



Full wwPDB NMR Structure Validation Report ⓘ

Feb 20, 2018 – 07:55 pm GMT

PDB ID : 1PPQ
Title : NMR structure of 16th module of Immune Adherence Receptor, Cr1 (Cd35)
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Deposited on : 2003-06-17

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 ⓘ 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
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
ShiftChecker : trunk30686
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk30686

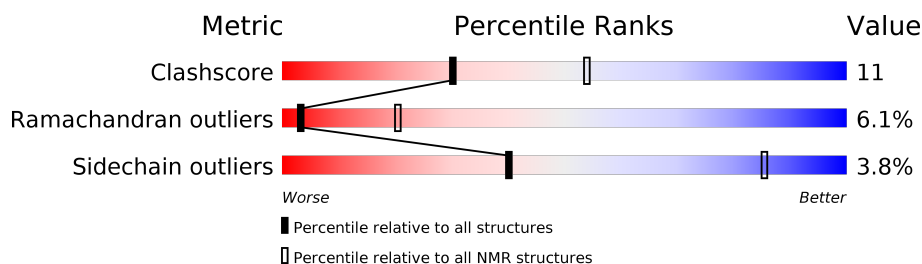
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 49%.

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	136279	12091
Ramachandran outliers	132675	10835
Sidechain outliers	132484	10811

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	68	

2 Ensemble composition and analysis

This entry contains 20 models. Model 1 is the overall representative, medoid model (most similar to other models). The authors have identified model 4 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:962-A:1024 (63)	0.69	1

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 6 single-model clusters were found.

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

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 1015 atoms, of which 506 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Complement receptor type 1.

Mol	Chain	Residues	Atoms							Trace
1	A	68	Total	C	H	N	O	S		0
			1015	313	506	93	98	5		

There are 5 discrepancies between the modelled and reference sequences:

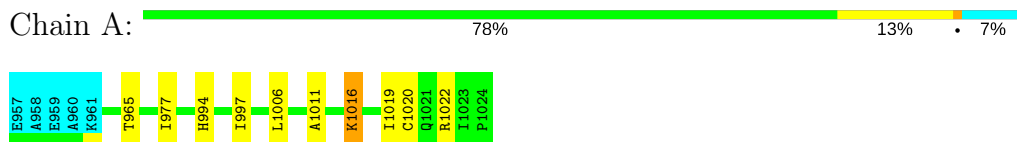
Chain	Residue	Modelled	Actual	Comment	Reference
A	957	GLU	-	CLONING ARTIFACT	UNP P17927
A	958	ALA	-	CLONING ARTIFACT	UNP P17927
A	959	GLU	-	CLONING ARTIFACT	UNP P17927
A	960	ALA	-	CLONING ARTIFACT	UNP P17927
A	987	THR	ASN	ENGINEERED	UNP P17927

4 Residue-property plots [i](#)

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: Complement receptor type 1

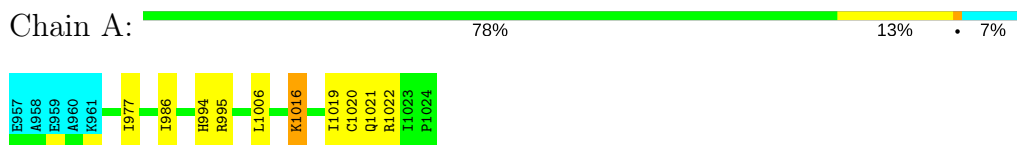


4.2 Scores per residue for each member of the ensemble

Colouring as in section [4.1](#) above.

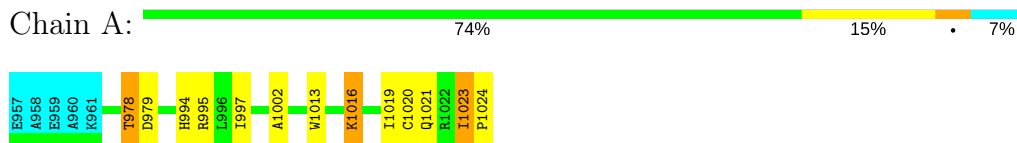
4.2.1 Score per residue for model 1 (medoid)

- Molecule 1: Complement receptor type 1



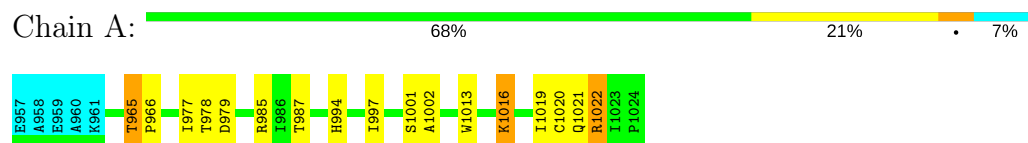
4.2.2 Score per residue for model 2

- Molecule 1: Complement receptor type 1



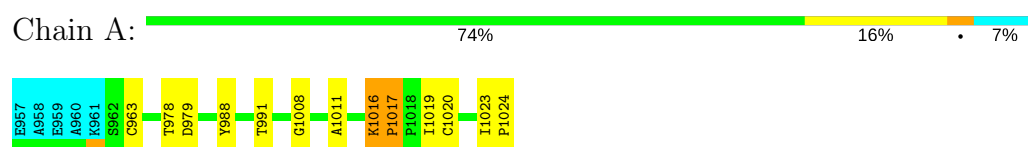
4.2.3 Score per residue for model 3

- Molecule 1: Complement receptor type 1



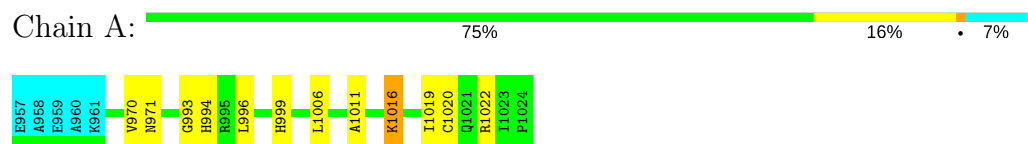
4.2.4 Score per residue for model 4

- Molecule 1: Complement receptor type 1



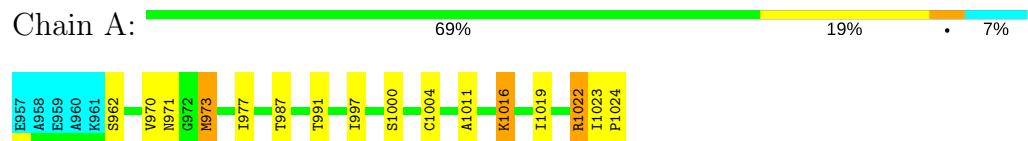
4.2.5 Score per residue for model 5

- Molecule 1: Complement receptor type 1



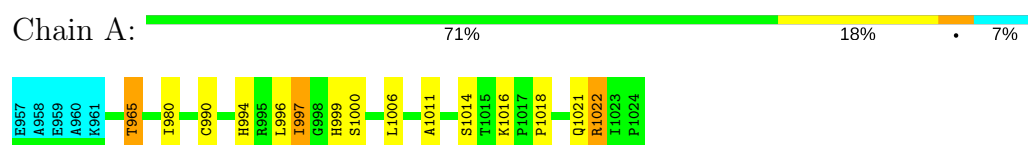
4.2.6 Score per residue for model 6

- Molecule 1: Complement receptor type 1



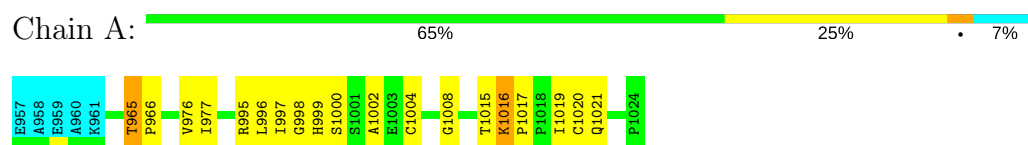
4.2.7 Score per residue for model 7

- Molecule 1: Complement receptor type 1



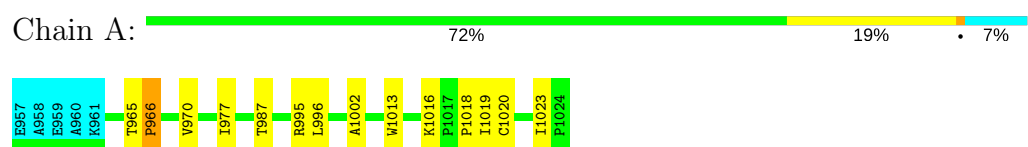
4.2.8 Score per residue for model 8

- Molecule 1: Complement receptor type 1



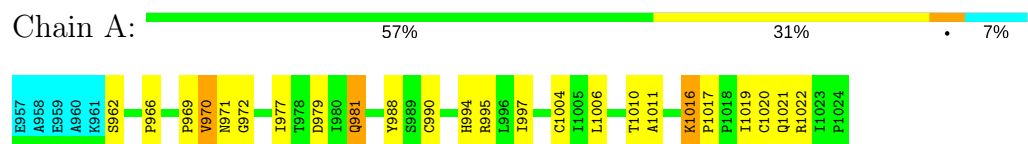
4.2.9 Score per residue for model 9

- Molecule 1: Complement receptor type 1



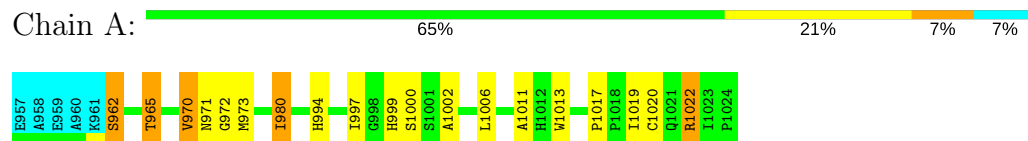
4.2.10 Score per residue for model 10

- Molecule 1: Complement receptor type 1



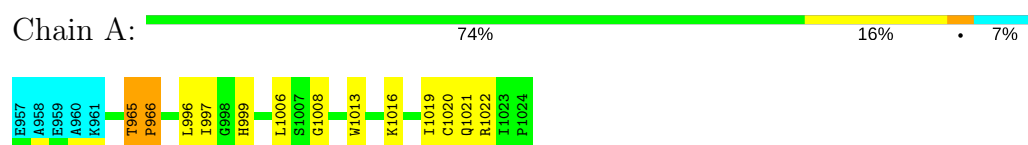
4.2.11 Score per residue for model 11

- Molecule 1: Complement receptor type 1



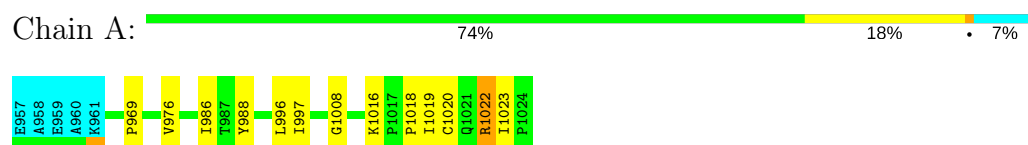
4.2.12 Score per residue for model 12

- Molecule 1: Complement receptor type 1



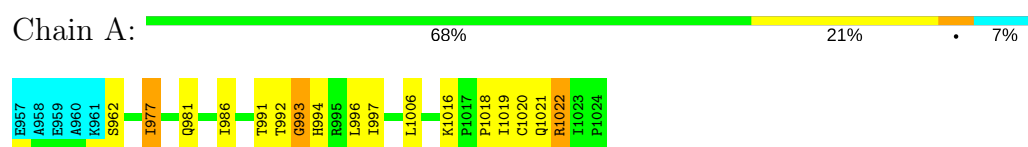
4.2.13 Score per residue for model 13

- Molecule 1: Complement receptor type 1



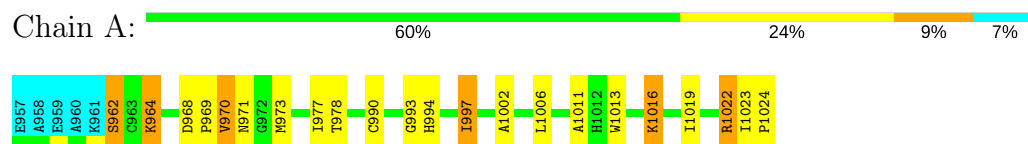
4.2.14 Score per residue for model 14

- Molecule 1: Complement receptor type 1



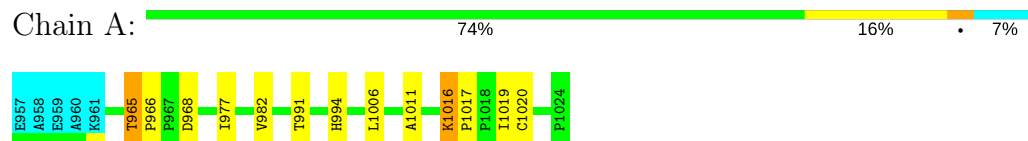
4.2.15 Score per residue for model 15

- Molecule 1: Complement receptor type 1



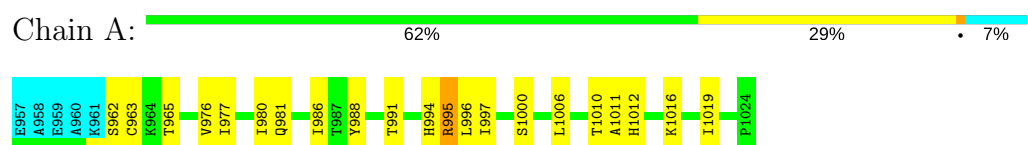
4.2.16 Score per residue for model 16

- Molecule 1: Complement receptor type 1



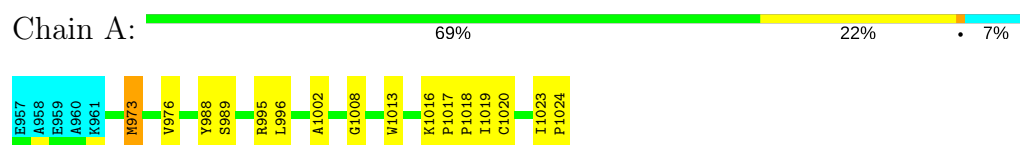
4.2.17 Score per residue for model 17

- Molecule 1: Complement receptor type 1



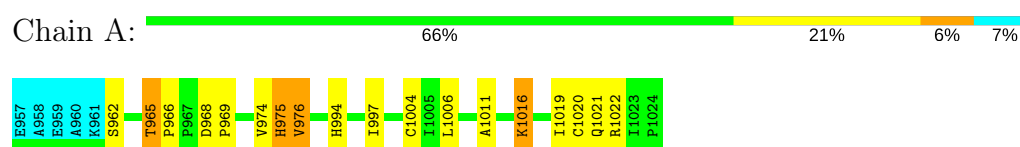
4.2.18 Score per residue for model 18

- Molecule 1: Complement receptor type 1



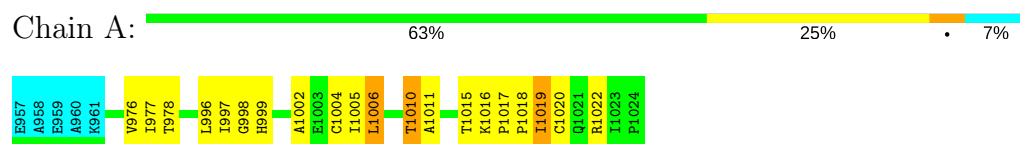
4.2.19 Score per residue for model 19

- Molecule 1: Complement receptor type 1



4.2.20 Score per residue for model 20

- Molecule 1: Complement receptor type 1



5 Refinement protocol and experimental data overview

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

Of the 60 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
CNS	structure solution	1.0
CNS	refinement	1.0

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 5900
Number of chemical shift lists	3
Total number of shifts	474
Number of shifts mapped to atoms	474
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	49%

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	472	469	465	10±3
All	All	9440	9380	9300	202

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 11.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:997:ILE:HD11	1:A:1021:GLN:HB2	0.69	1.65	19	4
1:A:997:ILE:HB	1:A:1019:ILE:HD13	0.65	1.68	13	1
1:A:997:ILE:HD13	1:A:1019:ILE:HG23	0.64	1.70	19	1
1:A:996:LEU:HD11	1:A:1018:PRO:HB2	0.64	1.69	13	2
1:A:965:THR:H	1:A:966:PRO:HD2	0.64	1.52	9	3
1:A:997:ILE:HD13	1:A:1019:ILE:HB	0.63	1.70	17	5
1:A:970:VAL:HG22	1:A:971:ASN:H	0.61	1.54	11	3
1:A:1002:ALA:HB2	1:A:1015:THR:HG23	0.61	1.71	20	1
1:A:1016:LYS:HD2	1:A:1016:LYS:H	0.61	1.55	19	4
1:A:1002:ALA:HB1	1:A:1013:TRP:HB3	0.61	1.72	3	6
1:A:1019:ILE:HG13	1:A:1020:CYS:H	0.60	1.57	20	1
1:A:965:THR:N	1:A:966:PRO:HD2	0.60	2.11	9	3
1:A:997:ILE:HD11	1:A:1021:GLN:HB3	0.57	1.75	8	2
1:A:1016:LYS:H	1:A:1016:LYS:HD3	0.57	1.59	4	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:969:PRO:HD2	1:A:974:VAL:HB	0.57	1.77	19	1
1:A:977:ILE:HD11	1:A:987:THR:HG23	0.56	1.76	3	3
1:A:1016:LYS:HB3	1:A:1018:PRO:HD2	0.55	1.78	20	1
1:A:977:ILE:HG22	1:A:978:THR:HG23	0.55	1.79	20	2
1:A:996:LEU:HD13	1:A:1000:SER:HA	0.54	1.78	17	1
1:A:1010:THR:HG22	1:A:1011:ALA:H	0.54	1.62	20	1
1:A:1019:ILE:HG23	1:A:1020:CYS:N	0.54	2.16	20	1
1:A:1019:ILE:HG13	1:A:1020:CYS:N	0.54	2.17	19	1
1:A:968:ASP:HA	1:A:974:VAL:HG11	0.54	1.80	19	1
1:A:977:ILE:HG12	1:A:986:ILE:HA	0.53	1.81	1	1
1:A:995:ARG:HG2	1:A:1023:ILE:HD11	0.53	1.79	2	1
1:A:998:GLY:HA2	1:A:1016:LYS:HD3	0.53	1.80	20	1
1:A:1022:ARG:H	1:A:1022:ARG:HD2	0.53	1.63	13	1
1:A:975:HIS:HD2	1:A:976:VAL:HG23	0.53	1.63	19	1
1:A:1019:ILE:HD12	1:A:1019:ILE:N	0.52	2.19	13	1
1:A:995:ARG:HB2	1:A:1023:ILE:HD11	0.52	1.80	18	2
1:A:970:VAL:HG22	1:A:971:ASN:ND2	0.51	2.20	5	2
1:A:965:THR:HB	1:A:966:PRO:HD3	0.51	1.82	3	3
1:A:989:SER:HA	1:A:996:LEU:HD11	0.51	1.83	18	1
1:A:995:ARG:HB3	1:A:1021:GLN:HE21	0.51	1.64	1	2
1:A:994:HIS:ND1	1:A:1022:ARG:HA	0.51	2.20	14	6
1:A:1016:LYS:HB2	1:A:1016:LYS:NZ	0.51	2.21	3	1
1:A:1023:ILE:HB	1:A:1024:PRO:HD3	0.50	1.82	2	3
1:A:1002:ALA:HB2	1:A:1015:THR:HG22	0.50	1.83	8	1
1:A:965:THR:HG22	1:A:980:ILE:HG21	0.49	1.83	7	2
1:A:978:THR:HG23	1:A:979:ASP:H	0.49	1.68	2	1
1:A:1023:ILE:N	1:A:1024:PRO:HD2	0.49	2.22	6	2
1:A:966:PRO:HD3	1:A:1013:TRP:NE1	0.49	2.22	9	3
1:A:997:ILE:HB	1:A:1019:ILE:HB	0.48	1.85	10	1
1:A:994:HIS:HB2	1:A:1020:CYS:SG	0.48	2.49	10	1
1:A:994:HIS:NE2	1:A:1022:ARG:HG2	0.48	2.24	7	1
1:A:997:ILE:N	1:A:997:ILE:HD12	0.47	2.24	10	2
1:A:972:GLY:HA2	1:A:990:CYS:HA	0.47	1.84	10	1
1:A:996:LEU:HD12	1:A:1019:ILE:O	0.47	2.10	13	3
1:A:1006:LEU:HG	1:A:1011:ALA:HB2	0.47	1.85	7	3
1:A:1022:ARG:H	1:A:1022:ARG:HD3	0.47	1.70	6	1
1:A:997:ILE:HD12	1:A:997:ILE:N	0.47	2.25	19	5
1:A:970:VAL:HG22	1:A:971:ASN:HD22	0.46	1.68	5	1
1:A:1006:LEU:HD12	1:A:1012:HIS:CD2	0.46	2.45	17	1
1:A:998:GLY:HA2	1:A:1016:LYS:NZ	0.46	2.24	8	1
1:A:994:HIS:HB3	1:A:1022:ARG:H	0.46	1.71	11	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:996:LEU:HD12	1:A:1018:PRO:HB2	0.46	1.87	7	1
1:A:996:LEU:HD21	1:A:1018:PRO:HB3	0.45	1.87	9	1
1:A:1019:ILE:HG22	1:A:1020:CYS:N	0.45	2.25	11	13
1:A:1006:LEU:HD23	1:A:1011:ALA:HB2	0.45	1.88	11	1
1:A:977:ILE:HG12	1:A:986:ILE:HG22	0.45	1.87	14	1
1:A:990:CYS:SG	1:A:994:HIS:HB2	0.45	2.51	10	2
1:A:978:THR:HG22	1:A:979:ASP:OD2	0.45	2.12	4	2
1:A:1006:LEU:HD12	1:A:1006:LEU:N	0.45	2.27	14	5
1:A:996:LEU:HD12	1:A:996:LEU:H	0.45	1.72	18	1
1:A:1006:LEU:N	1:A:1006:LEU:HD12	0.45	2.27	16	2
1:A:977:ILE:HD12	1:A:977:ILE:N	0.45	2.27	20	1
1:A:996:LEU:HG	1:A:1000:SER:HB2	0.44	1.89	7	1
1:A:964:LYS:HD2	1:A:964:LYS:N	0.44	2.27	15	1
1:A:966:PRO:HD3	1:A:1013:TRP:HE1	0.44	1.72	12	2
1:A:992:THR:HG22	1:A:993:GLY:N	0.44	2.27	14	1
1:A:997:ILE:H	1:A:997:ILE:HD12	0.44	1.71	6	1
1:A:1016:LYS:HD2	1:A:1016:LYS:N	0.44	2.28	10	5
1:A:995:ARG:NH1	1:A:997:ILE:HG13	0.44	2.28	17	1
1:A:991:THR:HG23	1:A:994:HIS:ND1	0.44	2.27	16	2
1:A:997:ILE:HG13	1:A:1019:ILE:HB	0.44	1.88	8	1
1:A:965:THR:N	1:A:966:PRO:CD	0.43	2.81	9	2
1:A:979:ASP:HB3	1:A:981:GLN:NE2	0.43	2.28	10	1
1:A:965:THR:H	1:A:966:PRO:CD	0.43	2.26	3	2
1:A:1019:ILE:CG1	1:A:1020:CYS:N	0.43	2.81	19	1
1:A:1016:LYS:HB2	1:A:1017:PRO:HD2	0.43	1.91	16	2
1:A:985:ARG:HD3	1:A:1001:SER:HB2	0.43	1.89	3	1
1:A:963:CYS:SG	1:A:1011:ALA:HB1	0.43	2.54	4	1
1:A:970:VAL:HG13	1:A:972:GLY:H	0.43	1.74	11	1
1:A:966:PRO:HG3	1:A:988:TYR:OH	0.43	2.14	10	1
1:A:970:VAL:HG13	1:A:971:ASN:HD22	0.43	1.72	6	1
1:A:995:ARG:HA	1:A:995:ARG:NE	0.43	2.29	10	1
1:A:996:LEU:HD13	1:A:997:ILE:N	0.43	2.28	20	1
1:A:997:ILE:HB	1:A:1019:ILE:H	0.43	1.73	8	1
1:A:1016:LYS:H	1:A:1016:LYS:HD2	0.43	1.74	16	1
1:A:997:ILE:HG21	1:A:1018:PRO:HB2	0.42	1.91	20	1
1:A:976:VAL:HA	1:A:986:ILE:HG22	0.42	1.91	17	2
1:A:997:ILE:HD12	1:A:997:ILE:H	0.42	1.74	12	1
1:A:1018:PRO:O	1:A:1019:ILE:HG22	0.42	2.14	20	1
1:A:994:HIS:HB3	1:A:1021:GLN:O	0.42	2.14	10	1
1:A:995:ARG:HD3	1:A:1023:ILE:HG13	0.42	1.91	9	1
1:A:994:HIS:HB3	1:A:1020:CYS:HB3	0.42	1.92	1	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:1005:ILE:HD13	1:A:1006:LEU:HG	0.42	1.92	20	1
1:A:996:LEU:HD23	1:A:1018:PRO:HB2	0.42	1.90	18	1
1:A:1017:PRO:N	1:A:1018:PRO:CD	0.42	2.83	20	1
1:A:973:MET:SD	1:A:973:MET:N	0.41	2.93	11	2
1:A:969:PRO:O	1:A:970:VAL:HG12	0.41	2.16	10	1
1:A:963:CYS:HB2	1:A:980:ILE:HG22	0.41	1.93	17	1
1:A:994:HIS:HB2	1:A:1020:CYS:HB3	0.41	1.91	5	1
1:A:970:VAL:HG13	1:A:971:ASN:N	0.41	2.30	10	1
1:A:1004:CYS:SG	1:A:1011:ALA:HB1	0.41	2.55	19	2
1:A:996:LEU:HD12	1:A:999:HIS:N	0.41	2.31	8	1
1:A:970:VAL:O	1:A:971:ASN:HB2	0.41	2.15	6	1
1:A:1016:LYS:N	1:A:1016:LYS:HD3	0.41	2.31	15	1
1:A:997:ILE:HD12	1:A:1019:ILE:HB	0.41	1.92	15	1
1:A:1006:LEU:HA	1:A:1011:ALA:HA	0.41	1.91	5	1
1:A:979:ASP:HB3	1:A:981:GLN:HE22	0.41	1.76	10	1
1:A:994:HIS:CG	1:A:1022:ARG:HA	0.41	2.51	11	1
1:A:1022:ARG:HD3	1:A:1022:ARG:N	0.41	2.31	6	1
1:A:975:HIS:CD2	1:A:976:VAL:HG23	0.41	2.49	19	1
1:A:977:ILE:HD12	1:A:985:ARG:O	0.41	2.16	3	1
1:A:1019:ILE:O	1:A:1020:CYS:C	0.40	2.60	20	1
1:A:973:MET:N	1:A:973:MET:SD	0.40	2.94	18	1
1:A:1023:ILE:HD12	1:A:1023:ILE:O	0.40	2.15	13	1
1:A:1016:LYS:HD3	1:A:1016:LYS:C	0.40	2.37	3	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	62/68 (91%)	45±3 (73±6%)	13±3 (21±5%)	4±2 (6±4%)	3	20
All	All	1240/1360 (91%)	905 (73%)	259 (21%)	76 (6%)	3	20

All 26 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	1022	ARG	8
1	A	965	THR	7
1	A	962	SER	7
1	A	1008	GLY	5
1	A	977	ILE	5
1	A	1017	PRO	5
1	A	976	VAL	4
1	A	1004	CYS	3
1	A	1000	SER	3
1	A	993	GLY	3
1	A	970	VAL	3
1	A	1006	LEU	2
1	A	969	PRO	2
1	A	999	HIS	2
1	A	1011	ALA	2
1	A	968	ASP	2
1	A	966	PRO	2
1	A	997	ILE	2
1	A	991	THR	2
1	A	975	HIS	1
1	A	1023	ILE	1
1	A	1010	THR	1
1	A	1014	SER	1
1	A	990	CYS	1
1	A	1019	ILE	1
1	A	980	ILE	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	56/59 (95%)	54±1 (96±2%)	2±1 (4±2%)	40	85
All	All	1120/1180 (95%)	1077 (96%)	43 (4%)	40	85

All 15 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	1016	LYS	18
1	A	988	TYR	4
1	A	999	HIS	3
1	A	973	MET	3
1	A	1022	ARG	3
1	A	1010	THR	2
1	A	994	HIS	2
1	A	1021	GLN	1
1	A	981	GLN	1
1	A	995	ARG	1
1	A	970	VAL	1
1	A	965	THR	1
1	A	964	LYS	1
1	A	978	THR	1
1	A	991	THR	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 49% for the well-defined parts and 47% for the entire structure.

7.1 Chemical shift list 1

File name: BMRB entry 5900

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	455
Number of shifts mapped to atoms	455
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
$^{13}\text{C}_\alpha$	0	—	None (insufficient data)
$^{13}\text{C}_\beta$	0	—	None (insufficient data)
$^{13}\text{C}'$	0	—	None (insufficient data)
^{15}N	56	3.08 ± 0.80	Should be applied

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 49%, i.e. 360 atoms were assigned a chemical shift out of a possible 734. 0 out of 6 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	167/303 (55%)	113/120 (94%)	0/126 (0%)	54/57 (95%)
Sidechain	177/379 (47%)	173/225 (77%)	0/139 (0%)	4/15 (27%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	16/52 (31%)	15/26 (58%)	0/17 (0%)	1/9 (11%)
Overall	360/734 (49%)	301/371 (81%)	0/282 (0%)	59/81 (73%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 47%, i.e. 371 atoms were assigned a chemical shift out of a possible 790. 0 out of 6 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	173/328 (53%)	117/130 (90%)	0/136 (0%)	56/62 (90%)
Sidechain	182/410 (44%)	178/243 (73%)	0/151 (0%)	4/16 (25%)
Aromatic	16/52 (31%)	15/26 (58%)	0/17 (0%)	1/9 (11%)
Overall	371/790 (47%)	310/399 (78%)	0/304 (0%)	61/87 (70%)

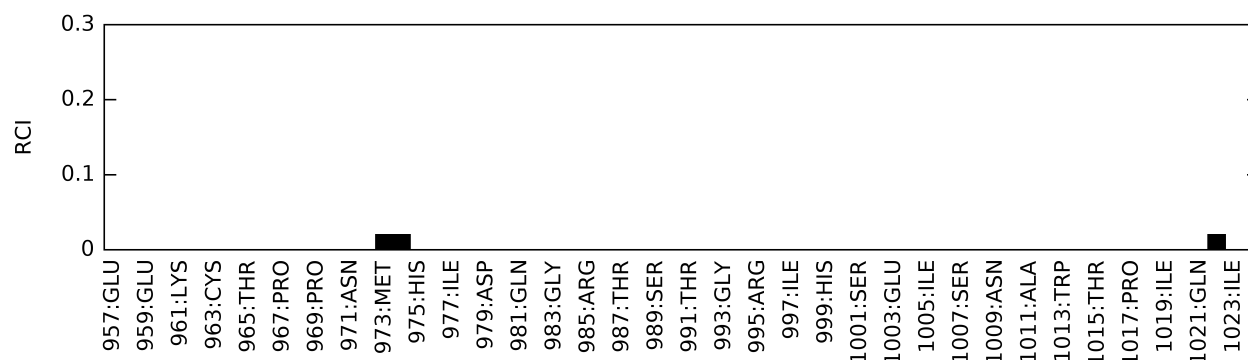
7.1.4 Statistically unusual chemical shifts [i](#)

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 5900

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	17
Number of shifts mapped to atoms	17
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

7.2.2 Chemical shift referencing [i](#)

No chemical shift referencing corrections were calculated (not enough data).

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 2%, i.e. 13 atoms were assigned a chemical shift out of a possible 734. 0 out of 6 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	9/303 (3%)	6/120 (5%)	0/126 (0%)	3/57 (5%)
Sidechain	4/379 (1%)	4/225 (2%)	0/139 (0%)	0/15 (0%)
Aromatic	0/52 (0%)	0/26 (0%)	0/17 (0%)	0/9 (0%)
Overall	13/734 (2%)	10/371 (3%)	0/282 (0%)	3/81 (4%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 2%, i.e. 13 atoms were assigned a chemical shift out of a possible 790. 0 out of 6 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	9/328 (3%)	6/130 (5%)	0/136 (0%)	3/62 (5%)
Sidechain	4/410 (1%)	4/243 (2%)	0/151 (0%)	0/16 (0%)
Aromatic	0/52 (0%)	0/26 (0%)	0/17 (0%)	0/9 (0%)
Overall	13/790 (2%)	10/399 (3%)	0/304 (0%)	3/87 (3%)

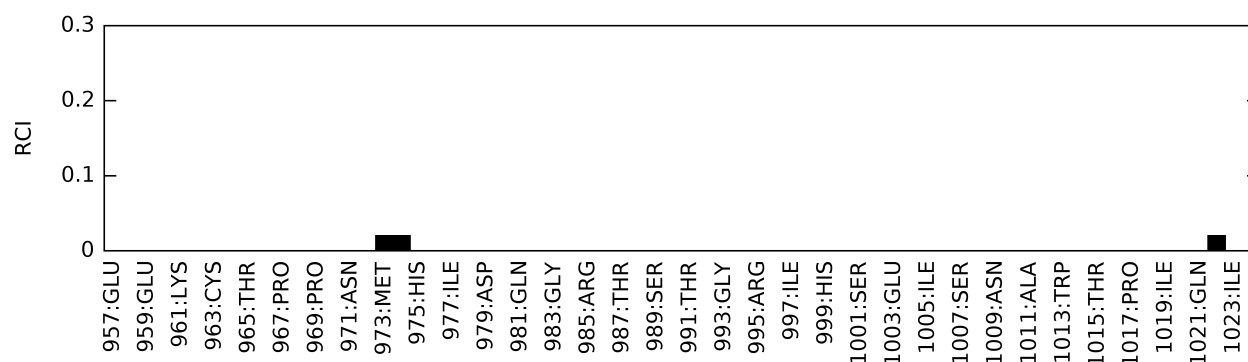
7.2.4 Statistically unusual chemical shifts [i](#)

There are no statistically unusual chemical shifts.

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 A:



7.3 Chemical shift list 3

File name: BMRB entry 5900

Chemical shift list name: *assigned_chem_shift_list_3*

7.3.1 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	2
Number of shifts mapped to atoms	2
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

7.3.2 Chemical shift referencing [i](#)

No chemical shift referencing corrections were calculated (not enough data).

7.3.3 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 0%, i.e. 2 atoms were assigned a chemical shift out of a possible 734. 0 out of 6 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	2/303 (1%)	1/120 (1%)	0/126 (0%)	1/57 (2%)
Sidechain	0/379 (0%)	0/225 (0%)	0/139 (0%)	0/15 (0%)
Aromatic	0/52 (0%)	0/26 (0%)	0/17 (0%)	0/9 (0%)
Overall	2/734 (0%)	1/371 (0%)	0/282 (0%)	1/81 (1%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 0%, i.e. 2 atoms were assigned a chemical shift out of a possible 790. 0 out of 6 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	2/328 (1%)	1/130 (1%)	0/136 (0%)	1/62 (2%)
Sidechain	0/410 (0%)	0/243 (0%)	0/151 (0%)	0/16 (0%)
Aromatic	0/52 (0%)	0/26 (0%)	0/17 (0%)	0/9 (0%)
Overall	2/790 (0%)	1/399 (0%)	0/304 (0%)	1/87 (1%)

7.3.4 Statistically unusual chemical shifts [i](#)

There are no statistically unusual chemical shifts.

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

No *random coil index* (RCI) plot could be generated from the current chemical shift list (assigned_chem_shift_list_3). RCI is only applicable to proteins.