Full wwPDB NMR Structure Validation Report (i)

Apr 27, 2016 – 01:37 AM BST

PDB ID	:	2LSJ
Title	:	Solution structure of the mouse Rev1 CTD in complex with the Rev1-interacting Region (RIR)of Pol Kappa
Authors	:	Liu, J.; Wojtaszek, J.; Zhou, P.
Deposited on	:	2012-05-01

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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

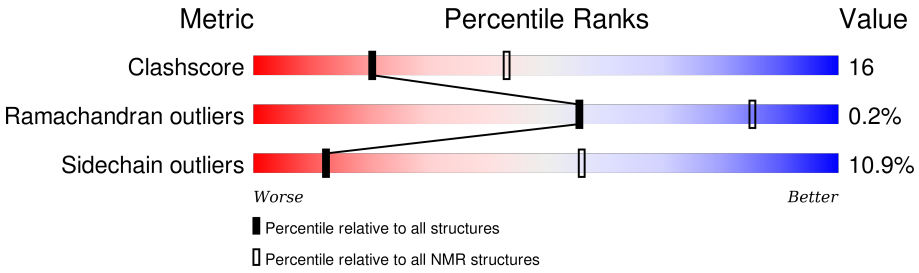
Cyrange	:	Kirchner and Güntert (2011)
NmrClust	:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Mogul	:	unknown
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	rb-20027457
Ideal 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 (i)

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

The overall completeness of chemical shifts assignment is 84%.

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 <=5%

Mol	Chain	Length	Quality of chain
1	A	119	48% 28% • • 18%
2	B	25	20% 8% 28% 44%

2 Ensemble composition and analysis

This entry contains 20 models. Model 12 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *lowest energy*.

The following residues are included in the computation of the global validation metrics.

Well-defined (core) protein residues			
Well-defined core	**Residue range (total)**	**Backbone RMSD (Å)**	**Medoid model**
1	A:25-A:116, B:208-B:214 (99)	0.15	12

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 4 clusters. No single-model clusters were found.

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

3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 1822 atoms, of which 919 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called DNA repair protein REV1.

Mol	Chain	Residues	Atoms						Trace
1	A	97	Total	C	H	N	O	S	0
			1575	502	794	121	153	5	

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	EXPRESSION TAG	UNP Q920Q2
A	2	SER	-	EXPRESSION TAG	UNP Q920Q2
A	3	GLY	-	EXPRESSION TAG	UNP Q920Q2
A	4	GLY	-	EXPRESSION TAG	UNP Q920Q2

- Molecule 2 is a protein called DNA polymerase kappa.

Mol	Chain	Residues	Atoms					Trace
2	B	14	Total	C	H	N	O	0
			247	76	125	24	22	

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	201	SER	-	EXPRESSION TAG	UNP Q9QUG2
B	202	HIS	-	EXPRESSION TAG	UNP Q9QUG2

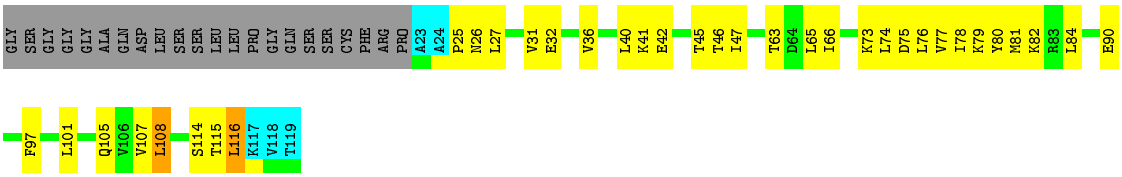
4 Residue-property plots

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.

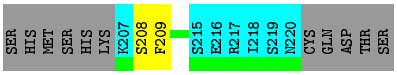
• Molecule 1: DNA repair protein REV1

Chain A:



• Molecule 2: DNA polymerase kappa

Chain B:



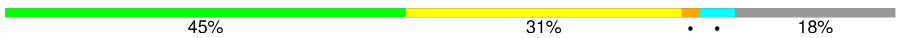
4.2 Scores per residue for each member of the ensemble

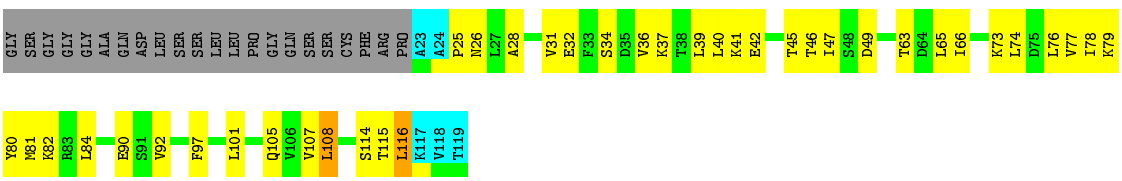
Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

• Molecule 1: DNA repair protein REV1

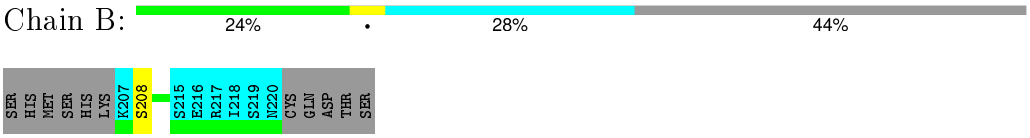
Chain A:





• Molecule 2: DNA polymerase kappa

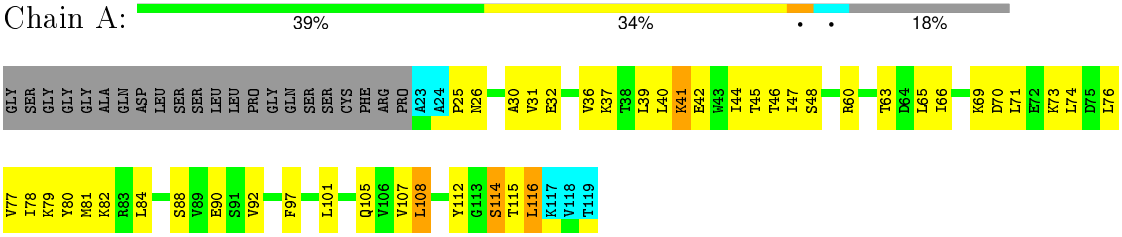
Chain B:



4.2.2 Score per residue for model 2

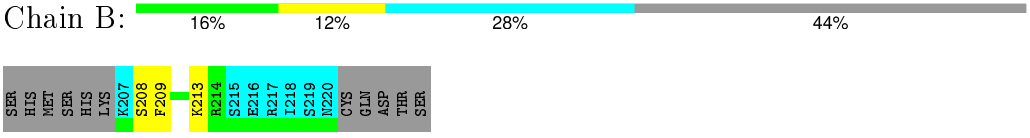
- Molecule 1: DNA repair protein REV1

Chain A:



- Molecule 2: DNA polymerase kappa

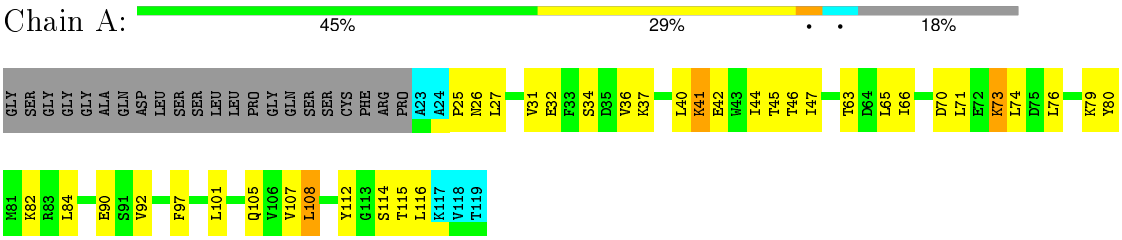
Chain B:



4.2.3 Score per residue for model 3

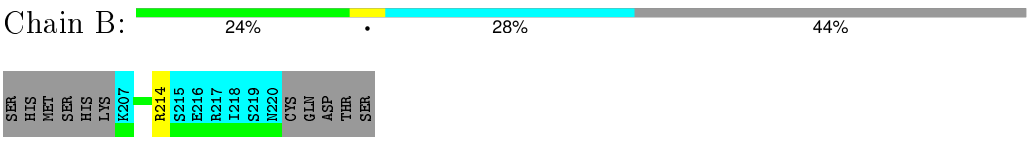
- Molecule 1: DNA repair protein REV1

Chain A:



- Molecule 2: DNA polymerase kappa

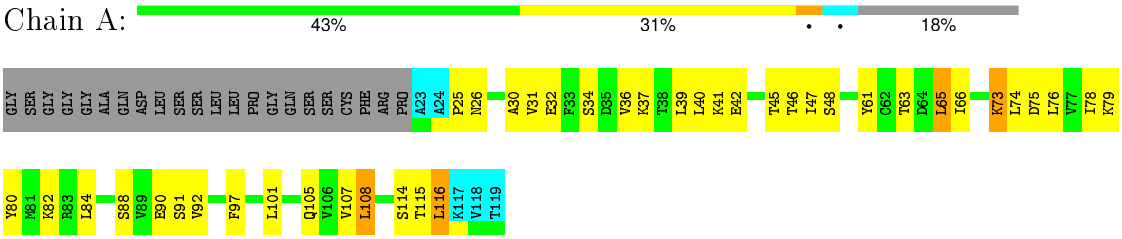
Chain B:



4.2.4 Score per residue for model 4

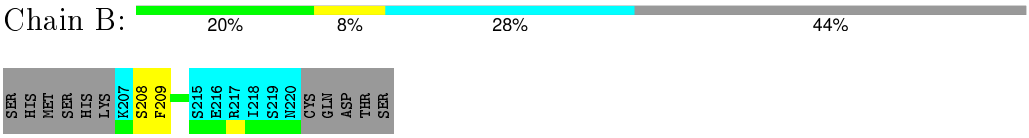
- Molecule 1: DNA repair protein REV1

Chain A:



- Molecule 2: DNA polymerase kappa

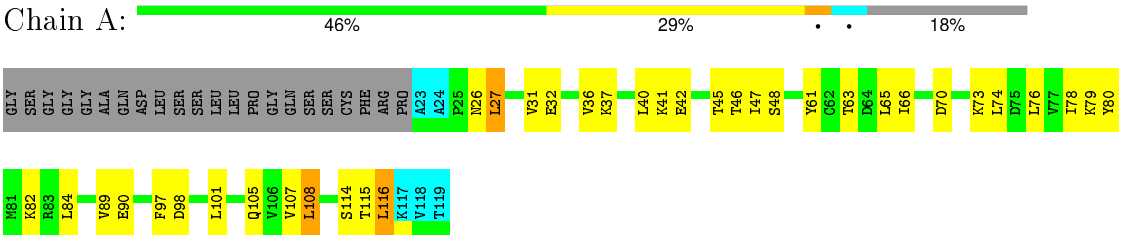
Chain B:



4.2.5 Score per residue for model 5

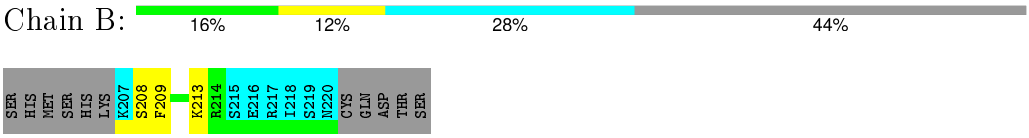
- Molecule 1: DNA repair protein REV1

Chain A:



- Molecule 2: DNA polymerase kappa

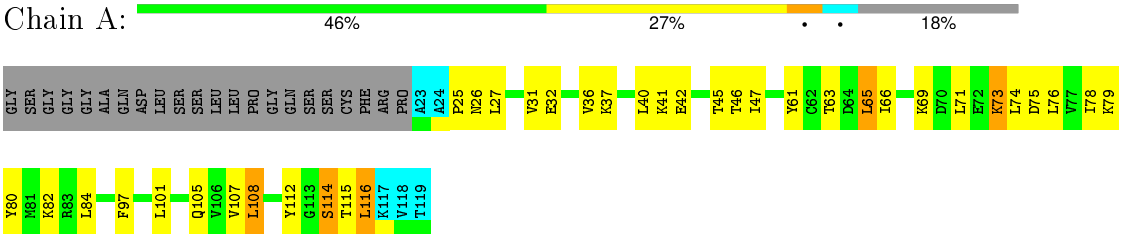
Chain B:



4.2.6 Score per residue for model 6

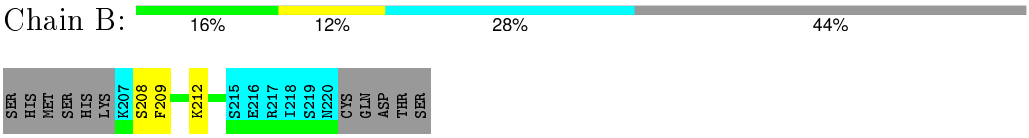
- Molecule 1: DNA repair protein REV1

Chain A:



- Molecule 2: DNA polymerase kappa

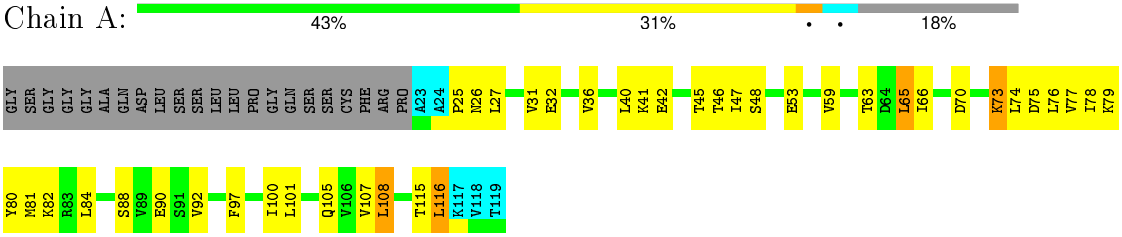
Chain B:



4.2.7 Score per residue for model 7

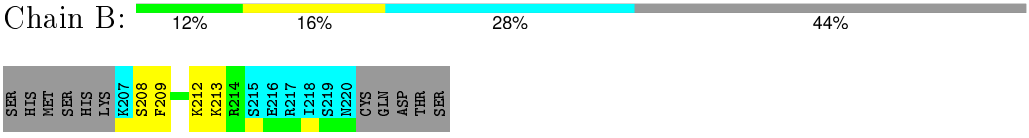
- Molecule 1: DNA repair protein REV1

Chain A:



- Molecule 2: DNA polymerase kappa

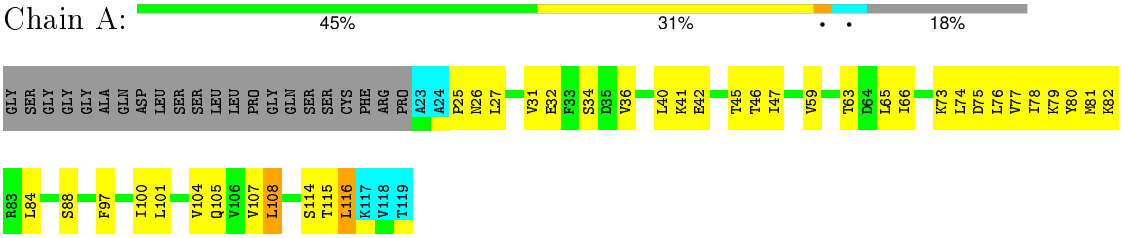
Chain B:



4.2.8 Score per residue for model 8

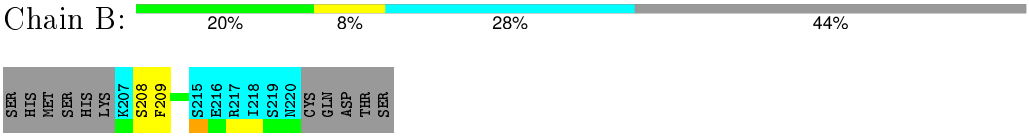
- Molecule 1: DNA repair protein REV1

Chain A:



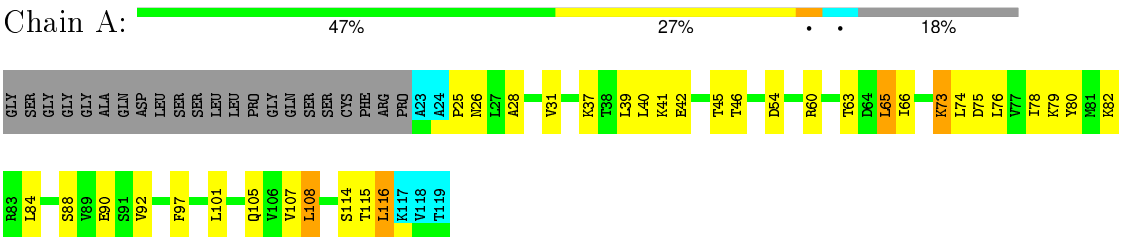
- Molecule 2: DNA polymerase kappa

Chain B:

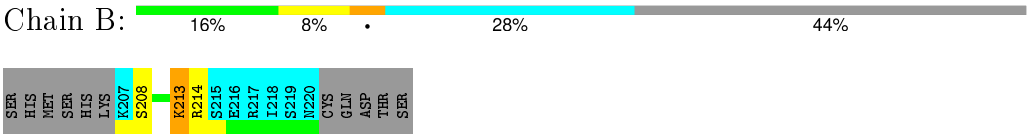


4.2.9 Score per residue for model 9

- Molecule 1: DNA repair protein REV1

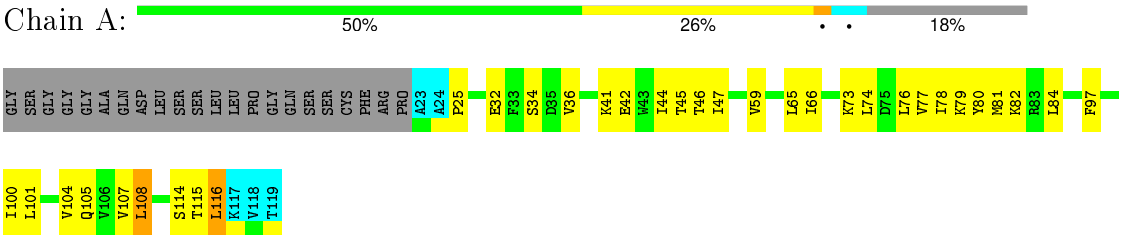


• Molecule 2: DNA polymerase kappa

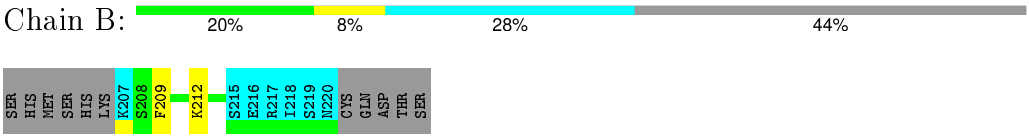


4.2.10 Score per residue for model 10

• Molecule 1: DNA repair protein REV1

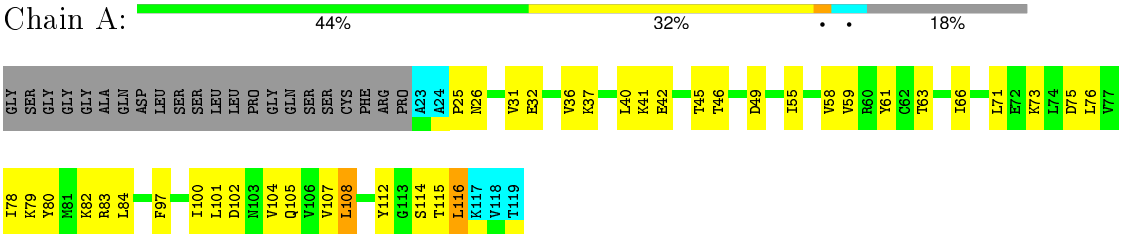


• Molecule 2: DNA polymerase kappa



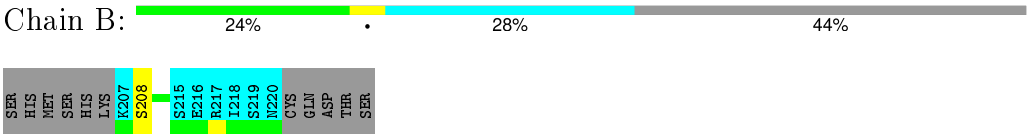
4.2.11 Score per residue for model 11

• Molecule 1: DNA repair protein REV1



• Molecule 2: DNA polymerase kappa

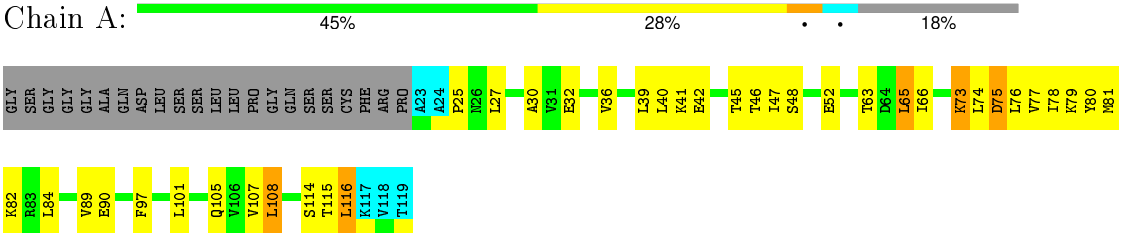
Chain B:



4.2.12 Score per residue for model 12 (medoid)

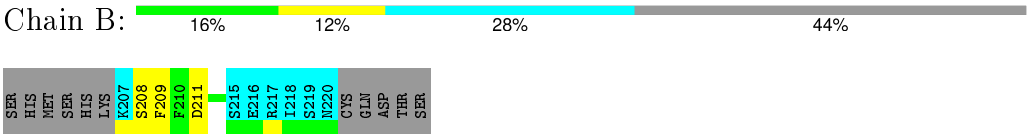
- Molecule 1: DNA repair protein REV1

Chain A:



- Molecule 2: DNA polymerase kappa

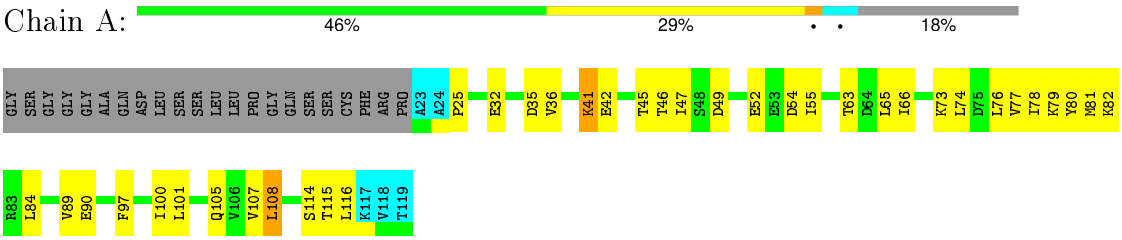
Chain B:



4.2.13 Score per residue for model 13

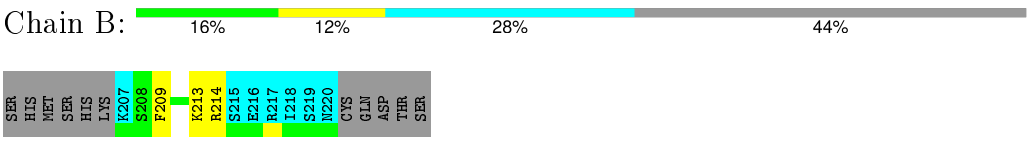
- Molecule 1: DNA repair protein REV1

Chain A:



- Molecule 2: DNA polymerase kappa

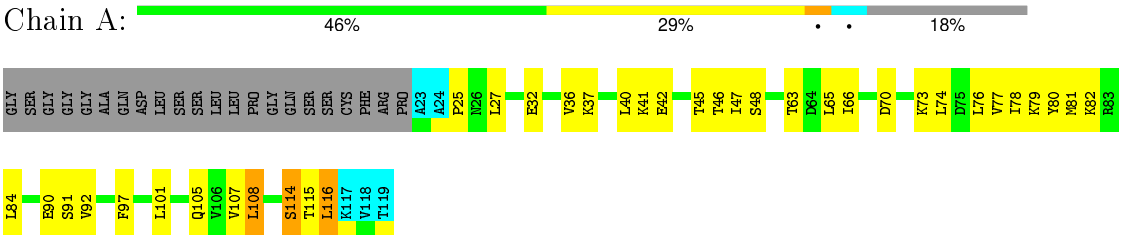
Chain B:



4.2.14 Score per residue for model 14

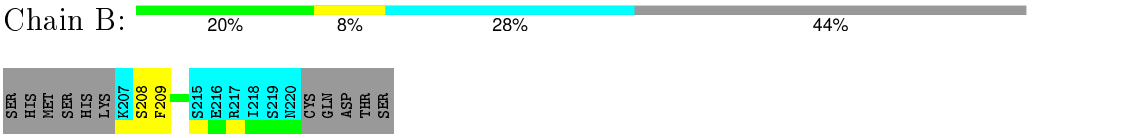
- Molecule 1: DNA repair protein REV1

Chain A:



- Molecule 2: DNA polymerase kappa

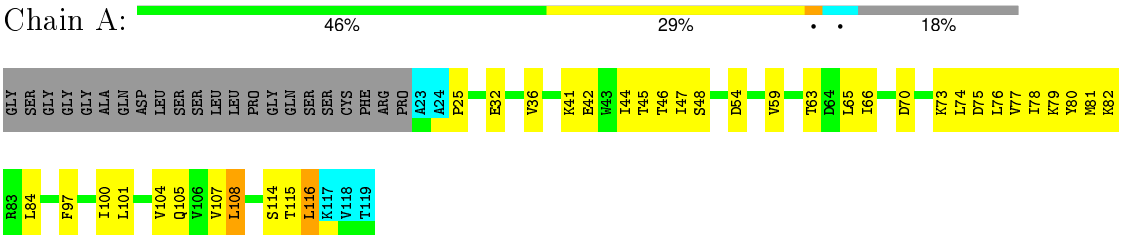
Chain B:



4.2.15 Score per residue for model 15

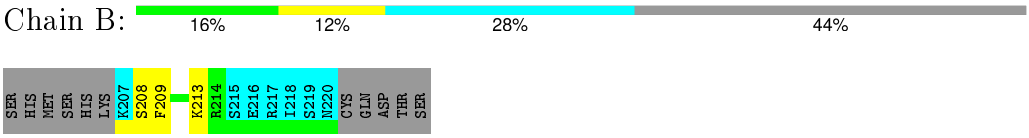
- Molecule 1: DNA repair protein REV1

Chain A:



- Molecule 2: DNA polymerase kappa

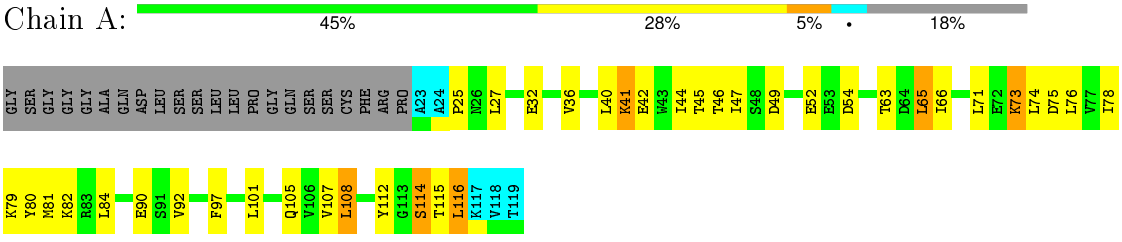
Chain B:



4.2.16 Score per residue for model 16

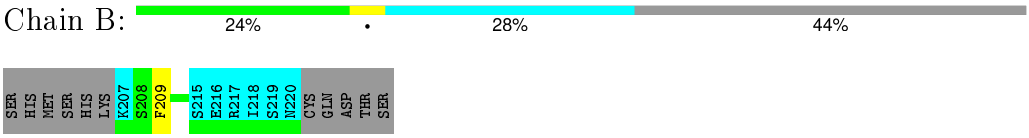
- Molecule 1: DNA repair protein REV1

Chain A:



- Molecule 2: DNA polymerase kappa

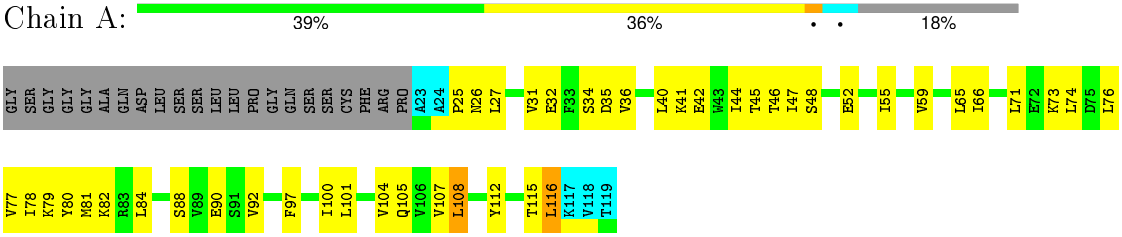
Chain B:



4.2.17 Score per residue for model 17

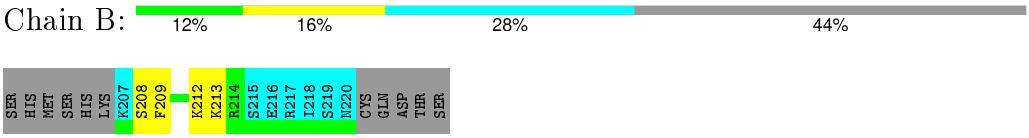
- Molecule 1: DNA repair protein REV1

Chain A:



- Molecule 2: DNA polymerase kappa

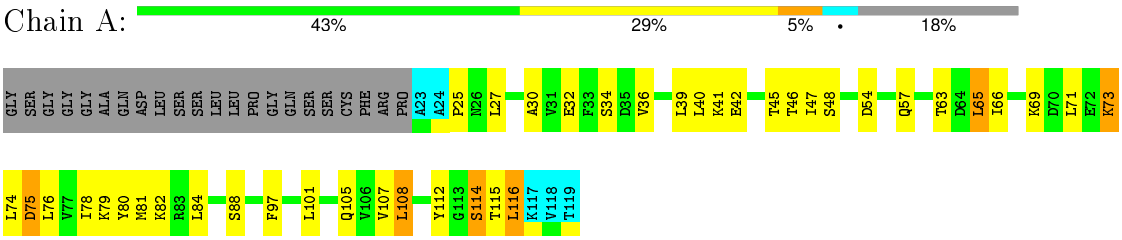
Chain B:



4.2.18 Score per residue for model 18

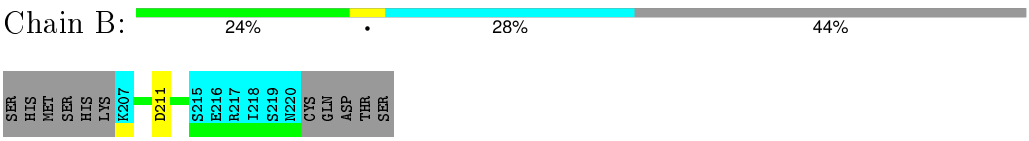
- Molecule 1: DNA repair protein REV1

Chain A:



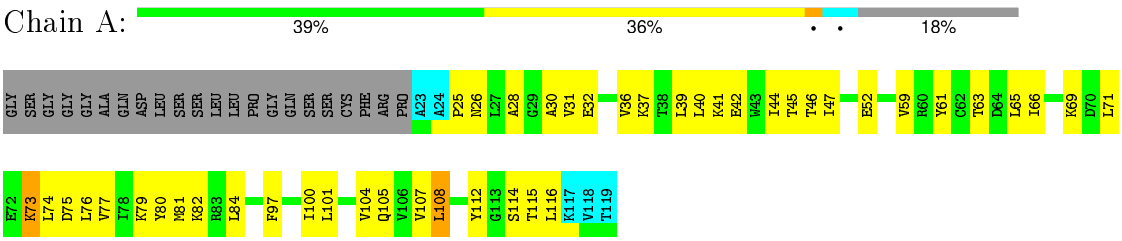
- Molecule 2: DNA polymerase kappa

Chain B:

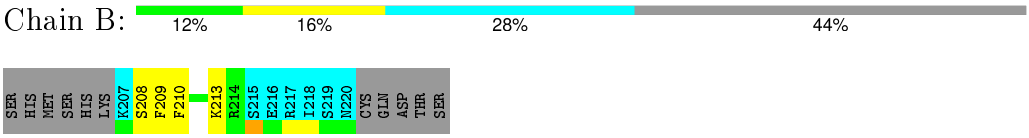


4.2.19 Score per residue for model 19

- Molecule 1: DNA repair protein REV1

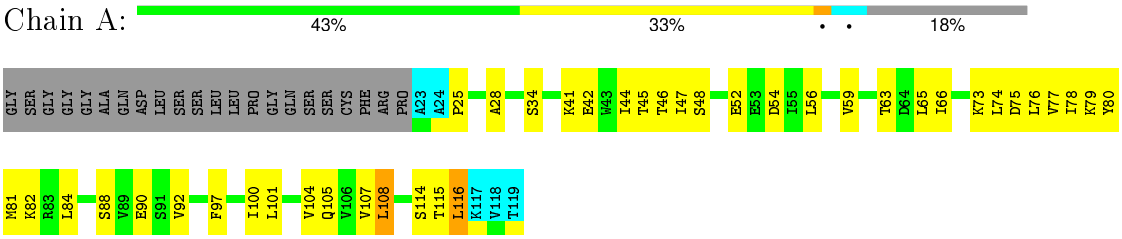


• Molecule 2: DNA polymerase kappa

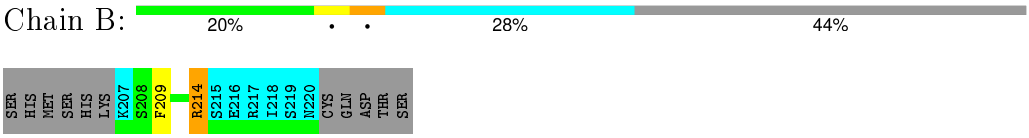


4.2.20 Score per residue for model 20

• Molecule 1: DNA repair protein REV1



• Molecule 2: DNA polymerase kappa



5 Refinement protocol and experimental data overview

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

Of the 100 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
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)	2lsj_cs.str
Number of chemical shift lists	1
Total number of shifts	1552
Number of shifts mapped to atoms	1552
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	84%

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	748	755	755	26±3
2	B	65	66	66	1±1
All	All	16260	16420	16420	523

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 16.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:78:ILE:HG21	1:A:116:LEU:HD22	0.78	1.54	2	16
1:A:97:PHE:CZ	1:A:101:LEU:HD11	0.71	2.21	7	20
1:A:42:GLU:O	1:A:46:THR:HG22	0.68	1.89	9	20
1:A:63:THR:HG22	1:A:107:VAL:HG11	0.67	1.66	9	15
1:A:28:ALA:HB3	1:A:39:LEU:HD13	0.67	1.67	9	2
1:A:108:LEU:HD21	1:A:115:THR:HA	0.66	1.67	13	20
1:A:65:LEU:HD23	1:A:74:LEU:HB2	0.65	1.68	7	19
1:A:71:LEU:HD11	1:A:112:TYR:CE2	0.64	2.28	18	6
1:A:32:GLU:O	1:A:36:VAL:HG23	0.64	1.93	2	18
1:A:65:LEU:HD11	1:A:73:LYS:HE2	0.61	1.71	12	5
1:A:105:GLN:HA	1:A:108:LEU:HD23	0.61	1.71	12	20
1:A:80:TYR:CE1	1:A:84:LEU:HD11	0.59	2.32	16	20
1:A:28:ALA:HB3	1:A:39:LEU:CD1	0.58	2.28	9	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:90:GLU:HB3	1:A:92:VAL:HG12	0.58	1.75	4	8
1:A:39:LEU:HD22	2:B:213:LYS:CE	0.58	2.27	9	1
1:A:44:ILE:HG22	1:A:44:ILE:O	0.58	1.98	3	6
1:A:71:LEU:HD11	1:A:112:TYR:CZ	0.58	2.34	18	7
1:A:37:LYS:HA	1:A:40:LEU:HD12	0.57	1.75	3	10
1:A:108:LEU:HD12	1:A:108:LEU:O	0.57	2.00	17	10
1:A:108:LEU:O	1:A:108:LEU:HD12	0.57	2.00	7	10
1:A:36:VAL:HG21	1:A:61:TYR:OH	0.56	2.01	6	3
1:A:73:LYS:HA	1:A:76:LEU:HD12	0.56	1.78	1	20
1:A:47:ILE:HD11	2:B:209:PHE:CD1	0.56	2.35	8	15
1:A:75:ASP:HA	1:A:116:LEU:HD21	0.56	1.77	12	3
1:A:26:ASN:ND2	1:A:31:VAL:HG22	0.55	2.17	2	12
1:A:73:LYS:O	1:A:77:VAL:HG23	0.54	2.03	17	4
1:A:41:LYS:O	1:A:45:THR:HG23	0.53	2.04	9	20
1:A:108:LEU:HD11	1:A:114:SER:O	0.53	2.04	20	18
1:A:27:LEU:HD21	1:A:40:LEU:HD21	0.52	1.80	7	8
1:A:41:LYS:HA	1:A:84:LEU:HD13	0.52	1.82	16	20
1:A:28:ALA:HB1	2:B:214:ARG:HB3	0.51	1.82	20	1
1:A:108:LEU:HD12	1:A:108:LEU:C	0.51	2.26	17	10
1:A:97:PHE:CE2	1:A:101:LEU:HD11	0.51	2.40	18	12
1:A:108:LEU:C	1:A:108:LEU:HD12	0.50	2.27	7	10
1:A:52:GLU:HA	1:A:55:ILE:HD12	0.50	1.83	17	1
1:A:77:VAL:HG12	1:A:81:MET:CE	0.50	2.36	8	12
1:A:63:THR:HG22	1:A:107:VAL:CG1	0.49	2.36	6	13
1:A:75:ASP:HA	1:A:116:LEU:HD11	0.49	1.82	18	1
1:A:55:ILE:O	1:A:58:VAL:HG22	0.49	2.08	11	1
1:A:90:GLU:HB3	1:A:92:VAL:HG22	0.48	1.85	2	2
1:A:55:ILE:HG23	1:A:100:ILE:HD11	0.48	1.85	13	1
1:A:89:VAL:HG13	1:A:90:GLU:CD	0.48	2.28	12	3
1:A:66:ILE:HD13	1:A:107:VAL:HG13	0.47	1.86	8	20
1:A:28:ALA:HB2	2:B:210:PHE:HB3	0.47	1.86	19	1
1:A:46:THR:HG23	1:A:47:ILE:HD12	0.47	1.86	17	6
1:A:59:VAL:HG22	1:A:100:ILE:HA	0.47	1.87	8	7
1:A:100:ILE:O	1:A:104:VAL:HG23	0.46	2.11	10	6
1:A:36:VAL:HG11	1:A:61:TYR:CE2	0.46	2.46	11	1
1:A:39:LEU:HD22	2:B:213:LYS:HE2	0.46	1.87	9	1
1:A:46:THR:HG23	1:A:47:ILE:CD1	0.45	2.42	3	7
1:A:78:ILE:CG2	1:A:116:LEU:HD22	0.45	2.35	2	6
1:A:27:LEU:HD12	1:A:61:TYR:CG	0.45	2.46	5	1
1:A:27:LEU:HD22	1:A:36:VAL:HG13	0.44	1.89	14	3
1:A:30:ALA:HB2	1:A:39:LEU:HD11	0.44	1.90	19	5

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:65:LEU:HD21	1:A:73:LYS:HG3	0.43	1.88	19	2
1:A:78:ILE:HD13	1:A:81:MET:CE	0.43	2.43	18	7
1:A:59:VAL:O	1:A:63:THR:HG23	0.43	2.13	8	1
1:A:65:LEU:HD21	1:A:73:LYS:CG	0.43	2.43	12	2
1:A:39:LEU:HD22	2:B:213:LYS:NZ	0.42	2.29	9	1
1:A:52:GLU:O	1:A:56:LEU:HD23	0.42	2.14	20	1
1:A:39:LEU:HD22	2:B:213:LYS:HZ1	0.42	1.73	9	1
1:A:63:THR:HG23	1:A:104:VAL:HG22	0.42	1.91	11	2
1:A:71:LEU:HD11	1:A:112:TYR:CE1	0.42	2.49	3	1
1:A:44:ILE:O	1:A:44:ILE:HG22	0.42	2.14	16	2
1:A:63:THR:CG2	1:A:107:VAL:HG11	0.42	2.41	9	4
1:A:59:VAL:HG22	1:A:100:ILE:HG23	0.42	1.90	11	1
1:A:26:ASN:CG	1:A:31:VAL:HG22	0.41	2.35	9	1
1:A:65:LEU:HD23	1:A:74:LEU:CB	0.41	2.43	4	3
1:A:65:LEU:HD11	1:A:73:LYS:CE	0.41	2.44	7	1
1:A:27:LEU:HD13	1:A:61:TYR:CG	0.41	2.50	6	1
1:A:78:ILE:HG21	1:A:116:LEU:CD2	0.41	2.43	9	2
1:A:66:ILE:HG23	1:A:112:TYR:CE1	0.41	2.50	3	1
1:A:63:THR:HG22	1:A:104:VAL:HA	0.40	1.93	11	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	92/119 (77%)	89±1 (97±1%)	3±1 (3±1%)	0±0 (0±0%)	56	85
2	B	7/25 (28%)	6±0 (89±6%)	1±0 (11±6%)	0±0 (0±0%)	100	100
All	All	1980/2880 (69%)	1906 (96%)	70 (4%)	4 (0%)	56	85

All 1 unique Ramachandran outliers are listed below.

Mol	Chain	Res	Type	Models (Total)
1	A	88	SER	4

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	87/106 (82%)	78±2 (90±2%)	9±2 (10±2%)	14 59
2	B	7/25 (28%)	5±1 (77±11%)	2±1 (23±11%)	3 30
All	All	1880/2620 (72%)	1675 (89%)	205 (11%)	12 56

All 31 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	79	LYS	20
1	A	116	LEU	20
1	A	108	LEU	20
1	A	82	LYS	20
2	B	208	SER	14
1	A	48	SER	10
1	A	75	ASP	10
1	A	73	LYS	9
1	A	34	SER	8
2	B	213	LYS	8
1	A	65	LEU	7
1	A	54	ASP	6
1	A	70	ASP	6
1	A	114	SER	5
1	A	49	ASP	4
2	B	212	LYS	4
2	B	214	ARG	4
1	A	41	LYS	4
1	A	69	LYS	4
1	A	52	GLU	4
1	A	88	SER	4
1	A	91	SER	2
1	A	60	ARG	2
2	B	211	ASP	2
1	A	35	ASP	2
1	A	57	GLN	1
1	A	83	ARG	1
1	A	27	LEU	1

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Mol	Chain	Res	Type	Models (Total)
1	A	102	ASP	1
1	A	98	ASP	1
1	A	53	GLU	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 84% for the well-defined parts and 84% for the entire structure.

7.1 Chemical shift list 1

File name: 2lsj_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	1552
Number of shifts mapped to atoms	1552
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	2

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	133	-0.57 ± 0.17	Should be applied
$^{13}C_{\beta}$	128	0.30 ± 0.06	None needed (< 0.5 ppm)
$^{13}C'$	0	—	—
^{15}N	121	0.32 ± 0.16	None needed (< 0.5 ppm)

7.1.3 Completeness of resonance assignments

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 84%, i.e. 1070 atoms were assigned a chemical shift out of a possible 1268. 22 out of 22 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	382/491 (78%)	191/196 (97%)	99/198 (50%)	92/97 (95%)
Sidechain	611/684 (89%)	375/396 (95%)	227/262 (87%)	9/26 (35%)

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	Total	^{1}H	^{13}C	^{15}N
Aromatic	77/93 (83%)	49/49 (100%)	26/42 (62%)	2/2 (100%)
Overall	1070/1268 (84%)	615/641 (96%)	352/502 (70%)	103/125 (82%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 84%, i.e. 1184 atoms were assigned a chemical shift out of a possible 1415. 23 out of 23 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	428/551 (78%)	214/220 (97%)	111/222 (50%)	103/109 (94%)
Sidechain	679/771 (88%)	418/447 (94%)	252/292 (86%)	9/32 (28%)
Aromatic	77/93 (83%)	49/49 (100%)	26/42 (62%)	2/2 (100%)
Overall	1184/1415 (84%)	681/716 (95%)	389/556 (70%)	114/143 (80%)

7.1.4 Statistically unusual chemical shifts (i)

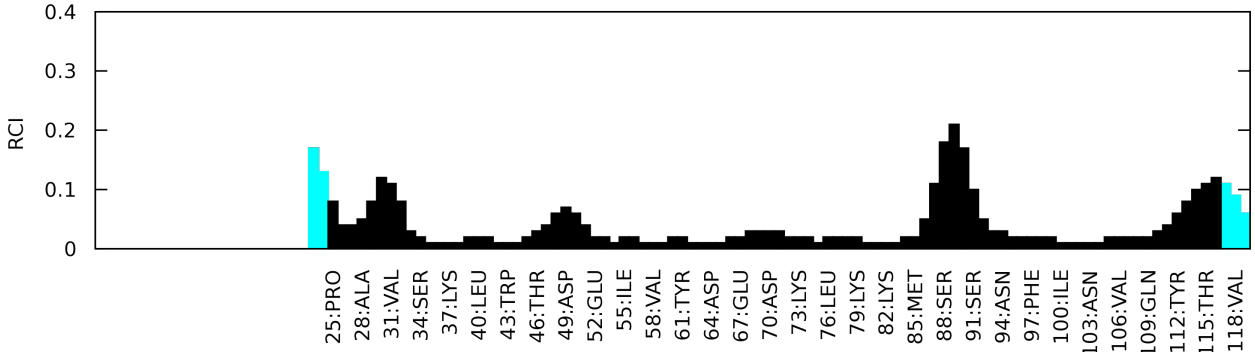
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

Mol	Chain	Res	Type	Atom	Shift, *ppm*	Expected range, *ppm*	Z-score
1	A	50	PRO	HG2	-0.19	3.48 – 0.38	-6.8
1	A	93	TRP	HH2	4.37	8.94 – 5.04	-6.7

7.1.5 Random Coil Index (RCI) plots (i)

The images below report *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:



Random coil index (RCI) for chain B: