



Full wwPDB NMR Structure Validation Report ⓘ

Apr 27, 2016 – 05:12 AM BST

PDB ID : 2RQF
Title : Solution structure of juvenile hormone binding protein from silkworm in complex with JH III
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Deposited on : 2009-04-27

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 : 1.7.1 (RC1), CSD as537be (2016)
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

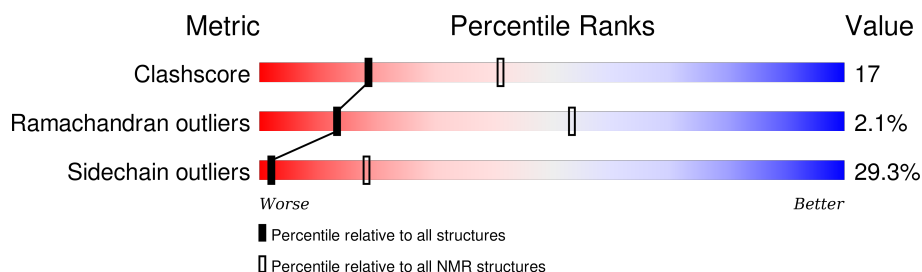
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 96%.

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	227	<div> <div>53%</div> <div>37%</div> <div>7%</div> <div>.</div> </div>

2 Ensemble composition and analysis

This entry contains 20 models. Model 1 is the overall representative, medoid model (most similar to other models).

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

Well-defined (core) protein residues			
Well-defined core	Residue range (total)	Backbone RMSD (Å)	Medoid model
1	A:5-A:225 (221)	0.22	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 4 clusters and 3 single-model clusters were found.

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

3 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 3521 atoms, of which 1766 are hydrogens and 0 are deuteriums.

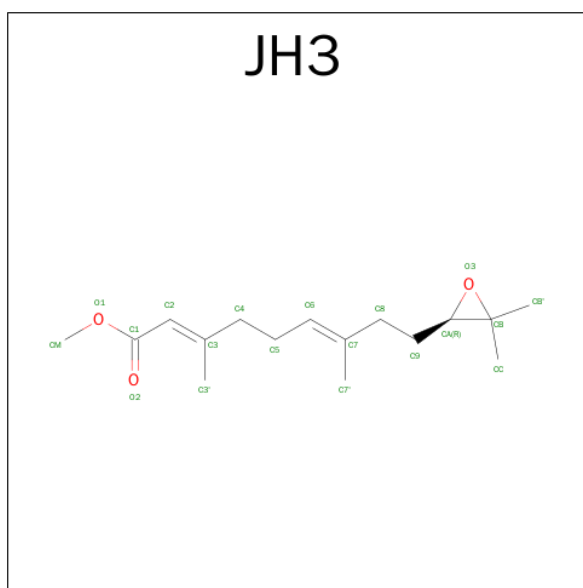
- Molecule 1 is a protein called Hemolymph juvenile hormone binding protein.

Mol	Chain	Residues	Atoms						Trace
1	A	227	Total	C	H	N	O	S	0
			3476	1094	1740	285	349	8	

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	EXPRESSION TAG	UNP Q9U556
A	-1	SER	-	EXPRESSION TAG	UNP Q9U556

- Molecule 2 is METHYL (2E,6E)-9-[(2R)-3,3-DIMETHYLOXIRAN-2-YL]-3,7-DIMETHYLNONA-2,6-DIENOATE (three-letter code: JH3) (formula: C₁₆H₂₆O₃).



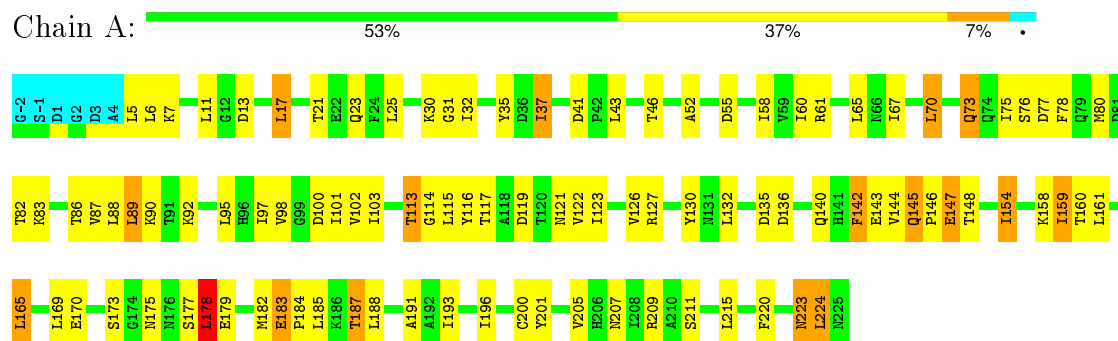
Mol	Chain	Residues	Atoms			
2	A	1	Total	C	H	O
			45	16	26	3

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: Hemolymph juvenile hormone binding protein

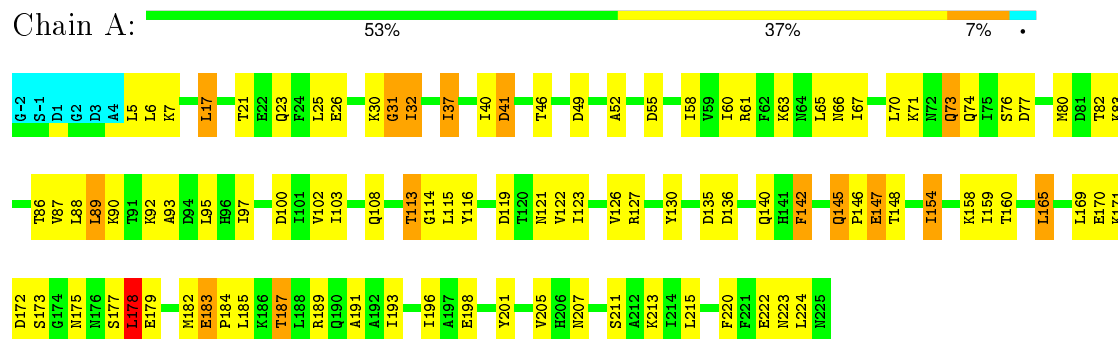


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

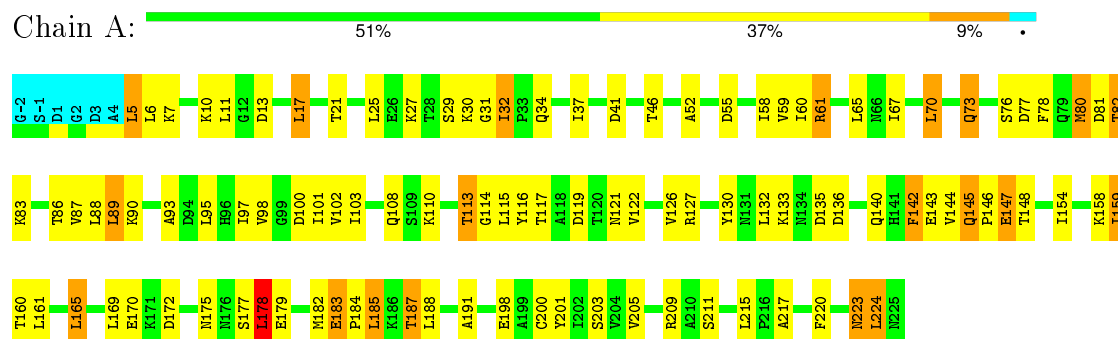
4.2.1 Score per residue for model 1 (medoid)

- Molecule 1: Hemolymph juvenile hormone binding protein



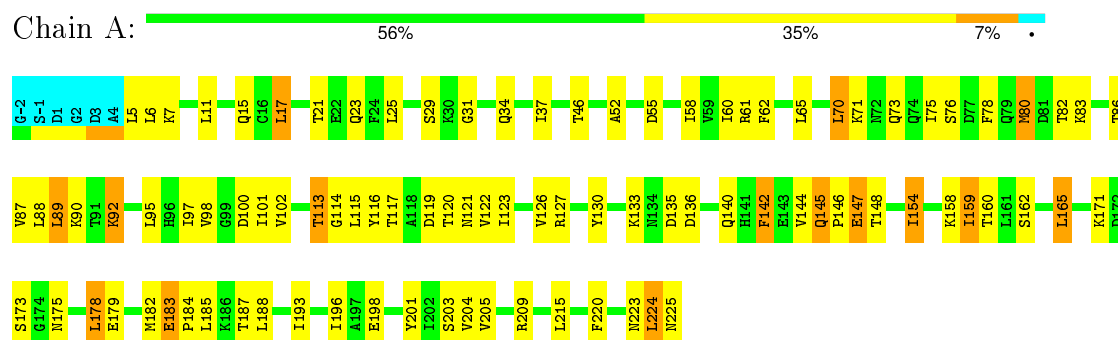
4.2.2 Score per residue for model 2

- Molecule 1: Hemolymph juvenile hormone binding protein



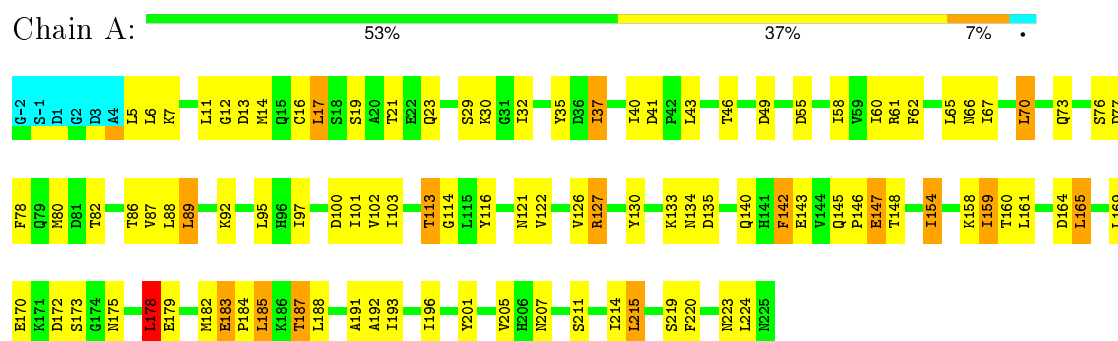
4.2.3 Score per residue for model 3

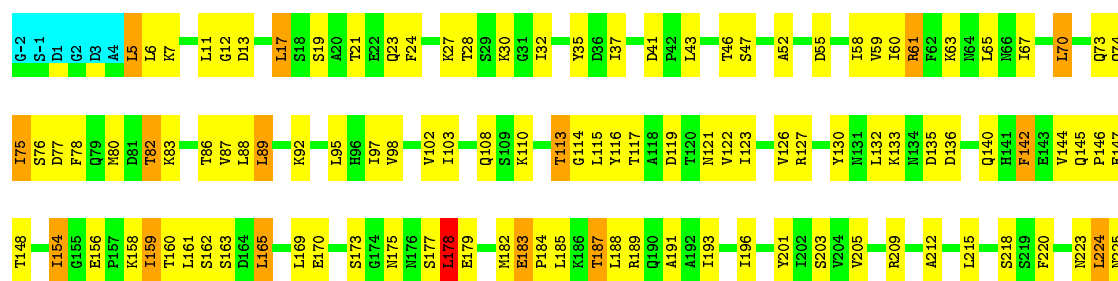
- Molecule 1: Hemolymph juvenile hormone binding protein



4.2.4 Score per residue for model 4

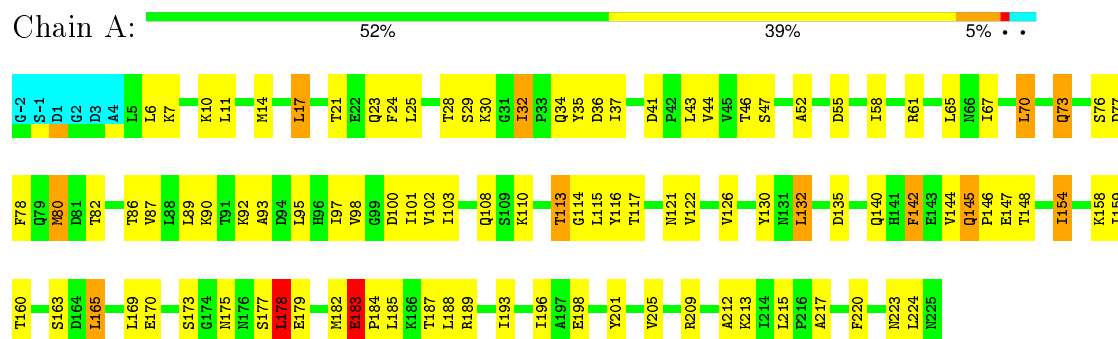
- Molecule 1: Hemolymph juvenile hormone binding protein





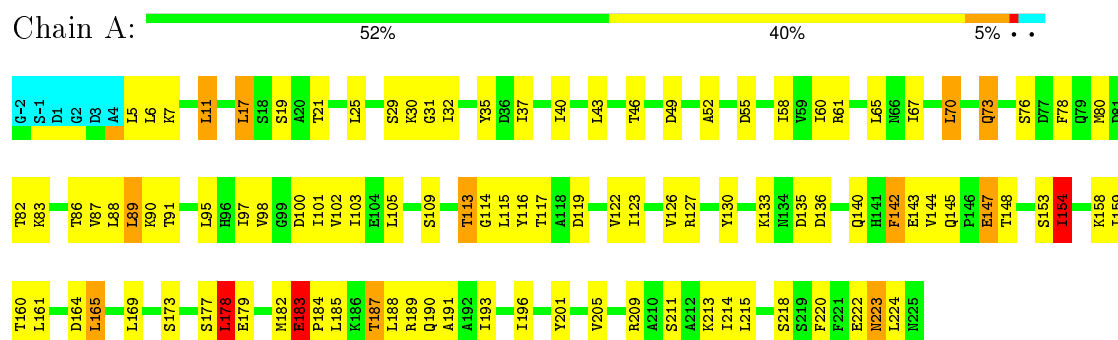
4.2.8 Score per residue for model 8

- Molecule 1: Hemolymph juvenile hormone binding protein



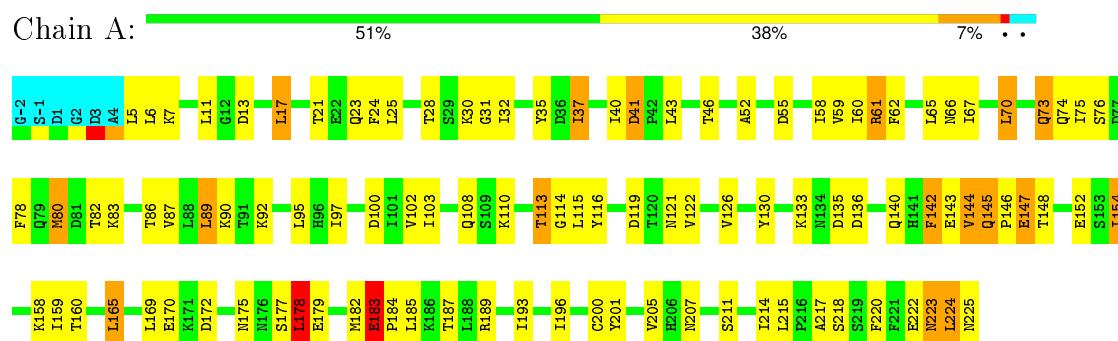
4.2.9 Score per residue for model 9

- Molecule 1: Hemolymph juvenile hormone binding protein



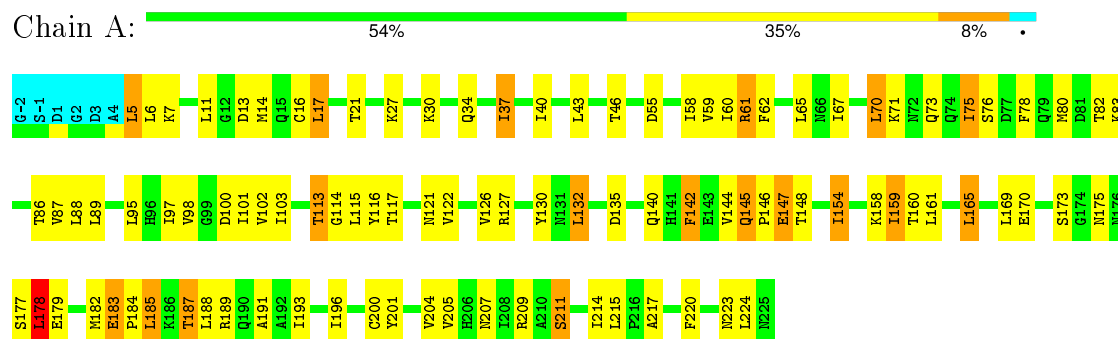
4.2.10 Score per residue for model 10

- Molecule 1: Hemolymph juvenile hormone binding protein



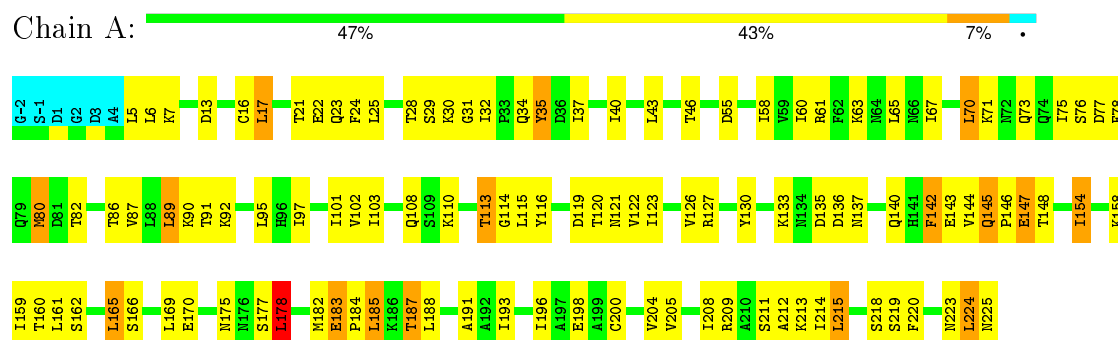
4.2.11 Score per residue for model 11

- Molecule 1: Hemolymph juvenile hormone binding protein



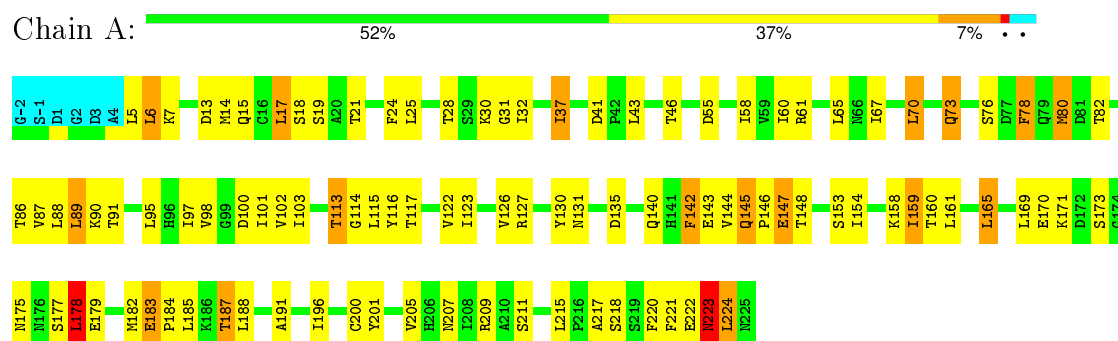
4.2.12 Score per residue for model 12

- Molecule 1: Hemolymph juvenile hormone binding protein



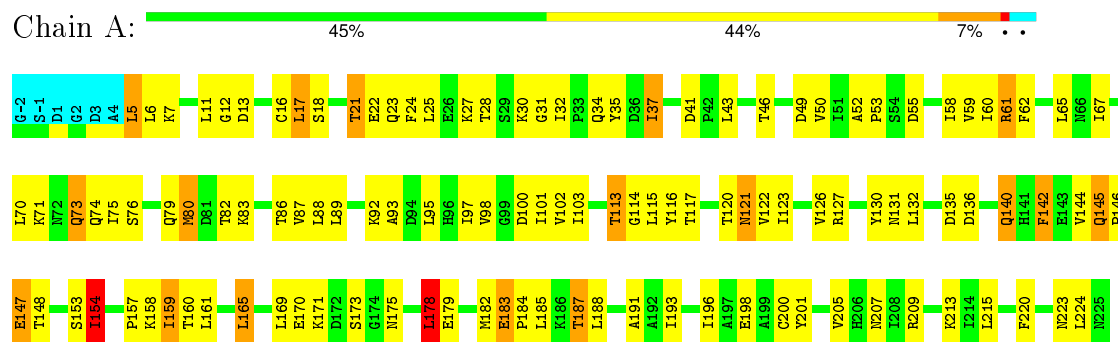
4.2.13 Score per residue for model 13

- Molecule 1: Hemolymph juvenile hormone binding protein



4.2.14 Score per residue for model 14

- Molecule 1: Hemolymph juvenile hormone binding protein



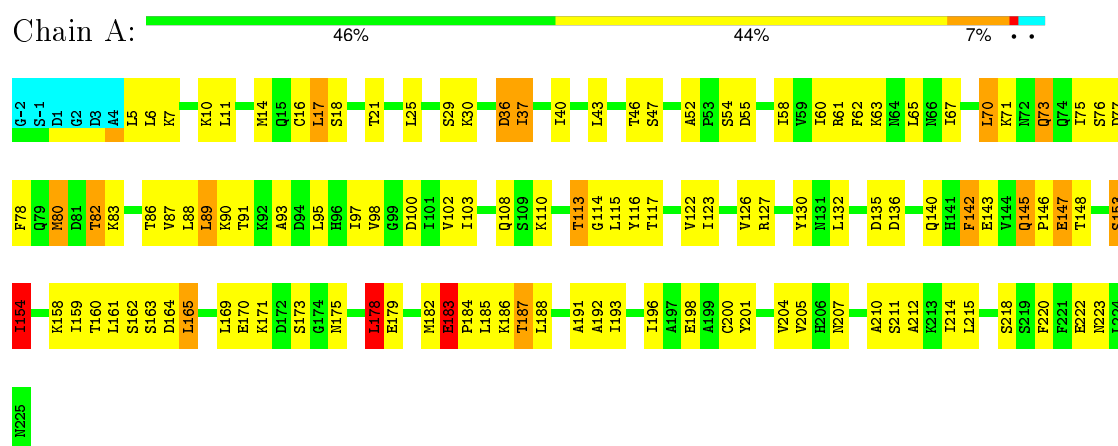
4.2.15 Score per residue for model 15

- Molecule 1: Hemolymph juvenile hormone binding protein



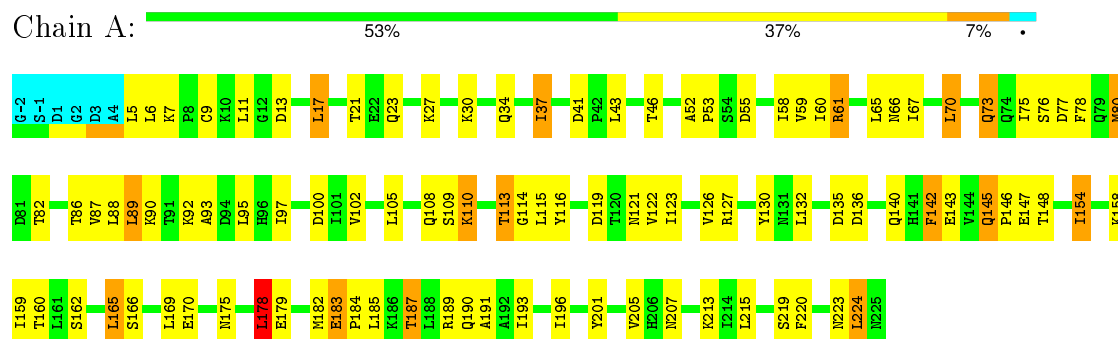
4.2.16 Score per residue for model 16

- Molecule 1: Hemolymph juvenile hormone binding protein



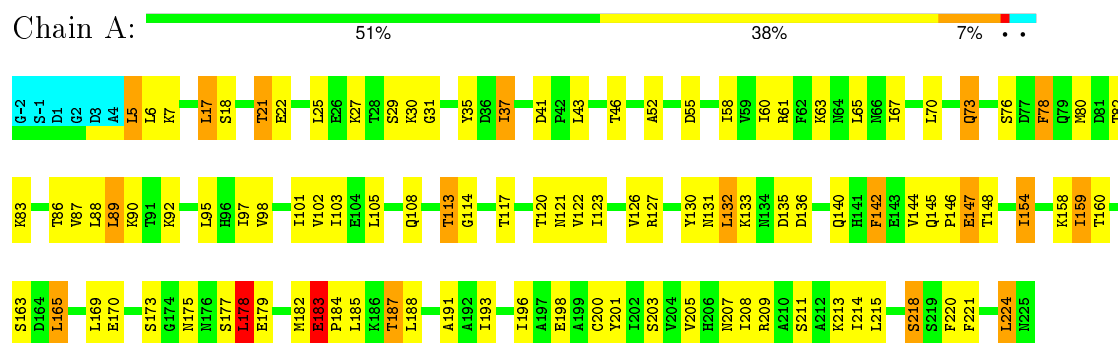
4.2.17 Score per residue for model 17

- Molecule 1: Hemolymph juvenile hormone binding protein



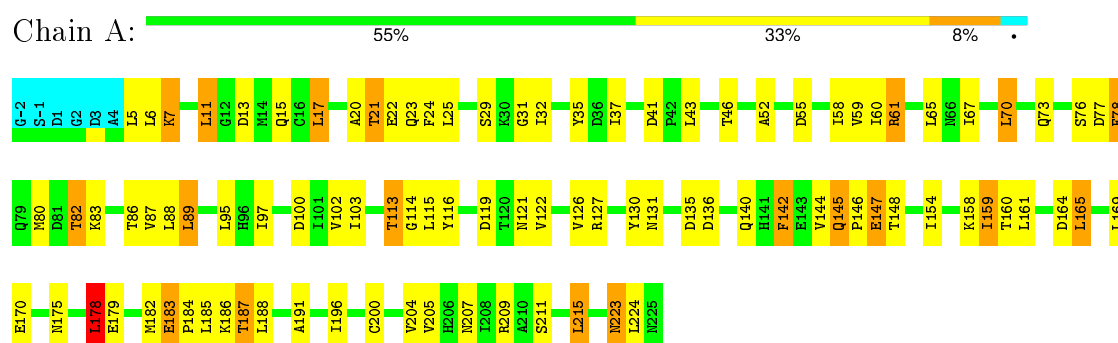
4.2.18 Score per residue for model 18

- Molecule 1: Hemolymph juvenile hormone binding protein



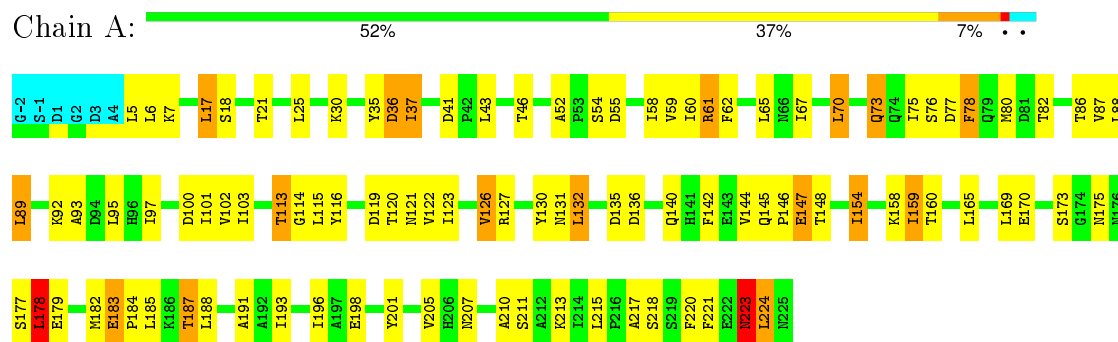
4.2.19 Score per residue for model 19

- Molecule 1: Hemolymph juvenile hormone binding protein



4.2.20 Score per residue for model 20

- Molecule 1: Hemolymph juvenile hormone binding protein



5 Refinement protocol and experimental data overview

The models were refined using the following method: *torsion angle dynamics*.

Of the 100 calculated structures, 20 were deposited, based on the following criterion: *structures with the least restraint violations*.

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

Software name	Classification	Version
CYANA	structure solution	2.1
CYANA	refinement	2.1

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 11073
Number of chemical shift lists	1
Total number of shifts	2926
Number of shifts mapped to atoms	2900
Number of unparsed shifts	0
Number of shifts with mapping errors	26
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	96%

No validations of the models with respect to experimental NMR restraints is performed at this time.

6 Model quality ⓘ

6.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: JH3

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	1701	1716	1716	57±6
2	A	19	26	26	7±2
All	All	34400	34840	34840	1175

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 17.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:70:LEU:HD12	1:A:95:LEU:HD21	0.95	1.37	19	19
1:A:144:VAL:HG12	2:A:300:JH3:HB'	0.93	1.37	19	8
1:A:25:LEU:HD21	1:A:204:VAL:HG13	0.92	1.39	12	2
1:A:102:VAL:HG22	1:A:113:THR:HG23	0.91	1.43	13	19
1:A:17:LEU:HD11	2:A:300:JH3:H3'	0.86	1.46	9	18
1:A:95:LEU:HD12	1:A:122:VAL:HG21	0.83	1.47	16	19
1:A:132:LEU:HD21	1:A:224:LEU:HD22	0.83	1.48	11	3
1:A:70:LEU:HD13	1:A:95:LEU:HD21	0.75	1.58	14	1
1:A:75:ILE:HD11	1:A:89:LEU:HD13	0.74	1.58	7	2
1:A:154:ILE:HG22	1:A:193:ILE:HG21	0.74	1.60	18	15
1:A:217:ALA:HB1	1:A:224:LEU:HD13	0.73	1.61	11	4

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:67:ILE:HG22	1:A:95:LEU:HD22	0.71	1.60	19	12
1:A:89:LEU:HD11	2:A:300:JH3:HMA	0.71	1.62	2	4
1:A:187:THR:HG22	1:A:191:ALA:HB2	0.70	1.64	15	15
1:A:221:PHE:CE2	1:A:224:LEU:HD12	0.69	2.21	18	2
1:A:142:PHE:CD1	2:A:300:JH3:HB'B	0.69	2.23	3	12
2:A:300:JH3:C2	2:A:300:JH3:H7'B	0.67	2.20	19	11
1:A:31:GLY:O	1:A:32:ILE:HD13	0.67	1.90	15	2
1:A:62:PHE:CE2	1:A:101:ILE:HD12	0.66	2.25	14	1
1:A:58:ILE:HG21	1:A:184:PRO:HB3	0.66	1.67	16	10
1:A:11:LEU:HD12	1:A:223:ASN:OD1	0.66	1.91	5	1
1:A:37:ILE:HG22	1:A:207:ASN:CB	0.65	2.21	10	12
1:A:35:TYR:CD1	1:A:214:ILE:HD13	0.65	2.26	18	1
1:A:142:PHE:CE2	1:A:224:LEU:HD11	0.65	2.27	8	3
1:A:95:LEU:HD12	1:A:122:VAL:CG2	0.65	2.21	7	19
1:A:142:PHE:CZ	1:A:224:LEU:HD11	0.64	2.26	11	3
1:A:87:VAL:HG23	1:A:130:TYR:CD1	0.64	2.27	13	19
1:A:35:TYR:CZ	1:A:214:ILE:HG21	0.64	2.28	9	2
1:A:60:ILE:HD12	1:A:103:ILE:CD1	0.64	2.23	12	9
1:A:25:LEU:HD21	1:A:204:VAL:CG1	0.64	2.21	12	1
1:A:17:LEU:CD1	2:A:300:JH3:H3'	0.63	2.22	12	18
1:A:60:ILE:HG23	1:A:103:ILE:HD13	0.63	1.71	2	8
1:A:65:LEU:HD22	1:A:97:ILE:CG2	0.63	2.22	12	20
1:A:142:PHE:CD2	2:A:300:JH3:HCA	0.63	2.28	4	1
1:A:11:LEU:HD23	1:A:80:MET:HE2	0.63	1.69	8	1
1:A:161:LEU:HD12	1:A:178:LEU:CD1	0.63	2.24	9	7
1:A:144:VAL:HG11	1:A:209:ARG:HA	0.63	1.70	8	7
1:A:89:LEU:HD11	2:A:300:JH3:CM	0.62	2.24	16	16
1:A:102:VAL:CG2	1:A:113:THR:HG23	0.62	2.22	12	8
1:A:80:MET:HB2	1:A:87:VAL:HG22	0.62	1.70	4	1
1:A:58:ILE:HG22	1:A:60:ILE:HD11	0.62	1.71	19	15
1:A:67:ILE:CG2	1:A:95:LEU:HD22	0.61	2.25	13	11
1:A:217:ALA:HB1	1:A:224:LEU:CD1	0.61	2.25	11	2
1:A:11:LEU:HD11	1:A:223:ASN:O	0.61	1.94	10	6
1:A:37:ILE:HG22	1:A:207:ASN:CG	0.61	2.15	4	11
1:A:70:LEU:CD1	1:A:95:LEU:HD21	0.61	2.21	19	11
1:A:60:ILE:HG21	1:A:188:LEU:HD11	0.61	1.72	12	3
1:A:97:ILE:CD1	1:A:196:ILE:HD13	0.61	2.26	15	19
1:A:187:THR:O	1:A:191:ALA:HB3	0.61	1.95	17	4
1:A:187:THR:HG22	1:A:191:ALA:CB	0.61	2.25	2	11
1:A:6:LEU:HD11	1:A:220:PHE:CE2	0.61	2.31	12	2
1:A:142:PHE:CG	2:A:300:JH3:HB'B	0.61	2.30	14	6

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:98:VAL:HG22	1:A:117:THR:HG23	0.61	1.70	18	11
1:A:11:LEU:HD23	1:A:80:MET:CE	0.60	2.26	8	2
1:A:11:LEU:HD12	1:A:12:GLY:N	0.60	2.11	14	3
1:A:17:LEU:HD13	1:A:78:PHE:CE2	0.60	2.30	7	8
1:A:132:LEU:HD21	1:A:224:LEU:CD1	0.60	2.26	20	1
1:A:6:LEU:HD21	1:A:220:PHE:CD2	0.60	2.31	9	17
1:A:31:GLY:C	1:A:32:ILE:HD13	0.60	2.17	1	2
1:A:88:LEU:HD13	1:A:127:ARG:HG2	0.60	1.73	6	16
1:A:80:MET:HG3	1:A:87:VAL:HG22	0.60	1.73	10	5
1:A:17:LEU:HD13	1:A:78:PHE:CZ	0.59	2.32	20	9
1:A:120:THR:HG21	1:A:193:ILE:HD11	0.59	1.73	18	6
1:A:25:LEU:HD13	1:A:73:GLN:OE1	0.59	1.98	13	12
1:A:17:LEU:HD22	1:A:78:PHE:CD2	0.59	2.33	16	7
1:A:154:ILE:CG2	1:A:193:ILE:HG21	0.59	2.27	14	16
1:A:132:LEU:HD21	1:A:224:LEU:HD13	0.59	1.73	18	4
1:A:18:SER:HA	1:A:75:ILE:HD12	0.59	1.74	20	3
1:A:89:LEU:HD11	2:A:300:JH3:HM	0.59	1.72	12	3
1:A:102:VAL:HG22	1:A:113:THR:HB	0.59	1.74	6	1
1:A:78:PHE:HB2	1:A:89:LEU:HD12	0.58	1.74	10	1
1:A:147:GLU:HG2	1:A:205:VAL:HG21	0.58	1.75	12	11
1:A:80:MET:CG	1:A:87:VAL:HG22	0.58	2.29	13	9
1:A:147:GLU:HG3	1:A:205:VAL:HG21	0.58	1.76	19	5
2:A:300:JH3:H7'B	2:A:300:JH3:C2	0.58	2.29	7	9
1:A:114:GLY:N	1:A:165:LEU:HD23	0.57	2.14	10	17
1:A:6:LEU:HD21	1:A:220:PHE:CE2	0.57	2.35	16	7
1:A:40:ILE:HD13	1:A:204:VAL:CG1	0.57	2.30	16	2
1:A:20:ALA:HB1	1:A:24:PHE:CZ	0.57	2.34	19	1
1:A:6:LEU:HD13	1:A:24:PHE:CZ	0.57	2.34	19	1
1:A:87:VAL:HG23	1:A:130:TYR:CD2	0.57	2.35	7	1
1:A:59:VAL:HG12	1:A:61:ARG:HD2	0.56	1.76	17	9
1:A:208:ILE:HG21	2:A:300:JH3:H7'	0.56	1.78	6	2
1:A:199:ALA:HA	1:A:202:ILE:HD12	0.56	1.76	15	1
1:A:115:LEU:HD23	1:A:116:TYR:N	0.56	2.16	5	16
1:A:208:ILE:HG22	2:A:300:JH3:HCB	0.55	1.76	5	2
1:A:159:ILE:HD13	1:A:185:LEU:HD13	0.55	1.77	4	4
1:A:37:ILE:HG22	1:A:207:ASN:HB3	0.55	1.78	17	10
1:A:32:ILE:HG22	1:A:34:GLN:HG2	0.55	1.77	8	1
1:A:144:VAL:HG21	1:A:209:ARG:HB3	0.55	1.77	15	1
1:A:87:VAL:HG23	1:A:130:TYR:CE1	0.55	2.36	14	2
1:A:17:LEU:HD13	1:A:78:PHE:CE1	0.55	2.36	18	1
1:A:114:GLY:N	1:A:165:LEU:HD12	0.55	2.17	20	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:80:MET:HE1	1:A:224:LEU:HD21	0.55	1.79	15	3
1:A:217:ALA:O	1:A:224:LEU:HD12	0.54	2.02	8	1
1:A:24:PHE:CZ	1:A:28:THR:HG21	0.54	2.36	12	1
1:A:17:LEU:HD13	1:A:78:PHE:CD2	0.54	2.38	11	2
1:A:200:CYS:O	1:A:204:VAL:HG23	0.54	2.02	12	2
1:A:144:VAL:CG1	2:A:300:JH3:HB'	0.54	2.27	2	2
1:A:88:LEU:HD22	1:A:127:ARG:NH2	0.54	2.17	9	1
1:A:169:LEU:HD12	1:A:178:LEU:HD11	0.54	1.78	9	19
2:A:300:JH3:CC	2:A:300:JH3:H7'	0.54	2.33	14	1
1:A:114:GLY:HA3	1:A:165:LEU:HD23	0.53	1.79	3	19
1:A:60:ILE:HD12	1:A:103:ILE:HD12	0.53	1.80	2	6
1:A:5:LEU:HD23	1:A:27:LYS:CB	0.53	2.33	17	1
1:A:43:LEU:HD22	1:A:200:CYS:SG	0.53	2.43	15	3
2:A:300:JH3:H7'B	2:A:300:JH3:H2	0.53	1.79	5	1
1:A:208:ILE:CG2	2:A:300:JH3:HCB	0.53	2.34	5	1
1:A:60:ILE:HG21	1:A:188:LEU:CD1	0.53	2.34	14	3
1:A:62:PHE:CD2	1:A:65:LEU:HD11	0.53	2.38	5	3
1:A:122:VAL:HG22	1:A:193:ILE:HG23	0.52	1.79	18	6
1:A:88:LEU:HD22	1:A:127:ARG:HH11	0.52	1.64	1	1
2:A:300:JH3:H2	2:A:300:JH3:H7'B	0.52	1.81	12	2
1:A:43:LEU:HD12	1:A:44:VAL:N	0.52	2.19	8	1
1:A:114:GLY:CA	1:A:165:LEU:HD23	0.52	2.35	3	19
1:A:201:TYR:O	1:A:205:VAL:HG23	0.52	2.05	1	16
1:A:6:LEU:HD23	1:A:215:LEU:CD1	0.52	2.34	19	1
1:A:75:ILE:CD1	1:A:89:LEU:HD11	0.52	2.34	3	2
1:A:60:ILE:HD12	1:A:103:ILE:HD13	0.52	1.82	6	3
1:A:43:LEU:O	1:A:67:ILE:HD12	0.52	2.04	11	15
1:A:88:LEU:HD13	1:A:127:ARG:CG	0.52	2.34	3	3
1:A:80:MET:CE	1:A:224:LEU:HD21	0.52	2.34	12	3
1:A:142:PHE:HB3	1:A:212:ALA:HB1	0.51	1.81	12	5
1:A:101:ILE:HD11	1:A:103:ILE:HD11	0.51	1.82	18	1
1:A:208:ILE:HG21	2:A:300:JH3:H9	0.51	1.81	5	1
1:A:215:LEU:HD12	1:A:219:SER:HB2	0.51	1.80	12	2
1:A:82:THR:HG23	1:A:130:TYR:OH	0.51	2.04	19	5
1:A:97:ILE:HD13	1:A:196:ILE:HD13	0.51	1.81	11	4
1:A:58:ILE:HG23	1:A:105:LEU:CD2	0.51	2.35	9	2
1:A:144:VAL:HA	2:A:300:JH3:HB'	0.51	1.82	7	1
1:A:103:ILE:HD13	1:A:165:LEU:HD11	0.51	1.82	1	4
1:A:58:ILE:HG21	1:A:184:PRO:CB	0.51	2.36	13	7
1:A:60:ILE:HD12	1:A:103:ILE:HG13	0.51	1.83	16	1
1:A:92:LYS:HB3	1:A:123:ILE:HG23	0.51	1.83	18	10

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:101:ILE:HD11	1:A:188:LEU:HD11	0.51	1.81	6	9
1:A:144:VAL:HG21	1:A:209:ARG:HG2	0.51	1.82	2	5
1:A:142:PHE:CZ	1:A:224:LEU:HD13	0.51	2.40	15	1
1:A:11:LEU:HD23	1:A:80:MET:HE1	0.50	1.81	2	1
1:A:58:ILE:HG22	1:A:60:ILE:CD1	0.50	2.37	17	4
1:A:120:THR:CG2	1:A:121:ASN:N	0.50	2.75	14	1
1:A:11:LEU:HD23	1:A:80:MET:SD	0.50	2.47	3	2
1:A:58:ILE:HG21	1:A:184:PRO:HG3	0.50	1.82	6	3
1:A:24:PHE:O	1:A:28:THR:HG23	0.49	2.07	15	7
1:A:17:LEU:HD11	1:A:78:PHE:CE2	0.49	2.42	4	1
1:A:5:LEU:HD23	1:A:27:LYS:HB2	0.49	1.83	5	7
1:A:221:PHE:CD1	1:A:224:LEU:HD11	0.49	2.42	15	1
1:A:144:VAL:HG23	1:A:144:VAL:O	0.49	2.07	15	1
1:A:147:GLU:OE2	1:A:205:VAL:HG11	0.49	2.08	19	1
1:A:144:VAL:HG21	1:A:209:ARG:CG	0.49	2.37	2	6
1:A:144:VAL:HG11	1:A:209:ARG:HG2	0.49	1.85	14	1
1:A:67:ILE:HG23	1:A:97:ILE:HG13	0.48	1.86	12	1
1:A:123:ILE:HD12	1:A:153:SER:HB3	0.48	1.85	14	4
1:A:52:ALA:HB3	1:A:58:ILE:HB	0.48	1.86	1	16
2:A:300:JH3:H7'	2:A:300:JH3:HCB	0.48	1.85	14	1
1:A:80:MET:HE2	1:A:130:TYR:CZ	0.48	2.43	7	1
1:A:188:LEU:O	1:A:192:ALA:HB3	0.48	2.08	16	2
1:A:70:LEU:HD22	1:A:200:CYS:SG	0.48	2.48	15	4
1:A:159:ILE:HD11	1:A:188:LEU:HB3	0.48	1.84	12	9
1:A:88:LEU:HD13	1:A:127:ARG:HG3	0.48	1.85	4	1
1:A:127:ARG:NH2	1:A:150:THR:HG21	0.48	2.23	5	1
1:A:31:GLY:HA2	1:A:37:ILE:HG22	0.48	1.84	12	3
1:A:73:GLN:HA	1:A:93:ALA:HB2	0.48	1.84	8	9
1:A:35:TYR:HB2	1:A:37:ILE:HD11	0.48	1.86	15	1
1:A:88:LEU:HD22	1:A:127:ARG:NH1	0.48	2.23	1	1
1:A:183:GLU:HA	1:A:184:PRO:C	0.47	2.30	20	20
1:A:103:ILE:HG22	1:A:103:ILE:O	0.47	2.09	14	1
1:A:17:LEU:HD23	1:A:18:SER:N	0.47	2.23	13	1
1:A:142:PHE:CE1	2:A:300:JH3:HB'B	0.47	2.45	11	1
1:A:120:THR:OG1	1:A:157:PRO:HA	0.47	2.08	14	1
1:A:17:LEU:CG	2:A:300:JH3:H3'	0.47	2.39	17	2
1:A:223:ASN:CG	1:A:223:ASN:O	0.47	2.53	13	2
1:A:211:SER:HA	1:A:214:ILE:HD12	0.47	1.85	11	1
1:A:35:TYR:CE1	1:A:214:ILE:HG21	0.47	2.45	18	1
1:A:6:LEU:HD21	1:A:220:PHE:CG	0.47	2.45	9	2
1:A:21:THR:HG22	1:A:22:GLU:N	0.47	2.25	19	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:36:ASP:OD2	1:A:210:ALA:HB1	0.47	2.10	20	2
1:A:218:SER:HA	1:A:221:PHE:CE1	0.46	2.45	18	1
1:A:144:VAL:HG12	2:A:300:JH3:CB'	0.46	2.41	6	6
1:A:217:ALA:HB1	1:A:221:PHE:CE2	0.46	2.45	20	2
1:A:58:ILE:HD13	1:A:184:PRO:HB3	0.46	1.88	16	1
1:A:101:ILE:HG23	1:A:165:LEU:HD13	0.46	1.87	20	1
2:A:300:JH3:HCB	2:A:300:JH3:H7'	0.46	1.87	8	3
1:A:6:LEU:HD13	1:A:24:PHE:CE1	0.46	2.46	19	1
1:A:147:GLU:CD	1:A:205:VAL:HG21	0.46	2.31	5	2
1:A:126:VAL:HG22	1:A:201:TYR:CE2	0.46	2.46	20	1
1:A:89:LEU:HD22	2:A:300:JH3:HMA	0.46	1.88	3	1
1:A:122:VAL:CG2	1:A:193:ILE:HG23	0.46	2.40	14	5
1:A:53:PRO:HD2	1:A:187:THR:HG21	0.46	1.88	17	2
1:A:62:PHE:HE2	1:A:101:ILE:HD12	0.46	1.70	14	1
1:A:120:THR:HG22	1:A:121:ASN:N	0.46	2.26	14	1
1:A:73:GLN:OE1	1:A:73:GLN:N	0.45	2.49	12	1
1:A:58:ILE:CG2	1:A:60:ILE:HD11	0.45	2.41	3	4
1:A:159:ILE:HD13	1:A:185:LEU:CD1	0.45	2.41	4	2
1:A:62:PHE:CG	1:A:65:LEU:HD11	0.45	2.46	10	6
1:A:78:PHE:HB3	1:A:89:LEU:HD12	0.45	1.88	3	1
1:A:89:LEU:HG	2:A:300:JH3:H3'B	0.45	1.87	15	1
1:A:101:ILE:CD1	1:A:188:LEU:HD11	0.45	2.40	13	5
1:A:25:LEU:HD22	1:A:204:VAL:HG12	0.45	1.88	3	1
1:A:145:GLN:CB	1:A:146:PRO:HD2	0.45	2.41	15	17
1:A:161:LEU:HD12	1:A:178:LEU:HD11	0.45	1.87	9	1
1:A:144:VAL:HG11	1:A:209:ARG:CG	0.45	2.42	14	1
1:A:113:THR:C	1:A:165:LEU:HD23	0.45	2.32	7	16
1:A:60:ILE:HG22	1:A:62:PHE:CE1	0.45	2.47	5	2
1:A:103:ILE:HG22	1:A:105:LEU:HD21	0.45	1.86	18	1
1:A:105:LEU:HD12	1:A:110:LYS:HD2	0.45	1.88	17	2
1:A:161:LEU:CD1	1:A:169:LEU:HD12	0.45	2.41	12	6
1:A:161:LEU:HD12	1:A:169:LEU:HD12	0.45	1.88	4	3
1:A:25:LEU:HD22	1:A:204:VAL:CG1	0.44	2.42	3	1
1:A:223:ASN:N	1:A:223:ASN:HD22	0.44	2.10	20	1
1:A:159:ILE:HG21	1:A:185:LEU:CD1	0.44	2.43	12	3
1:A:24:PHE:CE1	1:A:28:THR:HG21	0.44	2.47	6	2
1:A:35:TYR:CD2	1:A:214:ILE:HD13	0.44	2.48	9	2
1:A:87:VAL:HG13	1:A:89:LEU:HD23	0.44	1.90	14	1
1:A:223:ASN:HD22	1:A:223:ASN:N	0.44	2.11	13	1
1:A:60:ILE:HG23	1:A:103:ILE:CD1	0.43	2.42	11	5
1:A:40:ILE:HD12	1:A:41:ASP:HB2	0.43	1.90	10	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:11:LEU:HD21	1:A:80:MET:CE	0.43	2.43	16	1
1:A:208:ILE:CG2	2:A:300:JH3:H7'	0.43	2.44	12	1
1:A:87:VAL:CG1	1:A:89:LEU:HD23	0.43	2.43	15	1
1:A:80:MET:CB	1:A:87:VAL:HG22	0.43	2.41	4	1
1:A:21:THR:CG2	1:A:22:GLU:N	0.43	2.81	12	3
1:A:59:VAL:HG12	1:A:61:ARG:CD	0.43	2.43	14	2
1:A:187:THR:HG22	1:A:191:ALA:HB3	0.43	1.89	16	1
1:A:58:ILE:HG23	1:A:105:LEU:HD23	0.43	1.91	9	1
1:A:116:TYR:CE2	1:A:188:LEU:HD12	0.43	2.49	4	1
1:A:87:VAL:HG12	1:A:89:LEU:HD23	0.42	1.90	13	2
1:A:17:LEU:HD11	2:A:300:JH3:C3'	0.42	2.40	19	1
1:A:6:LEU:HD12	1:A:7:LYS:H	0.42	1.74	19	1
1:A:101:ILE:CD1	1:A:103:ILE:HD11	0.42	2.43	18	1
1:A:35:TYR:CB	1:A:37:ILE:HD12	0.42	2.44	8	1
1:A:132:LEU:HD22	1:A:140:GLN:HE21	0.42	1.75	14	1
1:A:87:VAL:HG23	1:A:130:TYR:HD2	0.42	1.73	7	1
1:A:32:ILE:HG22	1:A:34:GLN:HG3	0.42	1.91	2	1
2:A:300:JH3:H7'	2:A:300:JH3:CC	0.42	2.45	11	1
1:A:142:PHE:CG	2:A:300:JH3:HCA	0.42	2.50	19	1
1:A:87:VAL:HG23	1:A:130:TYR:HD1	0.42	1.74	19	1
1:A:35:TYR:CD2	1:A:214:ILE:HD12	0.42	2.49	10	1
1:A:221:PHE:C	1:A:221:PHE:CD1	0.42	2.93	20	2
1:A:189:ARG:O	1:A:193:ILE:HD13	0.42	2.15	1	3
1:A:123:ILE:HD12	1:A:153:SER:CB	0.42	2.45	16	1
1:A:144:VAL:O	1:A:144:VAL:HG23	0.42	2.14	6	2
1:A:103:ILE:O	1:A:103:ILE:HG22	0.42	2.14	16	1
1:A:65:LEU:HD22	1:A:97:ILE:HG22	0.42	1.92	16	1
1:A:43:LEU:HD23	1:A:200:CYS:SG	0.42	2.55	16	8
1:A:189:ARG:HA	1:A:193:ILE:HD13	0.41	1.92	8	1
1:A:7:LYS:HE2	1:A:20:ALA:HB2	0.41	1.92	15	1
1:A:40:ILE:HD13	1:A:204:VAL:HG12	0.41	1.92	16	1
1:A:75:ILE:HG12	1:A:89:LEU:HD11	0.41	1.93	10	1
1:A:166:SER:HA	1:A:178:LEU:HD12	0.41	1.92	12	1
1:A:142:PHE:CE2	1:A:224:LEU:HD13	0.41	2.50	15	1
1:A:144:VAL:HG22	1:A:144:VAL:O	0.41	2.14	10	1
1:A:36:ASP:OD2	1:A:214:ILE:HD11	0.41	2.15	16	1
1:A:11:LEU:HD11	1:A:224:LEU:HA	0.41	1.92	5	1
1:A:17:LEU:HD22	1:A:78:PHE:CD1	0.41	2.51	5	1
1:A:80:MET:HG2	1:A:87:VAL:HG22	0.40	1.93	13	1
1:A:70:LEU:HD12	1:A:95:LEU:CD2	0.40	2.31	3	1
1:A:35:TYR:CE2	1:A:214:ILE:HG21	0.40	2.51	9	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:142:PHE:CB	1:A:212:ALA:HB1	0.40	2.47	12	1
1:A:70:LEU:HD13	1:A:200:CYS:SG	0.40	2.57	12	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	220/227 (97%)	195±2 (89±1%)	20±2 (9±1%)	5±1 (2±0%)	13	53
All	All	4400/4540 (97%)	3905 (89%)	401 (9%)	94 (2%)	13	53

All 8 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	135	ASP	20
1	A	140	GLN	20
1	A	178	LEU	20
1	A	183	GLU	20
1	A	31	GLY	8
1	A	154	ILE	3
1	A	223	ASN	2
1	A	177	SER	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	195/198 (98%)	138±4 (71±2%)	57±4 (29±2%)	2	18
All	All	3900/3960 (98%)	2758 (71%)	1142 (29%)	2	18

All 114 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	82	THR	20
1	A	17	LEU	20
1	A	154	ILE	20
1	A	7	LYS	20
1	A	215	LEU	20
1	A	178	LEU	20
1	A	55	ASP	20
1	A	148	THR	20
1	A	86	THR	20
1	A	187	THR	20
1	A	46	THR	20
1	A	76	SER	20
1	A	160	THR	20
1	A	142	PHE	20
1	A	182	MET	20
1	A	61	ARG	20
1	A	158	LYS	20
1	A	185	LEU	20
1	A	126	VAL	20
1	A	179	GLU	19
1	A	165	LEU	19
1	A	21	THR	19
1	A	159	ILE	19
1	A	73	GLN	19
1	A	175	ASN	19
1	A	113	THR	19
1	A	223	ASN	19
1	A	30	LYS	18
1	A	170	GLU	18
1	A	100	ASP	17
1	A	121	ASN	17
1	A	224	LEU	17
1	A	70	LEU	17
1	A	89	LEU	16
1	A	136	ASP	16
1	A	147	GLU	16
1	A	145	GLN	16
1	A	173	SER	15
1	A	80	MET	15
1	A	37	ILE	15
1	A	83	LYS	14

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Mol	Chain	Res	Type	Models (Total)
1	A	41	ASP	13
1	A	211	SER	13
1	A	32	ILE	12
1	A	13	ASP	12
1	A	90	LYS	12
1	A	77	ASP	12
1	A	5	LEU	12
1	A	119	ASP	11
1	A	143	GLU	11
1	A	177	SER	11
1	A	198	GLU	10
1	A	29	SER	10
1	A	108	GLN	10
1	A	133	LYS	9
1	A	23	GLN	8
1	A	218	SER	8
1	A	162	SER	8
1	A	213	LYS	8
1	A	71	LYS	7
1	A	110	LYS	7
1	A	132	LEU	7
1	A	183	GLU	7
1	A	163	SER	7
1	A	203	SER	6
1	A	14	MET	6
1	A	63	LYS	6
1	A	11	LEU	6
1	A	131	ASN	6
1	A	34	GLN	6
1	A	222	GLU	5
1	A	16	CYS	5
1	A	171	LYS	5
1	A	172	ASP	5
1	A	35	TYR	5
1	A	164	ASP	5
1	A	19	SER	5
1	A	66	ASN	5
1	A	91	THR	5
1	A	78	PHE	5
1	A	15	GLN	5
1	A	40	ILE	4
1	A	75	ILE	4

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Mol	Chain	Res	Type	Models (Total)
1	A	225	ASN	4
1	A	74	GLN	4
1	A	49	ASP	4
1	A	92	LYS	4
1	A	47	SER	3
1	A	36	ASP	3
1	A	189	ARG	3
1	A	10	LYS	3
1	A	186	LYS	3
1	A	50	VAL	2
1	A	54	SER	2
1	A	109	SER	2
1	A	127	ARG	2
1	A	79	GLN	2
1	A	190	GLN	2
1	A	152	GLU	1
1	A	156	GLU	1
1	A	137	ASN	1
1	A	134	ASN	1
1	A	26	GLU	1
1	A	6	LEU	1
1	A	166	SER	1
1	A	9	CYS	1
1	A	81	ASP	1
1	A	209	ARG	1
1	A	18	SER	1
1	A	112	PHE	1
1	A	144	VAL	1
1	A	101	ILE	1
1	A	153	SER	1
1	A	219	SER	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

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds for which Mogul statistics could be retrieved, the number of bonds that are observed in the model and the number of bonds that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length is the number of standard deviations the observed value is removed from the expected value. A bond length with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond lengths.

Mol	Type	Chain	Res	Link	Bond lengths		
					Counts	RMSZ	#Z>2
2	JH3	A	300	-	19,19,19	1.05±0.00	0±0 (0±0%)

In the following table, the Counts columns list the number of angles for which Mogul statistics could be retrieved, the number of angles that are observed in the model and the number of angles that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond angle is the number of standard deviations the observed value is removed from the expected value. A bond angle with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond angles.

Mol	Type	Chain	Res	Link	Bond angles		
					Counts	RMSZ	#Z>2
2	JH3	A	300	-	25,26,26	1.06±0.00	0±0 (0±0%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	JH3	A	300	-	-	0±0,17,25,25	0±0,0,1,1

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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 96% for the well-defined parts and 96% for the entire structure.

7.1 Chemical shift list 1

File name: BMRB entry 11073

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	2926
Number of shifts mapped to atoms	2900
Number of unparsed shifts	0
Number of shifts with mapping errors	26
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

The following assigned chemical shifts were not mapped to the molecules present in the coordinate file.

- Chain not found in structure. All 26 occurrences are reported below.

Chain	Res	Type	Atom	Shift Data		
				Value	Uncertainty	Ambiguity
UNMAPPED	1	JH3	H8A	1.435	0.012	2
UNMAPPED	1	JH3	HCA	-0.101	0.004	1
UNMAPPED	1	JH3	HC	-0.101	0.004	1
UNMAPPED	1	JH3	H4	1.968	0.015	2
UNMAPPED	1	JH3	HM	3.468	0.002	1
UNMAPPED	1	JH3	H5A	1.424	0.009	2
UNMAPPED	1	JH3	H4A	1.968	0.015	2
UNMAPPED	1	JH3	H3'A	1.184	0.003	1
UNMAPPED	1	JH3	HA	2.655	0.004	1
UNMAPPED	1	JH3	H3'	1.184	0.003	1
UNMAPPED	1	JH3	H3'B	1.184	0.003	1
UNMAPPED	1	JH3	HB'	-0.101	0.004	1
UNMAPPED	1	JH3	H7'A	1.15	0.004	1
UNMAPPED	1	JH3	H5	1.424	0.009	2

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Chain	Res	Type	Atom	Shift Data		
				Value	Uncertainty	Ambiguity
UNMAPPED	1	JH3	H9A	1.097	0.006	2
UNMAPPED	1	JH3	HB'B	-0.101	0.004	1
UNMAPPED	1	JH3	H2	6.104	0.005	1
UNMAPPED	1	JH3	HMB	3.468	0.002	1
UNMAPPED	1	JH3	HCB	-0.101	0.004	1
UNMAPPED	1	JH3	HB'A	-0.101	0.004	1
UNMAPPED	1	JH3	HMA	3.468	0.002	1
UNMAPPED	1	JH3	H7'B	1.15	0.004	1
UNMAPPED	1	JH3	H6	4.743	0.003	1
UNMAPPED	1	JH3	H9	1.097	0.006	2
UNMAPPED	1	JH3	H7'	1.15	0.004	1
UNMAPPED	1	JH3	H8	1.955	0.008	2

7.1.2 Chemical shift referencing ⓘ

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	227	-0.12 ± 0.08	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	213	0.17 ± 0.10	None needed (< 0.5 ppm)
$^{13}\text{C}'$	226	0.18 ± 0.09	None needed (< 0.5 ppm)
^{15}N	215	-0.14 ± 0.20	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 96%, i.e. 2527 atoms were assigned a chemical shift out of a possible 2641. 0 out of 36 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	1084/1085 (100%)	432/432 (100%)	441/442 (100%)	211/211 (100%)
Sidechain	1319/1411 (93%)	781/821 (95%)	512/539 (95%)	26/51 (51%)
Aromatic	124/145 (86%)	64/78 (82%)	59/63 (94%)	1/4 (25%)
Overall	2527/2641 (96%)	1277/1331 (96%)	1012/1044 (97%)	238/266 (89%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 96%, i.e. 2566 atoms were assigned a chemical shift out of a possible 2684. 0 out of 36 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	1110/1115 (100%)	442/444 (100%)	453/454 (100%)	215/217 (99%)
Sidechain	1332/1424 (94%)	788/828 (95%)	518/545 (95%)	26/51 (51%)
Aromatic	124/145 (86%)	64/78 (82%)	59/63 (94%)	1/4 (25%)
Overall	2566/2684 (96%)	1294/1350 (96%)	1030/1062 (97%)	242/272 (89%)

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:

