



Full wwPDB NMR Structure Validation Report ⓘ

Apr 26, 2016 – 06:53 PM BST

PDB ID : 1Z00
Title : Solution structure of the C-terminal domain of ERCC1 complexed with the C-terminal domain of XPF
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Deposited on : 2005-03-01

This is a Full wwPDB NMR Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/NMRValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

Cyrange : Kirchner and Güntert (2011)
NmrClust : Kelley et al. (1996)
MolProbity : 4.02b-467
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

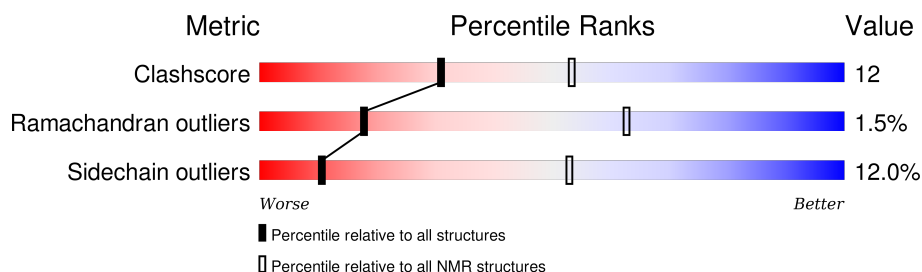
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	89	
2	B	84	

2 Ensemble composition and analysis

This entry contains 20 models. Model 15 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:231-A:295, B:833-B:894 (127)	0.15	15

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 2 clusters. No single-model clusters were found.

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

3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2614 atoms, of which 1318 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called DNA excision repair protein ERCC-1.

Mol	Chain	Residues	Atoms						Trace
1	A	84	Total	C	H	N	O	S	0
			1319	411	669	110	125	4	

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	219	MET	-	INITIATING METHIONINE	UNP P07992
A	298	GLY	-	EXPRESSION TAG	UNP P07992
A	299	GLY	-	EXPRESSION TAG	UNP P07992
A	300	LEU	-	EXPRESSION TAG	UNP P07992
A	301	GLU	-	EXPRESSION TAG	UNP P07992
A	302	HIS	-	EXPRESSION TAG	UNP P07992
A	303	HIS	-	EXPRESSION TAG	UNP P07992
A	304	HIS	-	EXPRESSION TAG	UNP P07992
A	305	HIS	-	EXPRESSION TAG	UNP P07992
A	306	HIS	-	EXPRESSION TAG	UNP P07992
A	307	HIS	-	EXPRESSION TAG	UNP P07992

- Molecule 2 is a protein called DNA repair endonuclease XPF.

Mol	Chain	Residues	Atoms						Trace
2	B	84	Total	C	H	N	O	S	0
			1295	405	649	111	126	4	

There is a discrepancy between the modelled and reference sequences:

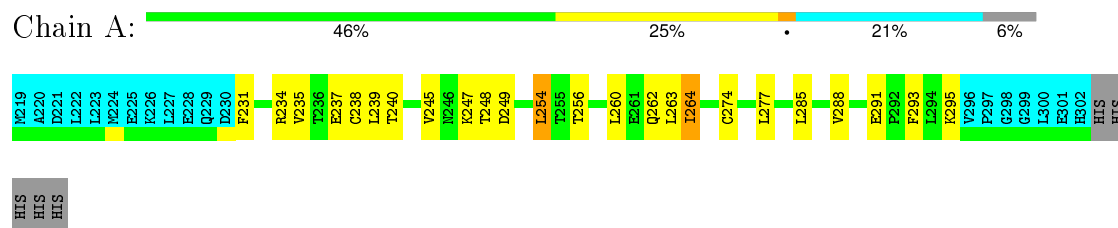
Chain	Residue	Modelled	Actual	Comment	Reference
B	822	MET	-	INITIATING METHIONINE	UNP Q92889

4 Residue-property plots

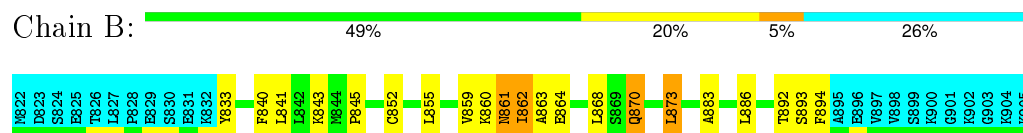
4.1 Average score per residue in the NMR ensemble

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 excision repair protein ERCC-1



- Molecule 2: DNA repair endonuclease XPF

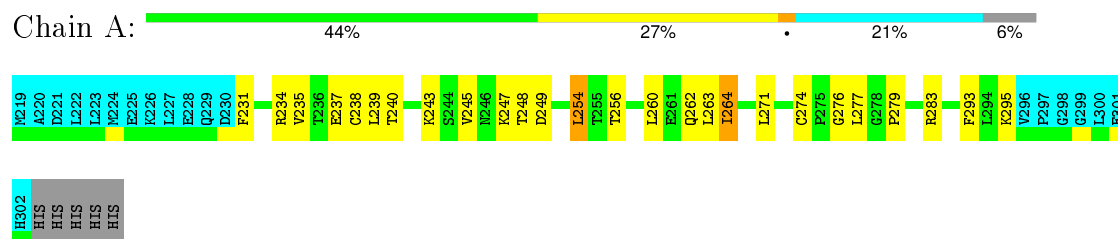


4.2 Scores per residue for each member of the ensemble

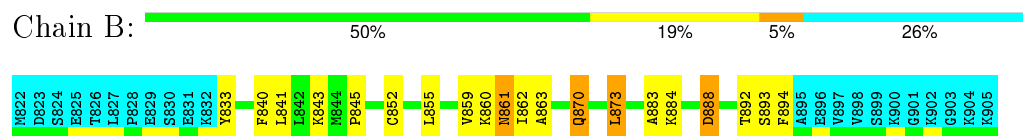
Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

- Molecule 1: DNA excision repair protein ERCC-1

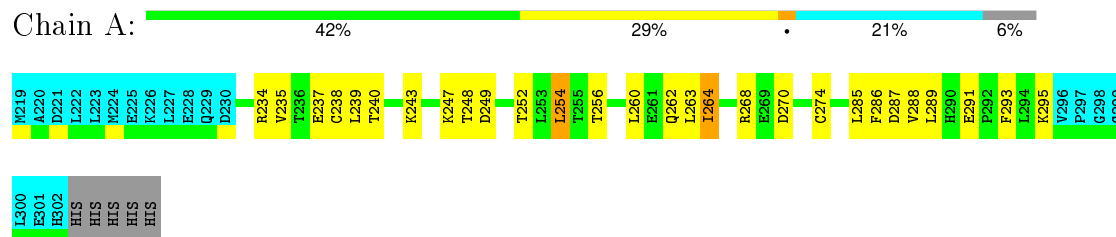


- Molecule 2: DNA repair endonuclease XPF

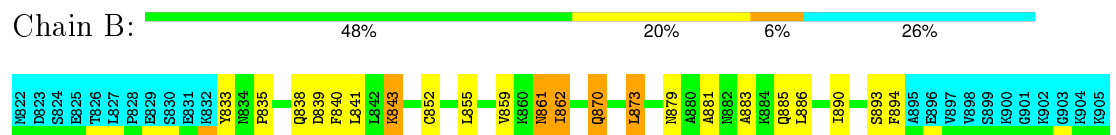


4.2.2 Score per residue for model 2

- Molecule 1: DNA excision repair protein ERCC-1

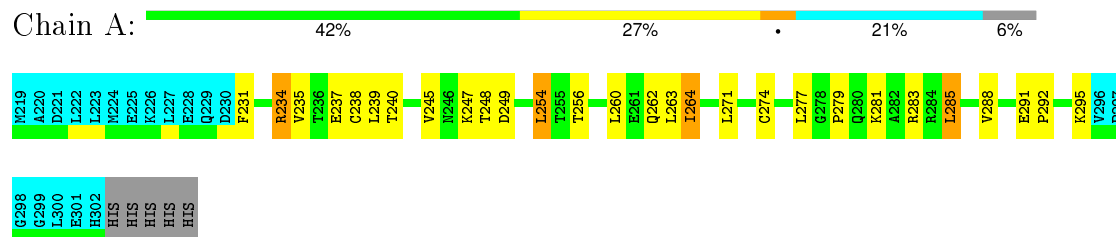


- Molecule 2: DNA repair endonuclease XPF

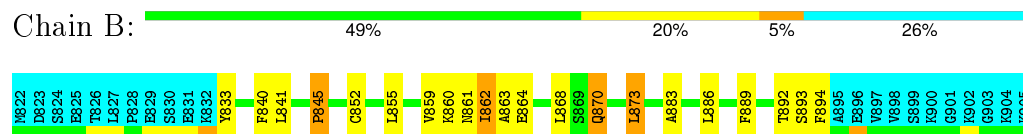


4.2.3 Score per residue for model 3

- Molecule 1: DNA excision repair protein ERCC-1

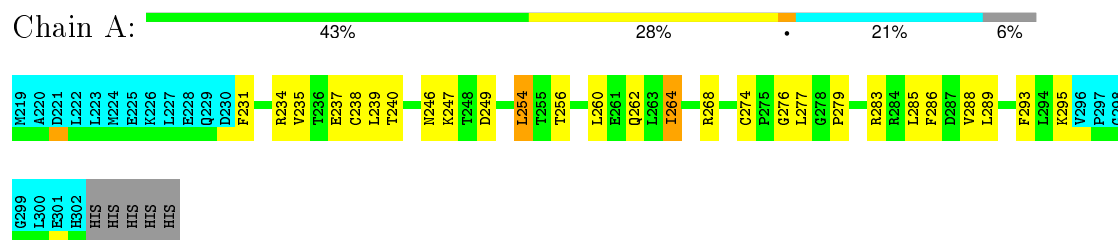


- Molecule 2: DNA repair endonuclease XPF

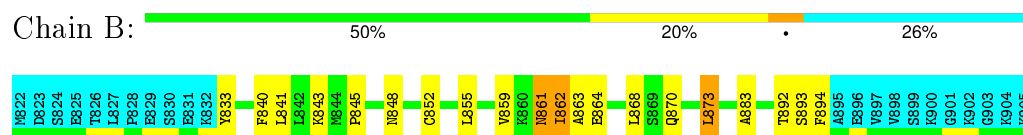


4.2.4 Score per residue for model 4

- Molecule 1: DNA excision repair protein ERCC-1

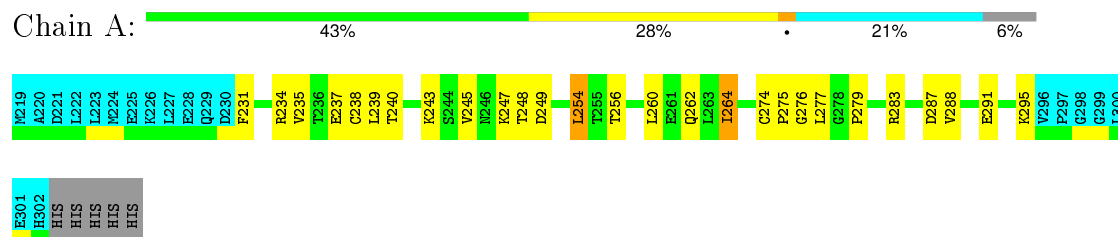


- Molecule 2: DNA repair endonuclease XPF

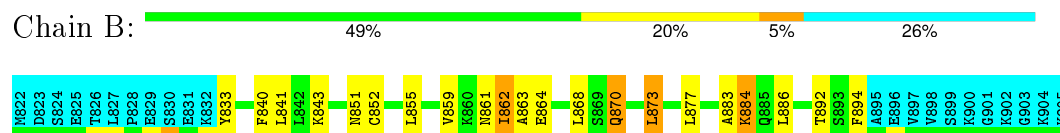


4.2.5 Score per residue for model 5

- Molecule 1: DNA excision repair protein ERCC-1

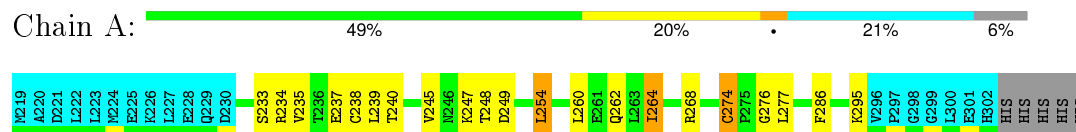


- Molecule 2: DNA repair endonuclease XPF



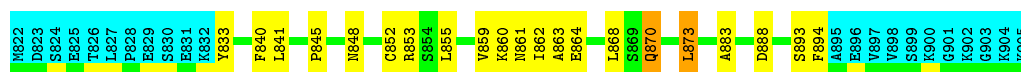
4.2.6 Score per residue for model 6

- Molecule 1: DNA excision repair protein ERCC-1



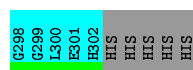
- Molecule 2: DNA repair endonuclease XPF



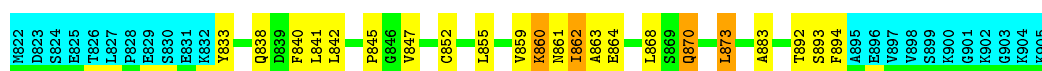


4.2.7 Score per residue for model 7

- Molecule 1: DNA excision repair protein ERCC-1



- Molecule 2: DNA repair endonuclease XPF

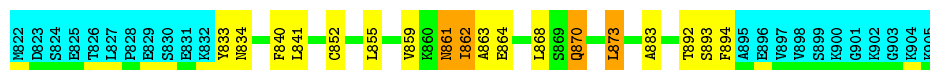


4.2.8 Score per residue for model 8

- Molecule 1: DNA excision repair protein ERCC-1



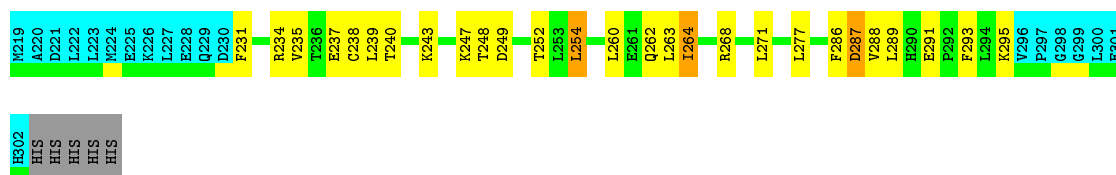
- Molecule 2: DNA repair endonuclease XPF



4.2.9 Score per residue for model 9

- Molecule 1: DNA excision repair protein ERCC-1



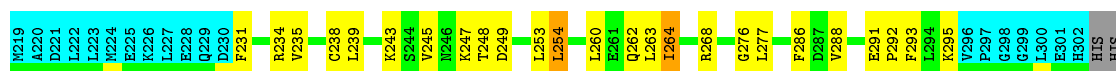


- Molecule 2: DNA repair endonuclease XPF

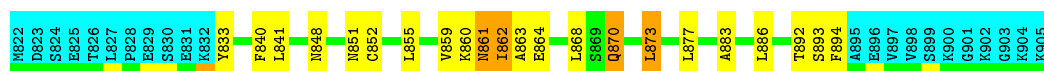


4.2.10 Score per residue for model 10

- Molecule 1: DNA excision repair protein ERCC-1

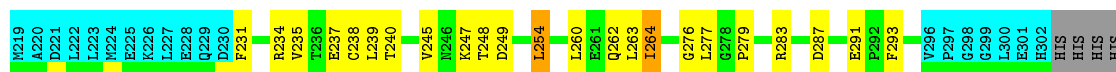


- Molecule 2: DNA repair endonuclease XPF



4.2.11 Score per residue for model 11

- Molecule 1: DNA excision repair protein ERCC-1



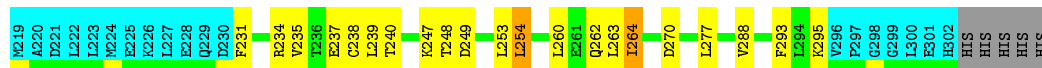
- Molecule 2: DNA repair endonuclease XPF





4.2.12 Score per residue for model 12

- Molecule 1: DNA excision repair protein ERCC-1

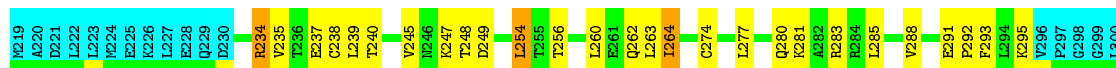


- Molecule 2: DNA repair endonuclease XPF

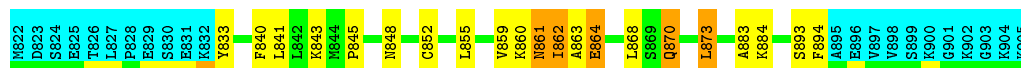


4.2.13 Score per residue for model 13

- Molecule 1: DNA excision repair protein ERCC-1



- Molecule 2: DNA repair endonuclease XPF



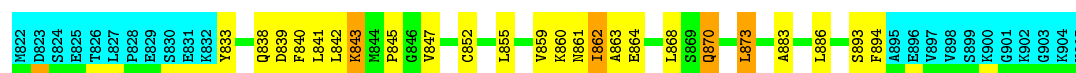
4.2.14 Score per residue for model 14

- Molecule 1: DNA excision repair protein ERCC-1



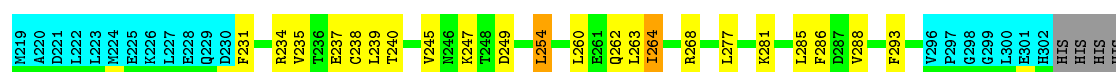
HIS

- Molecule 2: DNA repair endonuclease XPF

Chain B: 

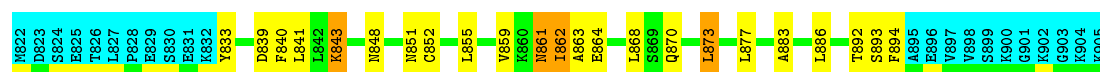
4.2.15 Score per residue for model 15 (medoid)

- Molecule 1: DNA excision repair protein ERCC-1

Chain A: 

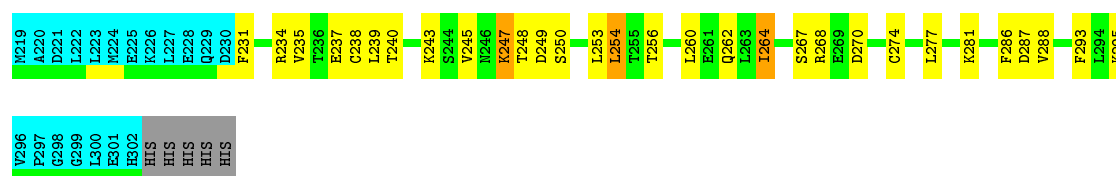
HIS

- Molecule 2: DNA repair endonuclease XPF

Chain B: 

4.2.16 Score per residue for model 16

- Molecule 1: DNA excision repair protein ERCC-1

Chain A: 

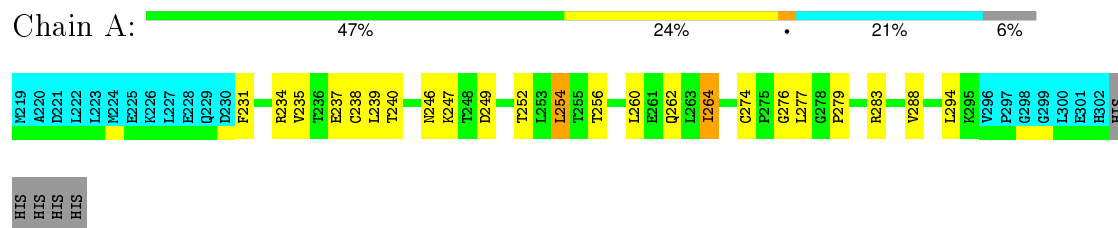
- Molecule 2: DNA repair endonuclease XPF

Chain B: 

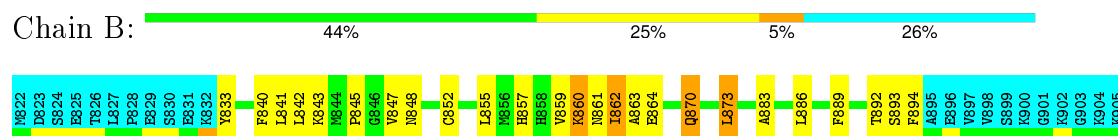
Y904
Y905

4.2.17 Score per residue for model 17

- Molecule 1: DNA excision repair protein ERCC-1

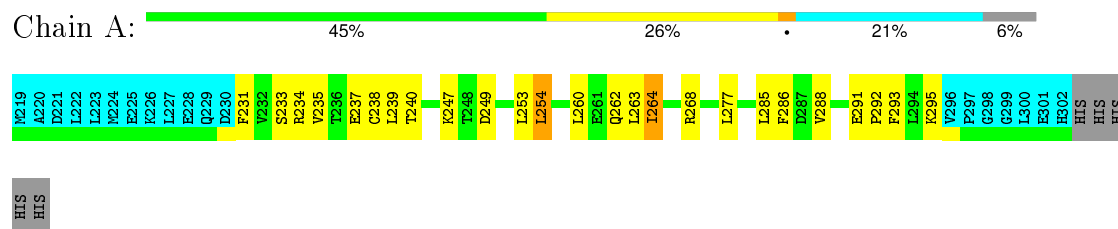


- Molecule 2: DNA repair endonuclease XPF

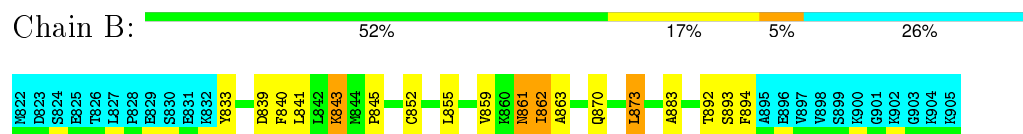


4.2.18 Score per residue for model 18

- Molecule 1: DNA excision repair protein ERCC-1



- Molecule 2: DNA repair endonuclease XPF



4.2.19 Score per residue for model 19

- Molecule 1: DNA excision repair protein ERCC-1





- HIS
-
- HIS

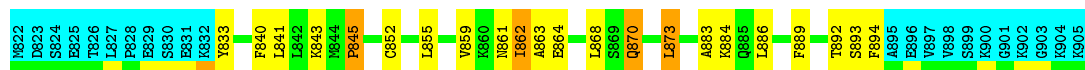


S899	
K900	
G901	
K902	
G903	
K904	
K905	

- | | |
|------|--|
| S899 | |
| K900 | |
| G901 | |
| K902 | |
| G903 | |
| K904 | |
| K905 | |



- | | |
|------|-----|
| E301 | HIS |
| H302 | HIS |
| | HIS |
| | HIS |
| | HIS |



5 Refinement protocol and experimental data overview

The models were refined using the following method: *water refinement in CNS*.

Of the 100 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
cyana	structure solution	2.0
CNS	refinement	1.1

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)	BMRB entry 6551
Number of chemical shift lists	2
Total number of shifts	1924
Number of shifts mapped to atoms	1924
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 [i](#)

6.1 Standard geometry [i](#)

There are no covalent bond-length or bond-angle outliers.

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	0.1±0.4
All	All	0	3

There are no bond-length outliers.

There are no bond-angle outliers.

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)
1	A	234	ARG	Sidechain	2
1	A	283	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	504	524	524	15±2
2	B	481	476	476	14±1
All	All	19700	20000	20000	461

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 12.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:873:LEU:HD13	2:B:883:ALA:HB1	0.72	1.60	17	20
2:B:838:GLN:O	2:B:842:LEU:HG	0.70	1.87	7	2
1:A:235:VAL:O	1:A:239:LEU:HG	0.64	1.92	17	20
1:A:254:LEU:HD22	2:B:894:PHE:CZ	0.62	2.30	19	18
1:A:249:ASP:OD1	1:A:277:LEU:HD13	0.61	1.96	18	19
2:B:864:GLU:O	2:B:868:LEU:HG	0.59	1.97	4	12
2:B:835:PRO:HA	2:B:838:GLN:OE1	0.58	1.98	19	1
2:B:841:LEU:HG	2:B:852:CYS:SG	0.57	2.39	10	17
2:B:855:LEU:O	2:B:859:VAL:HG12	0.57	1.99	9	20
1:A:235:VAL:HG12	1:A:260:LEU:HD23	0.56	1.77	15	14
2:B:873:LEU:CD1	2:B:883:ALA:HB1	0.56	2.30	7	20
1:A:231:PHE:CE2	2:B:892:THR:HG23	0.53	2.39	4	16
1:A:238:CYS:HB3	2:B:840:PHE:CZ	0.52	2.39	12	20
1:A:237:GLU:HA	1:A:240:THR:OG1	0.52	2.05	13	19
1:A:293:PHE:CE2	2:B:861:ASN:HA	0.52	2.39	16	12
2:B:847:VAL:HG12	2:B:852:CYS:SG	0.52	2.45	7	3
1:A:254:LEU:HD13	2:B:894:PHE:CE1	0.51	2.40	12	3
1:A:245:VAL:HG13	1:A:249:ASP:HB3	0.51	1.83	3	12
1:A:284:ARG:HA	1:A:287:ASP:OD2	0.51	2.06	20	1
1:A:287:ASP:O	1:A:291:GLU:HB2	0.50	2.06	5	5
1:A:260:LEU:O	1:A:264:ILE:HG22	0.50	2.06	12	20
1:A:291:GLU:OE2	1:A:292:PRO:HD2	0.50	2.06	13	5
1:A:279:PRO:O	1:A:283:ARG:HD3	0.50	2.07	11	7
1:A:231:PHE:CD2	2:B:894:PHE:HB3	0.49	2.42	12	3
1:A:256:THR:HG21	1:A:274:CYS:SG	0.49	2.47	7	11
1:A:264:ILE:HD11	2:B:863:ALA:HA	0.49	1.85	5	19
1:A:284:ARG:O	1:A:288:VAL:HG23	0.48	2.07	7	1
2:B:841:LEU:HD11	2:B:855:LEU:HD12	0.48	1.86	9	17
2:B:870:GLN:HA	2:B:873:LEU:HD11	0.48	1.85	10	15
1:A:268:ARG:HG3	1:A:286:PHE:CD1	0.48	2.44	15	3
1:A:254:LEU:HD22	2:B:894:PHE:CE1	0.48	2.43	16	4
1:A:285:LEU:HD12	1:A:288:VAL:CG2	0.48	2.39	13	4
1:A:249:ASP:CG	1:A:277:LEU:HD13	0.47	2.28	15	5
1:A:253:LEU:HD21	1:A:277:LEU:HD22	0.47	1.85	18	3
2:B:845:PRO:HG3	2:B:889:PHE:CG	0.47	2.45	3	5
2:B:839:ASP:O	2:B:843:LYS:HG2	0.47	2.09	2	4
1:A:289:LEU:HA	2:B:862:ILE:CD1	0.47	2.39	7	5
1:A:288:VAL:O	2:B:862:ILE:HD11	0.46	2.10	2	17
1:A:242:VAL:CG1	1:A:288:VAL:HG21	0.46	2.41	7	1
1:A:268:ARG:HG3	1:A:286:PHE:CD2	0.46	2.46	18	6
2:B:860:LYS:HD3	2:B:860:LYS:C	0.45	2.32	17	1
1:A:271:LEU:O	1:A:277:LEU:HD23	0.45	2.12	3	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:292:PRO:HA	2:B:860:LYS:O	0.45	2.11	7	1
2:B:886:LEU:O	2:B:890:ILE:HG13	0.44	2.11	19	2
1:A:245:VAL:HG21	1:A:285:LEU:HD23	0.44	1.87	3	2
1:A:274:CYS:SG	1:A:277:LEU:HB2	0.44	2.52	6	1
1:A:280:GLN:HG3	1:A:281:LYS:N	0.44	2.28	13	1
1:A:291:GLU:OE1	1:A:292:PRO:HD2	0.44	2.13	18	1
1:A:293:PHE:CZ	2:B:841:LEU:HD22	0.43	2.48	18	5
2:B:835:PRO:HA	2:B:838:GLN:HG2	0.43	1.89	9	3
2:B:851:ASN:HB3	2:B:877:LEU:CD2	0.43	2.44	19	4
1:A:235:VAL:HG11	2:B:894:PHE:CE2	0.43	2.49	15	1
2:B:884:LYS:O	2:B:888:ASP:HB2	0.42	2.13	1	1
1:A:267:SER:O	1:A:270:ASP:HB2	0.42	2.15	20	2
1:A:277:LEU:HD11	1:A:281:LYS:HB2	0.42	1.91	3	4
2:B:851:ASN:HB3	2:B:877:LEU:HD22	0.42	1.91	16	1
2:B:842:LEU:HA	2:B:852:CYS:SG	0.42	2.54	14	2
1:A:260:LEU:HB3	2:B:890:ILE:HA	0.42	1.92	2	1
2:B:884:LYS:C	2:B:884:LYS:HD3	0.42	2.35	11	2
2:B:844:MET:SD	2:B:845:PRO:HD2	0.41	2.56	11	1
1:A:249:ASP:O	1:A:253:LEU:HG	0.41	2.15	10	1
1:A:249:ASP:O	1:A:252:THR:HB	0.41	2.16	17	3
2:B:879:ASN:OD1	2:B:881:ALA:HB3	0.41	2.16	16	1
1:A:243:LYS:HA	1:A:243:LYS:HE3	0.41	1.93	10	1
1:A:237:GLU:OE1	2:B:843:LYS:HE3	0.41	2.16	2	1
1:A:295:LYS:HG3	2:B:834:ASN:OD1	0.41	2.15	8	1
2:B:881:ALA:O	2:B:885:GLN:HG3	0.40	2.15	19	2
1:A:294:LEU:HD22	2:B:833:TYR:CZ	0.40	2.51	17	1
2:B:884:LYS:HD3	2:B:884:LYS:C	0.40	2.37	13	1
1:A:247:LYS:HA	1:A:250:SER:OG	0.40	2.17	16	1

6.3 Torsion angles ⓘ

6.3.1 Protein backbone ⓘ

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	65/89 (73%)	60±1 (93±1%)	3±1 (5±2%)	1±1 (2±1%)	14	55

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	62/84 (74%)	60±1 (97±1%)	1±1 (2±1%)	1±0 (1±1%)	24	71
All	All	2540/3460 (73%)	2404 (95%)	97 (4%)	39 (2%)	18	63

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	295	LYS	16
2	B	845	PRO	13
1	A	276	GLY	9
1	A	275	PRO	1

6.3.2 Protein sidechains ⓘ

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	58/79 (73%)	51±1 (88±2%)	7±1 (12±2%)	11	54
2	B	52/71 (73%)	46±1 (88±3%)	7±1 (12±3%)	10	52
All	All	2200/3000 (73%)	1936 (88%)	264 (12%)	11	53

All 26 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)
2	B	873	LEU	20
1	A	264	ILE	20
2	B	870	GLN	20
1	A	254	LEU	20
2	B	861	ASN	20
1	A	247	LYS	20
1	A	262	GLN	20
2	B	862	ILE	19
1	A	248	THR	16
2	B	886	LEU	11
2	B	860	LYS	11
2	B	843	LYS	11

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Mol	Chain	Res	Type	Models (Total)
1	A	263	LEU	11
2	B	848	ASN	8
1	A	243	LYS	6
1	A	285	LEU	5
1	A	246	ASN	4
1	A	270	ASP	4
2	B	884	LYS	4
2	B	864	GLU	3
1	A	274	CYS	2
1	A	283	ARG	2
1	A	287	ASP	2
2	B	888	ASP	2
1	A	231	PHE	2
2	B	879	ASN	1

6.3.3 RNA [i](#)

There are no RNA molecules in this entry.

6.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.6 Ligand geometry [i](#)

There are no ligands in this entry.

6.7 Other polymers [i](#)

There are no such molecules in this entry.

6.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

7 Chemical shift validation [i](#)

The completeness of assignment taking into account all chemical shift lists is 84% for the well-defined parts and 83% for the entire structure.

7.1 Chemical shift list 1

File name: BMRB entry 6551

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	969
Number of shifts mapped to atoms	969
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
$^{13}\text{C}_\alpha$	82	-0.64 ± 0.10	Should be applied
$^{13}\text{C}_\beta$	78	0.06 ± 0.05	None needed (< 0.5 ppm)
$^{13}\text{C}'$	0	—	—
^{15}N	74	-0.28 ± 0.34	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 42%, i.e. 658 atoms were assigned a chemical shift out of a possible 1551. 16 out of 26 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	247/623 (40%)	124/248 (50%)	64/254 (25%)	59/121 (49%)
Sidechain	371/821 (45%)	226/480 (47%)	141/305 (46%)	4/36 (11%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	40/107 (37%)	22/59 (37%)	18/44 (41%)	0/4 (0%)
Overall	658/1551 (42%)	372/787 (47%)	223/603 (37%)	63/161 (39%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 41%, i.e. 826 atoms were assigned a chemical shift out of a possible 2033. 21 out of 34 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	309/824 (38%)	155/328 (47%)	81/336 (24%)	73/160 (46%)
Sidechain	477/1095 (44%)	291/641 (45%)	181/411 (44%)	5/43 (12%)
Aromatic	40/114 (35%)	22/63 (35%)	18/46 (39%)	0/5 (0%)
Overall	826/2033 (41%)	468/1032 (45%)	280/793 (35%)	78/208 (38%)

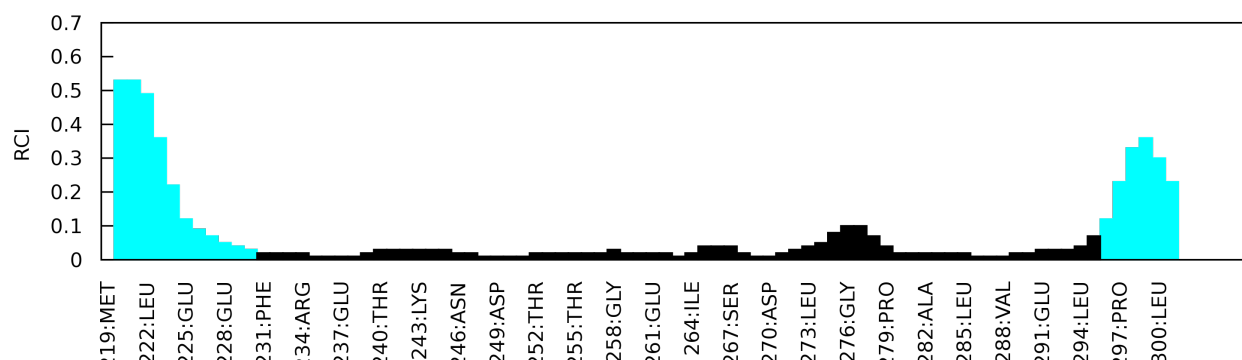
7.1.4 Statistically unusual chemical shifts [i](#)

There are no statistically unusual chemical shifts.

7.1.5 Random Coil Index (RCI) plots [i](#)

The image below reports *random coil index* values for the protein chains in the structure. The height of each bar gives a probability of a given residue to be disordered, as predicted from the available chemical shifts and the amino acid sequence. A value above 0.2 is an indication of significant predicted disorder. The colour of the bar shows whether the residue is in the well-defined core (black) or in the ill-defined residue ranges (cyan), as described in section 2 on ensemble composition.

Random coil index (RCI) for chain A:



7.2 Chemical shift list 2

File name: BMRB entry 6551

Chemical shift list name: *assigned_chem_shift_list_2*

7.2.1 Bookkeeping [i](#)

The following table shows the results of parsing the chemical shift list and reports the number of nuclei with statistically unusual chemical shifts.

Total number of shifts	955
Number of shifts mapped to atoms	955
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	1

7.2.2 Chemical shift referencing [i](#)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	83	-0.44 ± 0.15	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	78	-0.02 ± 0.13	None needed (< 0.5 ppm)
$^{13}\text{C}'$	0	—	—
^{15}N	77	0.88 ± 0.31	Should be applied

7.2.3 Completeness of resonance assignments [i](#)

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 41%, i.e. 643 atoms were assigned a chemical shift out of a possible 1551. 10 out of 26 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	240/623 (39%)	120/248 (48%)	62/254 (24%)	58/121 (48%)
Sidechain	352/821 (43%)	218/480 (45%)	125/305 (41%)	9/36 (25%)
Aromatic	51/107 (48%)	27/59 (46%)	24/44 (55%)	0/4 (0%)
Overall	643/1551 (41%)	365/787 (46%)	211/603 (35%)	67/161 (42%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 42%, i.e. 853 atoms were assigned a chemical shift out of a possible 2033. 13 out of 34 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	320/824 (39%)	160/328 (49%)	83/336 (25%)	77/160 (48%)

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	Total	¹ H	¹³ C	¹⁵ N
Sidechain	482/1095 (44%)	301/641 (47%)	172/411 (42%)	9/43 (21%)
Aromatic	51/114 (45%)	27/63 (43%)	24/46 (52%)	0/5 (0%)
Overall	853/2033 (42%)	488/1032 (47%)	279/793 (35%)	86/208 (41%)

7.2.4 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
2	B	856	MET	HG2	0.46	4.23 – 0.63	-5.5

7.2.5 Random Coil Index (RCI) plots [i](#)

The image below reports *random coil index* values for the protein chains in the structure. The height of each bar gives a probability of a given residue to be disordered, as predicted from the available chemical shifts and the amino acid sequence. A value above 0.2 is an indication of significant predicted disorder. The colour of the bar shows whether the residue is in the well-defined core (black) or in the ill-defined residue ranges (cyan), as described in section 2 on ensemble composition.

Random coil index (RCI) for chain B:

