILE:HD11	0.58	2.28	7	1
1:A:66:LEU:HD13	1:A:84:SER:OG	0.58	1.97	1	1
1:A:88:LEU:CD1	1:A:123:VAL:HG21	0.58	2.29	7	2
1:A:20:PHE:HA	1:A:23:ILE:HD12	0.58	1.76	12	9
1:A:70:VAL:HG21	1:A:81:MET:HG2	0.58	1.73	10	8
1:A:37:ILE:HG12	1:A:111:LEU:HD22	0.57	1.77	8	1
1:A:34:GLY:HA2	1:A:112:ILE:HD12	0.57	1.74	8	4
1:A:66:LEU:HD13	1:A:84:SER:HA	0.56	1.77	2	1
1:A:41:GLN:CD	1:A:108:ALA:HB2	0.56	2.20	3	1
1:A:51:TYR:CE2	1:A:98:ILE:HD13	0.56	2.35	13	3
1:A:19:VAL:HG21	1:A:126:SER:HA	0.56	1.76	13	3
1:A:35:ARG:O	1:A:39:LEU:HD23	0.56	2.00	11	1
1:A:59:PRO:HG2	1:A:91:LEU:HD13	0.56	1.76	3	2
1:A:12:ILE:CD1	1:A:133:VAL:HG21	0.55	2.32	4	6
1:A:16:LEU:HD12	1:A:71:PHE:HB2	0.55	1.78	12	1
1:A:88:LEU:HD12	1:A:123:VAL:HG21	0.54	1.78	5	1
1:A:8:HIS:HB3	1:A:12:ILE:HD13	0.53	1.80	2	10
1:A:131:GLU:O	1:A:134:ILE:HG22	0.53	2.04	10	3
1:A:12:ILE:HD11	1:A:133:VAL:HG21	0.52	1.80	12	3
1:A:79:GLU:O	1:A:82:THR:HG22	0.51	2.06	10	1
1:A:66:LEU:HD13	1:A:84:SER:CB	0.51	2.36	1	1
1:A:124:GLU:O	1:A:127:ILE:HD12	0.51	2.06	9	1
1:A:16:LEU:HD13	1:A:71:PHE:CD1	0.50	2.41	11	3
1:A:16:LEU:HD23	1:A:17:LYS:N	0.50	2.21	8	2
1:A:109:VAL:N	1:A:110:PRO:HD2	0.49	2.22	3	15
1:A:19:VAL:HG21	1:A:129:ILE:CD1	0.49	2.25	10	1
1:A:70:VAL:HG21	1:A:81:MET:CG	0.49	2.38	13	4
1:A:85:LYS:HG3	1:A:123:VAL:HG11	0.48	1.86	7	1
1:A:69:LEU:HD23	1:A:80:LYS:CD	0.48	2.38	2	3
1:A:81:MET:SD	1:A:127:ILE:HG22	0.48	2.48	12	3
1:A:120:LYS:O	1:A:123:VAL:HG12	0.47	2.10	1	2
1:A:59:PRO:HG3	1:A:91:LEU:HD22	0.47	1.85	4	1
1:A:37:ILE:CG1	1:A:111:LEU:HD22	0.47	2.40	8	1
1:A:58:GLU:N	1:A:59:PRO:HD2	0.47	2.25	1	15
1:A:41:GLN:NE2	1:A:108:ALA:HB2	0.47	2.25	3	1
1:A:19:VAL:HG23	1:A:129:ILE:CD1	0.47	2.40	1	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:16:LEU:HD12	1:A:71:PHE:CB	0.47	2.39	8	3
1:A:58:GLU:CB	1:A:59:PRO:CD	0.46	2.93	2	15
1:A:130:THR:O	1:A:133:VAL:HG12	0.46	2.11	2	5
1:A:56:VAL:HA	1:A:91:LEU:HD11	0.46	1.86	7	1
1:A:63:PHE:CD1	1:A:87:VAL:HG11	0.46	2.46	8	1
1:A:16:LEU:HD13	1:A:71:PHE:CG	0.46	2.46	11	2
1:A:88:LEU:HD11	1:A:123:VAL:HG21	0.46	1.87	2	1
1:A:101:LEU:HB3	1:A:102:ILE:HD12	0.45	1.89	15	15
1:A:37:ILE:HG22	1:A:108:ALA:HB1	0.45	1.89	7	1
1:A:69:LEU:HD23	1:A:80:LYS:CE	0.45	2.41	2	1
1:A:124:GLU:HG3	1:A:127:ILE:HD11	0.45	1.87	7	1
1:A:52:PHE:CE1	1:A:95:LEU:HD11	0.45	2.47	7	1
1:A:66:LEU:HD22	1:A:80:LYS:HD3	0.45	1.89	12	3
1:A:41:GLN:CG	1:A:108:ALA:HB2	0.45	2.41	7	1
1:A:41:GLN:HG3	1:A:108:ALA:HB2	0.44	1.89	7	2
1:A:71:PHE:CZ	1:A:129:ILE:HD13	0.44	2.46	10	1
1:A:56:VAL:HG23	1:A:91:LEU:HD21	0.44	1.89	13	1
1:A:41:GLN:OE1	1:A:108:ALA:HB2	0.43	2.13	1	2
1:A:15:ILE:HG22	1:A:129:ILE:CD1	0.43	2.44	9	1
1:A:39:LEU:HD13	1:A:43:GLY:O	0.43	2.13	11	1
1:A:124:GLU:HG2	1:A:127:ILE:HD11	0.43	1.88	7	1
1:A:45:GLY:HA3	1:A:102:ILE:HG21	0.43	1.89	5	1
1:A:91:LEU:HD12	1:A:91:LEU:O	0.43	2.14	3	1
1:A:9:ALA:CA	1:A:12:ILE:HG22	0.43	2.44	1	14
1:A:66:LEU:HD12	1:A:84:SER:HA	0.43	1.91	11	1
1:A:91:LEU:O	1:A:91:LEU:HD12	0.42	2.15	7	2
1:A:99:VAL:HG22	1:A:106:SER:HB2	0.42	1.92	15	1
1:A:69:LEU:HD11	1:A:73:LEU:HD12	0.41	1.91	4	1
1:A:33:ALA:HB1	1:A:115:TYR:CZ	0.41	2.50	15	1
1:A:34:GLY:CA	1:A:112:ILE:HD12	0.41	2.44	7	1
1:A:108:ALA:O	1:A:112:ILE:HG22	0.41	2.16	2	5
1:A:41:GLN:HE21	1:A:111:LEU:HD12	0.41	1.73	13	1
1:A:33:ALA:HB1	1:A:115:TYR:CE2	0.41	2.50	13	1
1:A:26:ILE:CG2	1:A:119:THR:HG23	0.41	2.45	11	1
1:A:52:PHE:CD2	1:A:53:VAL:HG23	0.41	2.51	8	1
1:A:50:LEU:O	1:A:54:VAL:HG23	0.40	2.15	13	2
1:A:16:LEU:HD22	1:A:71:PHE:CB	0.40	2.46	2	1

6.3 Torsion angles [i](#)

6.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all NMR entries. The Analysed column shows the number of residues for which the backbone conformation was analysed and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	128/140 (91%)	119±2 (93±1%)	6±1 (5±1%)	3±1 (2±1%)	12	51
All	All	1920/2100 (91%)	1788 (93%)	87 (5%)	45 (2%)	12	51

All 6 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	42	GLU	15
1	A	9	ALA	15
1	A	46	GLY	5
1	A	78	GLY	5
1	A	8	HIS	4
1	A	45	GLY	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	114/125 (91%)	80±4 (70±3%)	34±4 (30±3%)	2	17
All	All	1710/1875 (91%)	1194 (70%)	516 (30%)	2	17

All 74 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	133	VAL	15
1	A	97	LYS	15
1	A	12	ILE	15
1	A	111	LEU	15

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Mol	Chain	Res	Type	Models (Total)
1	A	118	PHE	14
1	A	63	PHE	14
1	A	93	GLU	13
1	A	22	LYS	13
1	A	20	PHE	13
1	A	116	MET	13
1	A	19	VAL	13
1	A	94	LYS	12
1	A	62	LYS	12
1	A	51	TYR	11
1	A	84	SER	11
1	A	80	LYS	10
1	A	35	ARG	10
1	A	104	SER	10
1	A	18	CYS	10
1	A	42	GLU	10
1	A	64	SER	10
1	A	135	ASN	9
1	A	14	HIS	9
1	A	89	LYS	9
1	A	60	CYS	9
1	A	100	GLU	8
1	A	50	LEU	8
1	A	130	THR	8
1	A	128	LYS	8
1	A	120	LYS	8
1	A	117	LEU	8
1	A	52	PHE	7
1	A	125	SER	7
1	A	25	LYS	7
1	A	40	SER	6
1	A	76	ASP	6
1	A	55	ASN	6
1	A	98	ILE	6
1	A	86	SER	6
1	A	8	HIS	6
1	A	61	LYS	6
1	A	16	LEU	6
1	A	101	LEU	6
1	A	85	LYS	6
1	A	126	SER	6
1	A	131	GLU	5

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Mol	Chain	Res	Type	Models (Total)
1	A	132	GLU	5
1	A	30	SER	5
1	A	121	GLU	5
1	A	77	SER	4
1	A	32	GLU	4
1	A	10	MET	4
1	A	17	LYS	4
1	A	69	LEU	4
1	A	58	GLU	4
1	A	53	VAL	4
1	A	91	LEU	3
1	A	26	ILE	3
1	A	95	LEU	3
1	A	24	CYS	3
1	A	38	GLU	3
1	A	124	GLU	3
1	A	73	LEU	2
1	A	106	SER	2
1	A	90	SER	2
1	A	107	SER	2
1	A	122	PHE	2
1	A	99	VAL	2
1	A	37	ILE	2
1	A	105	THR	2
1	A	13	ASP	1
1	A	39	LEU	1
1	A	134	ILE	1
1	A	41	GLN	1

6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

6.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

6.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.6 Ligand geometry

There are no ligands in this entry.

6.7 Other polymers

There are no such molecules in this entry.

6.8 Polymer linkage issues

There are no chain breaks in this entry.

7 Chemical shift validation

The completeness of assignment taking into account all chemical shift lists is 72% for the well-defined parts and 67% for the entire structure.

7.1 Chemical shift list 1

File name: 2lkg_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	1306
Number of shifts mapped to atoms	1306
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
$^{13}\text{C}_\alpha$	129	-0.92 ± 0.15	Should be applied
$^{13}\text{C}_\beta$	104	0.34 ± 0.06	None needed (< 0.5 ppm)
$^{13}\text{C}'$	0	—	—
^{15}N	122	0.93 ± 0.17	Should be applied

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 72%, i.e. 1106 atoms were assigned a chemical shift out of a possible 1538. 0 out of 25 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	479/630 (76%)	238/251 (95%)	124/256 (48%)	117/123 (95%)
Sidechain	599/816 (73%)	386/476 (81%)	207/320 (65%)	6/20 (30%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	28/92 (30%)	26/50 (52%)	2/40 (5%)	0/2 (0%)
Overall	1106/1538 (72%)	650/777 (84%)	333/616 (54%)	123/145 (85%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 67%, i.e. 1146 atoms were assigned a chemical shift out of a possible 1703. 0 out of 25 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	499/690 (72%)	248/275 (90%)	129/280 (46%)	122/135 (90%)
Sidechain	618/872 (71%)	399/511 (78%)	213/338 (63%)	6/23 (26%)
Aromatic	29/141 (21%)	27/78 (35%)	2/54 (4%)	0/9 (0%)
Overall	1146/1703 (67%)	674/864 (78%)	344/672 (51%)	128/167 (77%)

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:

