



Full wwPDB NMR Structure Validation Report ⓘ

Apr 27, 2016 – 06:48 AM BST

PDB ID : 4A52
Title : NMR structure of the imipenem-acylated L,D-transpeptidase from *Bacillus subtilis*
Authors : Lecoq, L.; Simorre, J.; Bougault, C.; Arthur, M.; Hugonnet, J.; Veckerle, C.; Pessey, O.
Deposited on : 2011-10-24

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

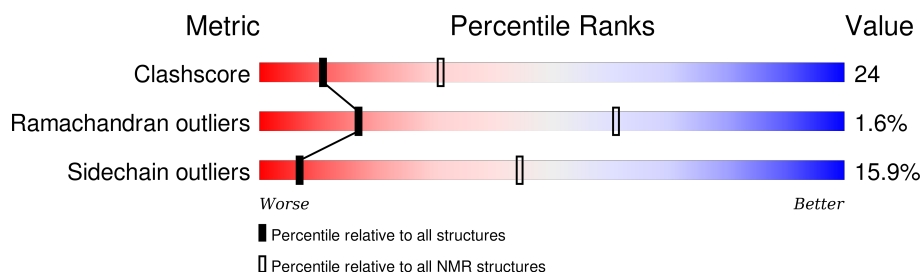
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 90%.

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	175	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA and RNA chains that are outliers for geometric criteria:

Mol	Chain	Compound	Res	Total models with violations	
				Chirality	Geometry
2	A	IM2	1142	20	-

2 Ensemble composition and analysis

This entry contains 20 models. Model 13 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative.

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:3-A:85, A:98-A:119, A:125-A:134, A:145-A:166 (137)	0.27	13

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 5 single-model clusters were found.

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

3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2499 atoms, of which 1202 are hydrogens and 0 are deuteriums.

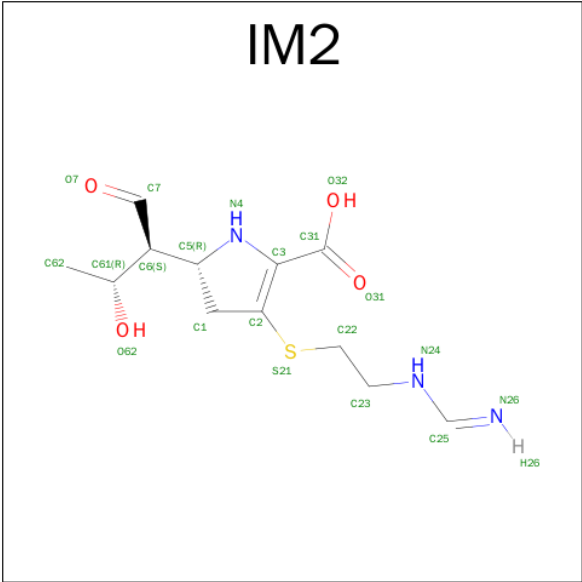
- Molecule 1 is a protein called PUTATIVE L, D-TRANSPEPTIDASE YKUD.

Mol	Chain	Residues	Atoms						Trace
1	A	169	Total	C	H	N	O	S	0
			2461	810	1184	230	234	3	

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	EXPRESSION TAG	UNP O34816
A	2	ARG	-	EXPRESSION TAG	UNP O34816
A	3	LYS	-	EXPRESSION TAG	UNP O34816
A	4	LEU	-	EXPRESSION TAG	UNP O34816
A	168	GLY	-	EXPRESSION TAG	UNP O34816
A	169	SER	-	EXPRESSION TAG	UNP O34816
A	170	HIS	-	EXPRESSION TAG	UNP O34816
A	171	HIS	-	EXPRESSION TAG	UNP O34816
A	172	HIS	-	EXPRESSION TAG	UNP O34816
A	173	HIS	-	EXPRESSION TAG	UNP O34816
A	174	HIS	-	EXPRESSION TAG	UNP O34816
A	175	HIS	-	EXPRESSION TAG	UNP O34816

- Molecule 2 is (5R)-5-[(1S,2R)-1-FORMYL-2-HYDROXYPROPYL]-3-[(2-{[(E)-IMINOMETHYL]AMINO}ETHYL)SULFANYL]-4,5-DIHYDRO-1H-PYRROLE-2-CARBOXYLIC ACID (three-letter code: IM2) (formula: C₁₂H₁₉N₃O₄S).



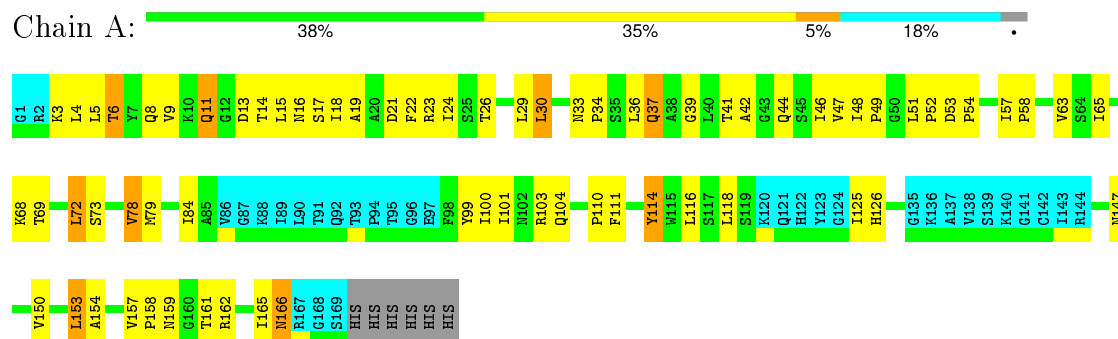
Mol	Chain	Residues	Atoms					
			Total	C	H	N	O	S
2	A	1	38	12	18	3	4	1

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: PUTATIVE L, D-TRANSPEPTIDASE YKUD

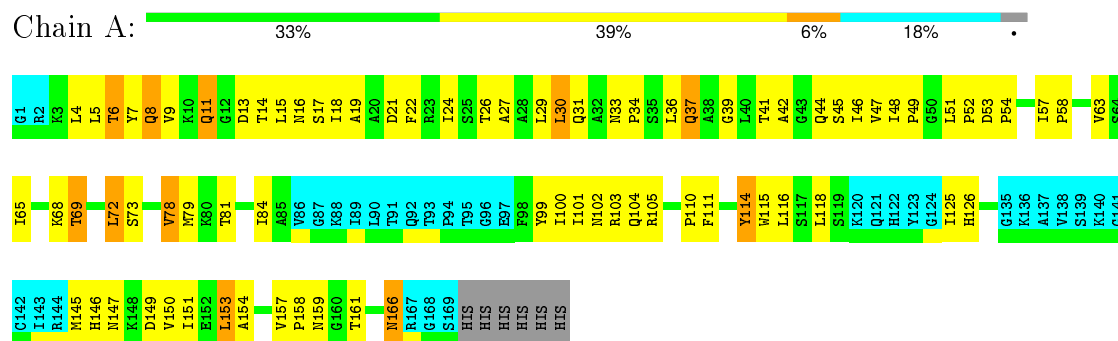


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

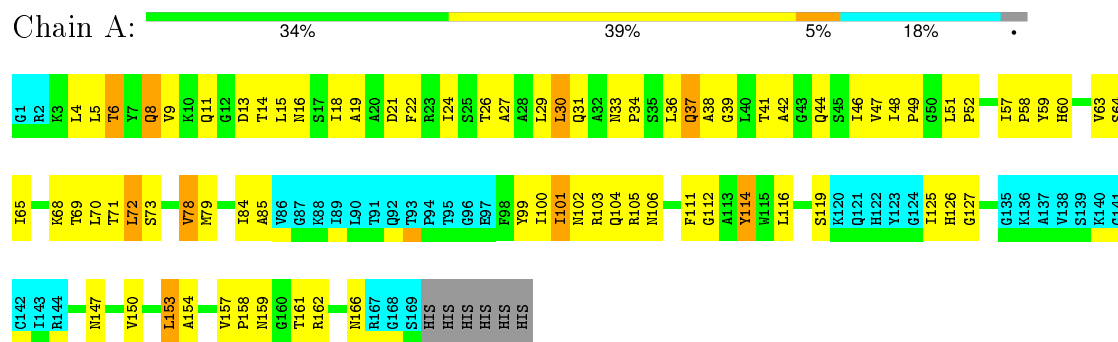
4.2.1 Score per residue for model 1

- Molecule 1: PUTATIVE L, D-TRANSPEPTIDASE YKUD



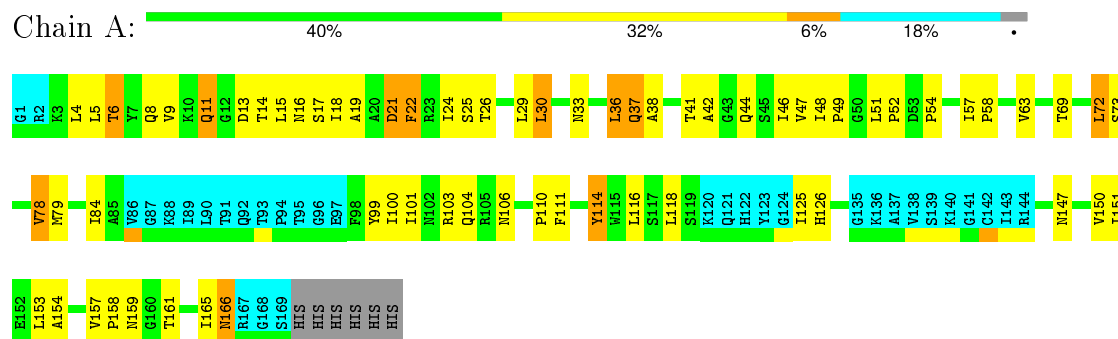
4.2.2 Score per residue for model 2

- Molecule 1: PUTATIVE L, D-TRANSPEPTIDASE YKUD



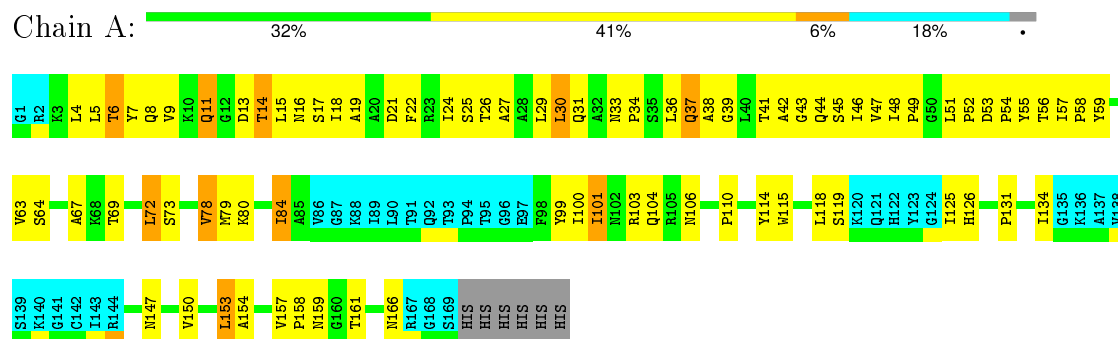
4.2.5 Score per residue for model 5

- Molecule 1: PUTATIVE L, D-TRANSPEPTIDASE YKUD



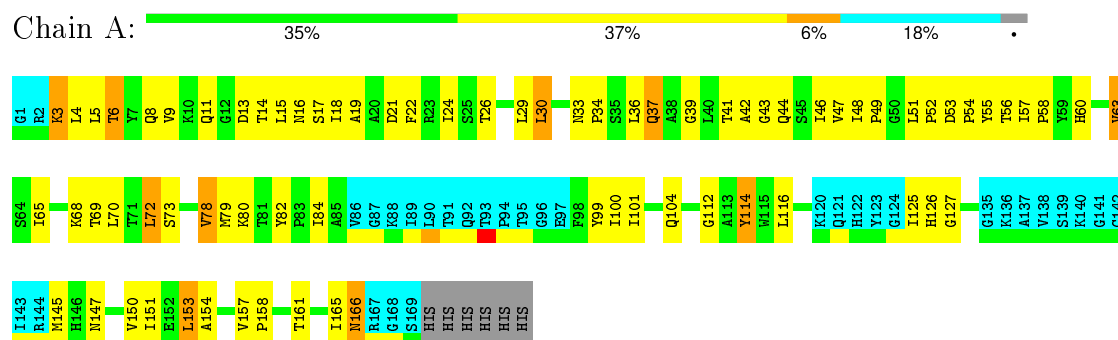
4.2.8 Score per residue for model 8

- Molecule 1: PUTATIVE L, D-TRANSPEPTIDASE YKUD



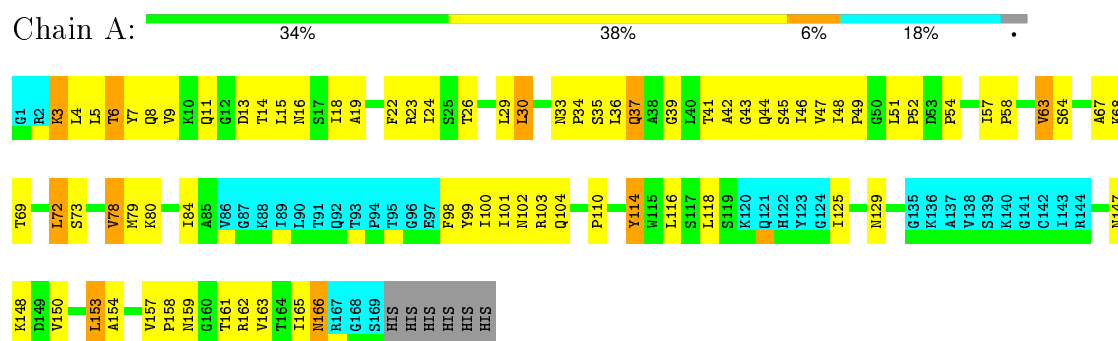
4.2.9 Score per residue for model 9

- Molecule 1: PUTATIVE L, D-TRANSPEPTIDASE YKUD



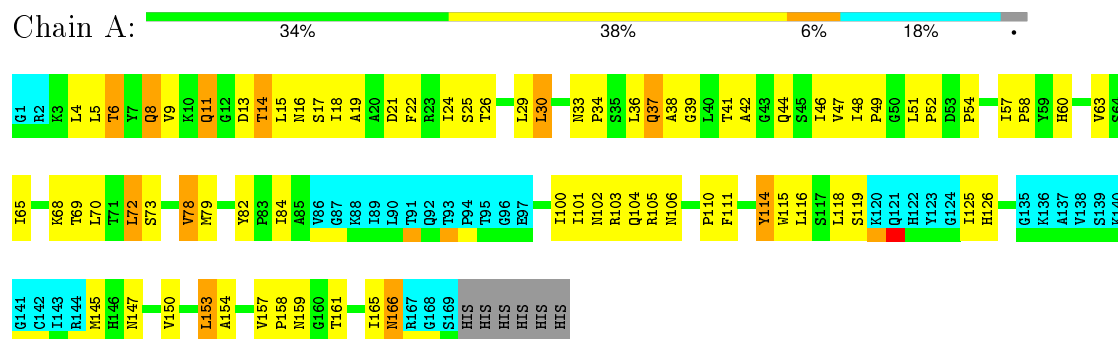
4.2.10 Score per residue for model 10

- Molecule 1: PUTATIVE L, D-TRANSPEPTIDASE YKUD



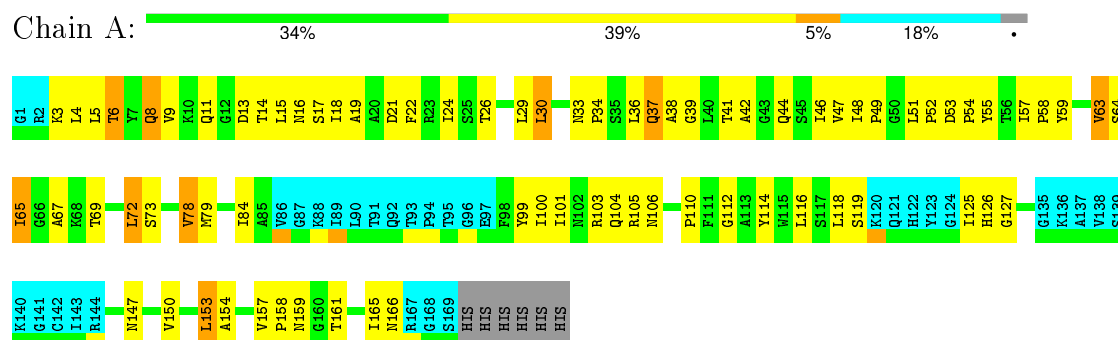
4.2.11 Score per residue for model 11

- Molecule 1: PUTATIVE L, D-TRANSPEPTIDASE YKUD



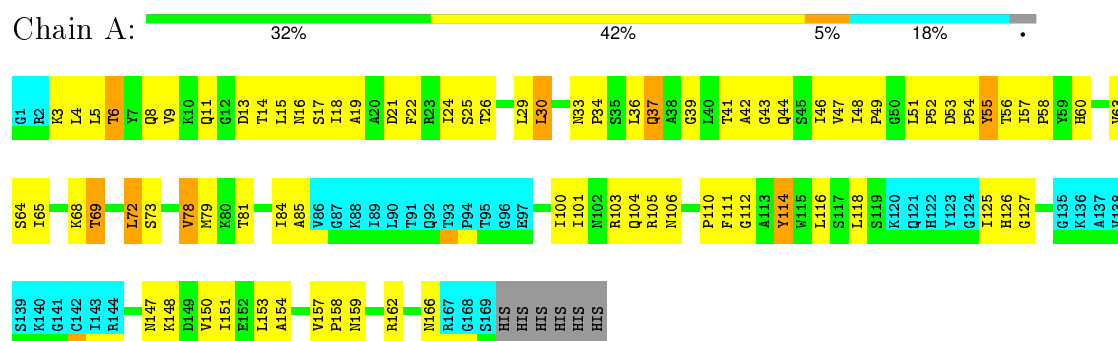
4.2.12 Score per residue for model 12

- Molecule 1: PUTATIVE L, D-TRANSPEPTIDASE YKUD



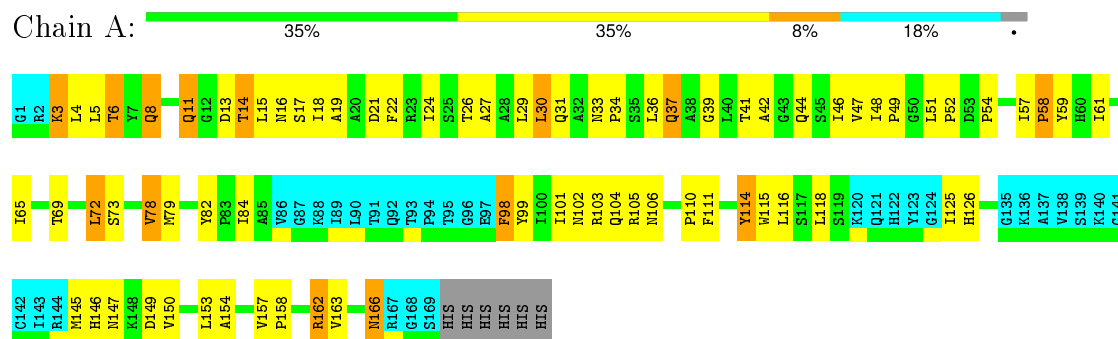
4.2.13 Score per residue for model 13 (medoid)

- Molecule 1: PUTATIVE L, D-TRANSPEPTIDASE YKUD



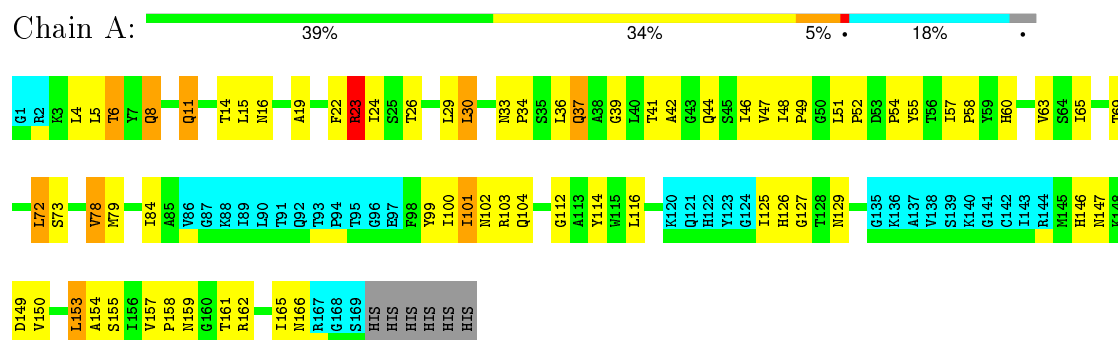
4.2.14 Score per residue for model 14

- Molecule 1: PUTATIVE L, D-TRANSPEPTIDASE YKUD



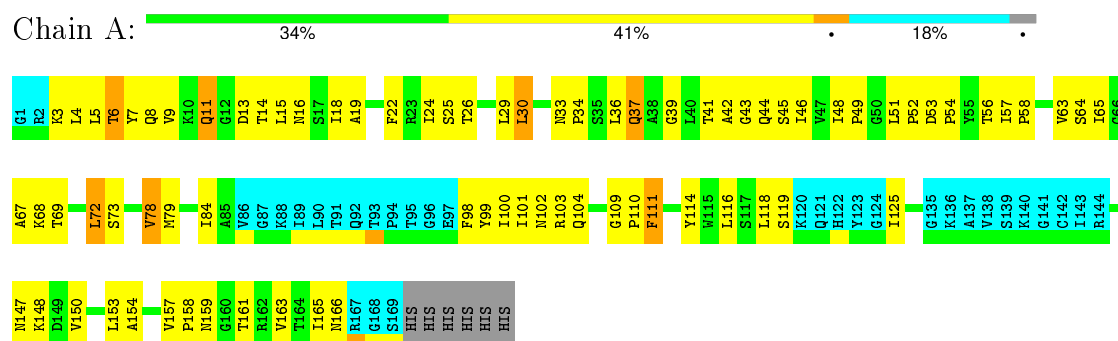
4.2.15 Score per residue for model 15

- Molecule 1: PUTATIVE L, D-TRANSPEPTIDASE YKUD



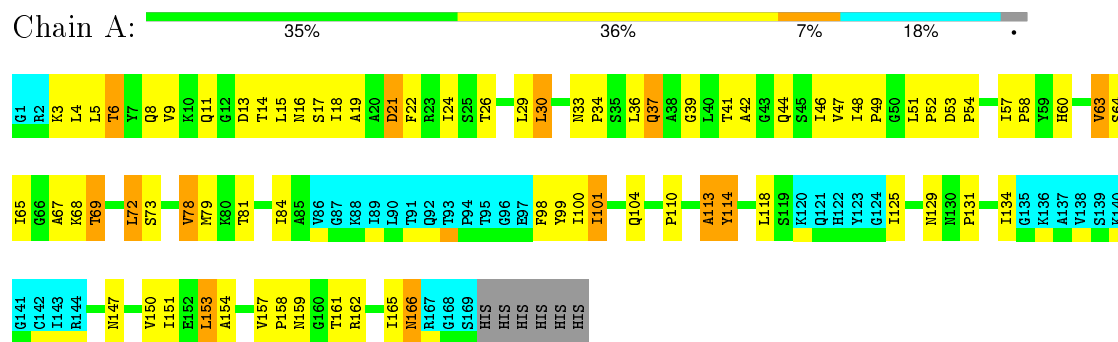
4.2.16 Score per residue for model 16

- Molecule 1: PUTATIVE L, D-TRANSPEPTIDASE YKUD



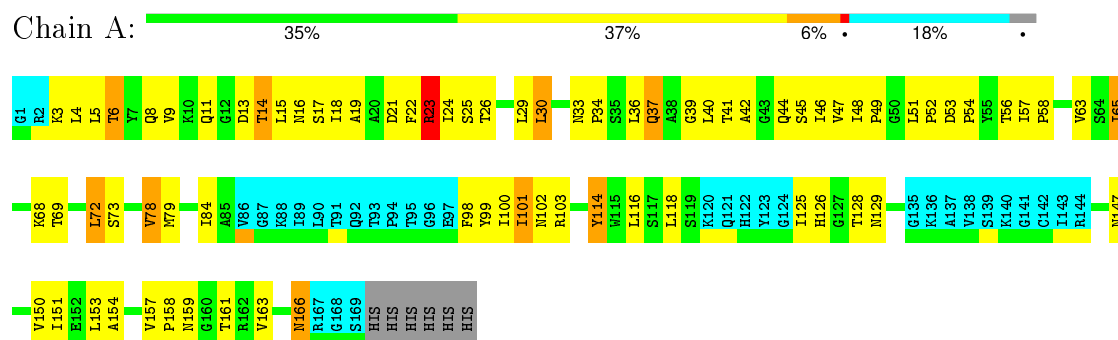
4.2.17 Score per residue for model 17

- Molecule 1: PUTATIVE L, D-TRANSPEPTIDASE YKUD



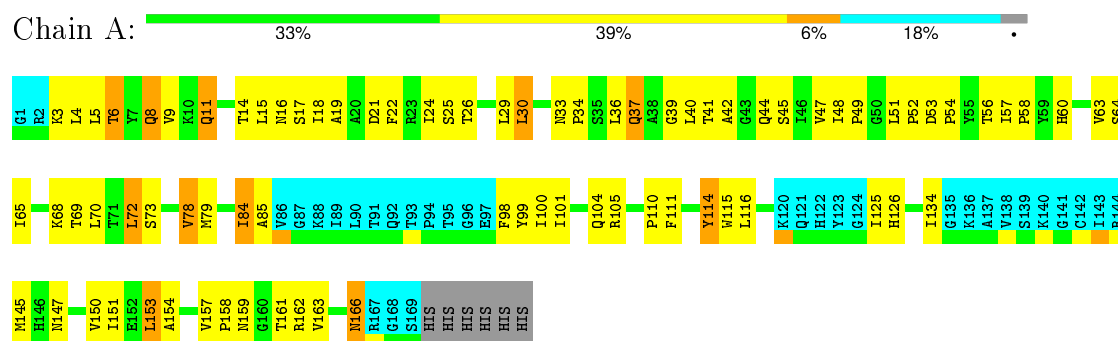
4.2.18 Score per residue for model 18

- Molecule 1: PUTATIVE L, D-TRANSPEPTIDASE YKUD



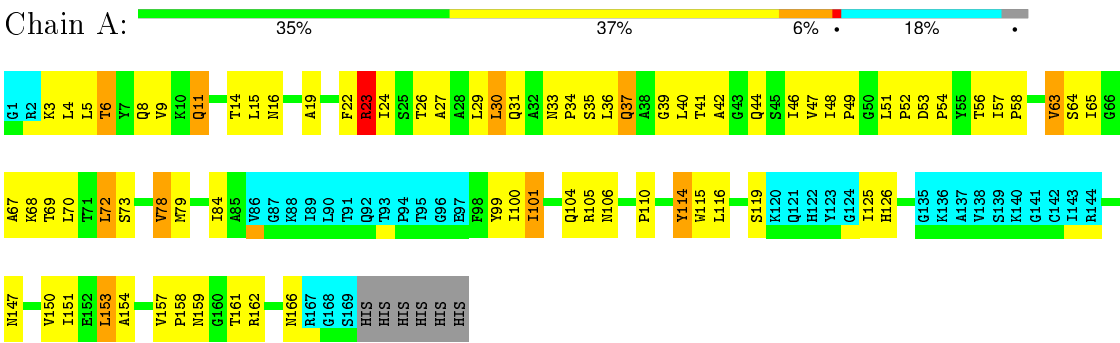
4.2.19 Score per residue for model 19

- Molecule 1: PUTATIVE L, D-TRANSPEPTIDASE YKUD



4.2.20 Score per residue for model 20

● Molecule 1: PUTATIVE L, D-TRANSPEPTIDASE YKUD



5 Refinement protocol and experimental data overview

The models were refined using the following method: *ITERATIVE STRUCTURE CALCULATION WITH ARIA2.3*.

Of the 20 calculated structures, 20 were deposited, based on the following criterion: *STRUCTURE WITH THE LOWEST ENERGY*.

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

Software name	Classification	Version
CNS1.2	refinement	
CNS 1.2	structure solution	
TALOS ANY	structure solution	
UNIO 10	structure solution	
NMRDRAW ANY	structure solution	
NMRPIPE ANY	structure solution	
CCPNMR ANALYSIS 2.2	structure solution	

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 18037
Number of chemical shift lists	1
Total number of shifts	1851
Number of shifts mapped to atoms	1851
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	90%

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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: IM2

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the (average) root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#Z>5	RMSZ	#Z>5
1	A	0.49±0.02	0±1/1065 (0.0±0.1%)	0.65±0.01	0±0/1458 (0.0±0.0%)
All	All	0.49	7/21300 (0.0%)	0.65	0/29160 (0.0%)

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±0.2
All	All	0	1

All unique bond outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
1	A	55	TYR	CE2-CZ	6.91	1.47	1.38	13	3
1	A	55	TYR	CE1-CZ	-6.31	1.30	1.38	13	4

There are no bond-angle outliers.

There are no chirality outliers.

All unique planar outliers are listed below.

Mol	Chain	Res	Type	Group	Models (Total)
1	A	55	TYR	Sidechain	1

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	1041	955	1070	50±4
2	A	20	18	16	2±1
All	All	21220	19460	21720	1036

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 24.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:44:GLN:OE1	1:A:46:ILE:HG23	0.79	1.76	6	1
1:A:11:GLN:HA	1:A:42:ALA:HB2	0.76	1.58	5	20
1:A:98:PHE:CE1	1:A:163:VAL:HG11	0.74	2.18	14	1
1:A:17:SER:O	1:A:21:ASP:HB2	0.72	1.84	1	12
1:A:59:TYR:HA	1:A:73:SER:O	0.70	1.86	2	5
1:A:30:LEU:HD11	1:A:37:GLN:N	0.69	2.03	14	20
1:A:116:LEU:HB2	1:A:125:ILE:O	0.69	1.88	12	17
1:A:34:PRO:O	1:A:37:GLN:HG3	0.67	1.89	20	18
1:A:22:PHE:O	1:A:24:ILE:HG23	0.67	1.90	15	19
1:A:99:TYR:HA	1:A:161:THR:O	0.67	1.88	4	16
1:A:98:PHE:CD1	1:A:163:VAL:HG11	0.67	2.25	14	1
1:A:82:TYR:HB3	1:A:145:MET:SD	0.67	2.30	14	3
1:A:98:PHE:CE2	1:A:163:VAL:HG21	0.66	2.25	14	1
2:A:1142:IM2:S21	2:A:1142:IM2:H25	0.66	2.30	11	1
1:A:103:ARG:HG2	1:A:116:LEU:HD23	0.66	1.68	4	3
1:A:5:LEU:HD12	1:A:54:PRO:HD3	0.65	1.66	1	10
1:A:51:LEU:HD21	1:A:159:ASN:O	0.64	1.93	4	18
1:A:100:ILE:HD11	1:A:125:ILE:HD12	0.64	1.70	4	18
1:A:4:LEU:HD13	1:A:49:PRO:HA	0.64	1.69	14	20
2:A:1142:IM2:H25	2:A:1142:IM2:S21	0.64	2.32	5	1
2:A:1142:IM2:H11	2:A:1142:IM2:O62	0.63	1.92	5	3
1:A:57:ILE:HD13	1:A:158:PRO:HG2	0.63	1.69	7	20
1:A:153:LEU:O	1:A:157:VAL:HG22	0.63	1.94	8	20
1:A:19:ALA:O	1:A:24:ILE:HG12	0.63	1.94	19	20
2:A:1142:IM2:O32	2:A:1142:IM2:S21	0.63	2.56	2	4
1:A:105:ARG:HG2	1:A:106:ASN:N	0.63	2.08	12	5

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:16:ASN:HA	1:A:26:THR:CG2	0.62	2.25	2	20
1:A:53:ASP:HB3	1:A:56:THR:HG23	0.62	1.70	13	8
2:A:1142:IM2:H623	2:A:1142:IM2:N4	0.62	2.10	4	1
1:A:104:GLN:HG3	1:A:105:ARG:O	0.61	1.95	19	4
1:A:30:LEU:HD11	1:A:37:GLN:CA	0.61	2.25	12	20
1:A:23:ARG:HD2	1:A:101:ILE:HD11	0.61	1.72	15	3
1:A:22:PHE:CD1	1:A:101:ILE:HD12	0.61	2.31	15	19
1:A:150:VAL:O	1:A:154:ALA:HB2	0.61	1.96	2	20
2:A:1142:IM2:N4	2:A:1142:IM2:H623	0.60	2.11	11	1
1:A:103:ARG:HB3	1:A:114:TYR:CE1	0.59	2.32	14	3
1:A:53:ASP:HB3	1:A:56:THR:HG22	0.59	1.74	16	2
1:A:51:LEU:HD23	1:A:52:PRO:HD2	0.59	1.74	5	20
1:A:41:THR:O	1:A:44:GLN:HB3	0.59	1.97	6	20
1:A:13:ASP:HB3	1:A:18:ILE:HD11	0.58	1.75	3	17
1:A:11:GLN:CA	1:A:42:ALA:HB2	0.58	2.27	17	14
1:A:104:GLN:HB3	1:A:115:TRP:CD1	0.58	2.34	6	1
1:A:3:LYS:O	1:A:52:PRO:HA	0.57	1.99	12	10
1:A:60:HIS:HB2	1:A:73:SER:OG	0.57	1.99	11	1
1:A:36:LEU:HA	1:A:39:GLY:O	0.57	1.99	15	19
1:A:166:ASN:HD22	1:A:166:ASN:N	0.56	1.99	11	3
1:A:98:PHE:CZ	1:A:118:LEU:HD11	0.56	2.36	14	1
1:A:147:ASN:O	1:A:150:VAL:HG12	0.56	2.00	16	20
1:A:8:GLN:HA	1:A:44:GLN:O	0.56	2.01	6	20
1:A:33:ASN:ND2	1:A:47:VAL:H	0.56	1.98	3	13
2:A:1142:IM2:S21	2:A:1142:IM2:O31	0.56	2.64	6	7
1:A:51:LEU:HD23	1:A:52:PRO:CD	0.55	2.31	5	20
1:A:14:THR:O	1:A:18:ILE:HD13	0.55	2.02	6	17
2:A:1142:IM2:O31	2:A:1142:IM2:S21	0.55	2.65	12	6
1:A:29:LEU:HD11	1:A:46:ILE:HD12	0.55	1.79	17	19
2:A:1142:IM2:S21	2:A:1142:IM2:O32	0.55	2.64	11	2
1:A:33:ASN:HD21	1:A:47:VAL:H	0.54	1.45	3	19
1:A:8:GLN:NE2	1:A:43:GLY:HA2	0.54	2.18	10	8
1:A:63:VAL:HG13	1:A:165:ILE:HG13	0.54	1.80	12	3
1:A:36:LEU:N	1:A:36:LEU:CD2	0.53	2.71	5	1
1:A:102:ASN:O	1:A:116:LEU:HA	0.53	2.04	16	5
1:A:166:ASN:N	1:A:166:ASN:HD22	0.53	2.01	3	7
1:A:68:LYS:HG3	1:A:68:LYS:O	0.53	2.04	10	1
2:A:1142:IM2:H41	2:A:1142:IM2:H622	0.53	1.64	2	1
1:A:22:PHE:CD1	1:A:101:ILE:HG13	0.53	2.38	7	1
1:A:103:ARG:HG2	1:A:116:LEU:CD2	0.52	2.34	4	3
1:A:61:ILE:HB	1:A:163:VAL:HB	0.52	1.80	14	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:33:ASN:HB3	1:A:36:LEU:CD2	0.52	2.34	5	1
1:A:111:PHE:CE1	1:A:115:TRP:HB2	0.52	2.39	11	1
1:A:72:LEU:HD22	1:A:79:MET:SD	0.51	2.45	3	20
1:A:98:PHE:CZ	1:A:163:VAL:HG11	0.51	2.40	14	1
1:A:23:ARG:HD2	1:A:101:ILE:CD1	0.51	2.35	15	3
1:A:112:GLY:HA3	1:A:127:GLY:C	0.51	2.26	15	6
1:A:118:LEU:HD11	1:A:163:VAL:HG11	0.51	1.81	18	3
1:A:5:LEU:HD23	1:A:48:ILE:CG1	0.51	2.35	7	20
1:A:4:LEU:CD1	1:A:49:PRO:HA	0.50	2.36	17	7
1:A:103:ARG:HG2	1:A:116:LEU:HD12	0.50	1.83	14	1
1:A:53:ASP:OD1	1:A:54:PRO:HD2	0.50	2.06	6	3
1:A:15:LEU:HG	1:A:26:THR:CG2	0.50	2.37	8	20
1:A:29:LEU:O	1:A:33:ASN:HB2	0.50	2.07	16	20
1:A:63:VAL:O	1:A:165:ILE:HA	0.49	2.06	17	2
1:A:5:LEU:HG	1:A:6:THR:N	0.49	2.22	8	20
1:A:115:TRP:CH2	2:A:1142:IM2:H25	0.49	2.41	1	1
2:A:1142:IM2:S21	2:A:1142:IM2:C25	0.49	3.00	11	1
1:A:102:ASN:ND2	1:A:103:ARG:H	0.49	2.05	14	2
1:A:102:ASN:CG	1:A:103:ARG:H	0.49	2.10	2	3
1:A:37:GLN:HE21	1:A:38:ALA:N	0.49	2.06	8	6
1:A:65:ILE:O	1:A:68:LYS:HG2	0.48	2.08	19	3
1:A:166:ASN:HD22	1:A:166:ASN:H	0.48	1.51	14	4
1:A:166:ASN:H	1:A:166:ASN:HD22	0.48	1.51	10	6
1:A:100:ILE:CG1	1:A:161:THR:HB	0.48	2.38	9	2
1:A:114:TYR:CD2	1:A:151:ILE:HG13	0.48	2.43	1	9
1:A:104:GLN:HB3	1:A:115:TRP:HB3	0.48	1.85	20	4
1:A:65:ILE:CG1	1:A:165:ILE:HG23	0.48	2.38	11	2
1:A:53:ASP:CG	1:A:54:PRO:HD2	0.47	2.29	8	7
1:A:73:SER:HA	1:A:78:VAL:HA	0.47	1.86	15	19
1:A:18:ILE:HG12	1:A:40:LEU:CD2	0.47	2.39	18	1
1:A:27:ALA:O	1:A:31:GLN:HG3	0.47	2.09	8	6
2:A:1142:IM2:N4	2:A:1142:IM2:H622	0.47	2.24	2	1
1:A:60:HIS:HB3	1:A:73:SER:OG	0.47	2.09	3	2
1:A:64:SER:HA	1:A:166:ASN:O	0.47	2.09	17	1
1:A:22:PHE:HD1	1:A:101:ILE:HD12	0.47	1.70	19	10
1:A:13:ASP:CB	1:A:18:ILE:HD11	0.47	2.40	11	7
1:A:113:ALA:HB1	1:A:151:ILE:CD1	0.47	2.40	17	1
2:A:1142:IM2:N26	2:A:1142:IM2:H222	0.46	2.25	19	1
1:A:64:SER:HB2	1:A:67:ALA:HB3	0.46	1.87	8	2
1:A:9:VAL:HG11	1:A:40:LEU:HD23	0.46	1.87	19	2
1:A:103:ARG:HB2	1:A:114:TYR:CE1	0.46	2.45	2	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:4:LEU:O	1:A:53:ASP:HB2	0.46	2.10	1	1
1:A:158:PRO:HD2	1:A:161:THR:OG1	0.46	2.10	15	10
1:A:63:VAL:HB	1:A:70:LEU:CB	0.46	2.41	9	6
1:A:61:ILE:HB	1:A:163:VAL:CB	0.46	2.41	14	1
2:A:1142:IM2:N26	2:A:1142:IM2:C22	0.45	2.79	19	1
1:A:146:HIS:HB2	1:A:149:ASP:OD1	0.45	2.11	1	2
1:A:60:HIS:HB2	1:A:73:SER:HB2	0.45	1.88	15	5
1:A:129:ASN:H	2:A:1142:IM2:C25	0.45	2.24	18	1
1:A:103:ARG:HB2	1:A:114:TYR:CZ	0.45	2.46	11	1
1:A:103:ARG:NH1	1:A:155:SER:HA	0.45	2.27	15	1
1:A:5:LEU:HD23	1:A:48:ILE:HG13	0.45	1.88	7	11
1:A:72:LEU:O	1:A:78:VAL:HA	0.45	2.11	9	9
1:A:98:PHE:HB2	1:A:163:VAL:HG13	0.45	1.89	19	5
1:A:146:HIS:HB3	1:A:149:ASP:OD1	0.45	2.11	15	2
2:A:1142:IM2:C62	2:A:1142:IM2:N4	0.45	2.80	11	1
1:A:33:ASN:HB3	1:A:36:LEU:HD23	0.45	1.88	5	1
1:A:22:PHE:O	1:A:23:ARG:HD3	0.45	2.12	20	2
1:A:22:PHE:HA	1:A:101:ILE:HD12	0.44	1.89	20	1
1:A:51:LEU:HD11	1:A:101:ILE:HG13	0.44	1.88	10	3
1:A:13:ASP:HB3	1:A:18:ILE:CD1	0.44	2.41	13	12
1:A:64:SER:O	1:A:68:LYS:N	0.44	2.50	10	4
2:A:1142:IM2:O62	2:A:1142:IM2:N4	0.43	2.51	7	1
1:A:72:LEU:HG	1:A:153:LEU:HD12	0.43	1.89	4	5
1:A:44:GLN:HG2	1:A:45:SER:N	0.43	2.28	6	1
2:A:1142:IM2:C25	2:A:1142:IM2:S21	0.43	3.05	5	1
1:A:131:PRO:O	1:A:134:ILE:HB	0.43	2.13	8	2
1:A:103:ARG:NH2	1:A:158:PRO:HA	0.43	2.29	3	1
1:A:99:TYR:CE2	1:A:162:ARG:HG2	0.43	2.49	17	1
1:A:69:THR:HB	1:A:81:THR:CG2	0.43	2.43	13	3
1:A:145:MET:CG	1:A:150:VAL:HB	0.42	2.43	19	1
1:A:3:LYS:HE2	1:A:56:THR:CG2	0.42	2.44	20	1
1:A:18:ILE:HG21	1:A:40:LEU:HD21	0.42	1.90	19	1
1:A:21:ASP:HB3	1:A:119:SER:O	0.42	2.14	2	1
1:A:44:GLN:HG3	1:A:45:SER:N	0.42	2.29	19	2
1:A:3:LYS:HE2	1:A:3:LYS:H	0.42	1.74	18	1
1:A:64:SER:HB2	1:A:67:ALA:CB	0.42	2.44	17	3
1:A:30:LEU:HD11	1:A:37:GLN:HA	0.42	1.92	12	1
1:A:65:ILE:HG12	1:A:165:ILE:HG23	0.41	1.91	16	1
1:A:7:TYR:O	1:A:45:SER:HA	0.41	2.14	8	4
1:A:26:THR:O	1:A:30:LEU:HB2	0.41	2.15	12	5
1:A:3:LYS:N	1:A:3:LYS:HD2	0.41	2.30	3	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:166:ASN:N	1:A:166:ASN:ND2	0.41	2.68	17	1
1:A:100:ILE:HB	1:A:161:THR:HB	0.41	1.92	17	4
1:A:64:SER:HB3	1:A:67:ALA:CB	0.41	2.45	16	2
1:A:105:ARG:CG	1:A:106:ASN:N	0.41	2.84	2	1
1:A:111:PHE:CE2	1:A:115:TRP:HB2	0.41	2.50	1	1
1:A:63:VAL:HB	1:A:165:ILE:HG13	0.41	1.92	17	1
1:A:166:ASN:ND2	1:A:166:ASN:N	0.41	2.69	11	1
1:A:54:PRO:O	1:A:162:ARG:HD2	0.41	2.15	14	1
1:A:85:ALA:HB3	2:A:1142:IM2:H51	0.41	1.93	19	1
1:A:99:TYR:H	1:A:119:SER:HB2	0.41	1.76	8	1
1:A:15:LEU:HA	1:A:40:LEU:HD13	0.41	1.92	18	1
1:A:103:ARG:HG2	1:A:116:LEU:CD1	0.41	2.45	14	1
1:A:58:PRO:O	1:A:59:TYR:CG	0.41	2.74	14	1
1:A:5:LEU:HB2	1:A:51:LEU:HD22	0.41	1.92	5	1
1:A:3:LYS:H	1:A:3:LYS:HE2	0.41	1.76	7	1
1:A:109:GLY:C	1:A:111:PHE:H	0.41	2.19	16	1
1:A:100:ILE:HB	1:A:161:THR:CB	0.41	2.46	12	1
1:A:53:ASP:HB3	1:A:56:THR:CG2	0.40	2.44	9	1
1:A:107:PRO:HG3	1:A:115:TRP:NE1	0.40	2.31	6	1
1:A:98:PHE:CD1	1:A:99:TYR:N	0.40	2.90	14	1
1:A:18:ILE:HA	1:A:21:ASP:HB2	0.40	1.93	2	1
1:A:24:ILE:CD1	1:A:29:LEU:HB2	0.40	2.46	6	2

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	137/175 (78%)	121±2 (89±1%)	13±2 (10±1%)	2±1 (2±0%)	17	61
All	All	2740/3500 (78%)	2429 (89%)	268 (10%)	43 (2%)	17	61

All 5 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	58	PRO	20
1	A	110	PRO	16
1	A	23	ARG	3
1	A	119	SER	3
1	A	113	ALA	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	114/144 (79%)	96±2 (84±2%)	18±2 (16±2%)	7	44
All	All	2280/2880 (79%)	1917 (84%)	363 (16%)	7	44

All 41 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	114	TYR	20
1	A	69	THR	20
1	A	6	THR	20
1	A	37	GLN	20
1	A	166	ASN	20
1	A	72	LEU	20
1	A	78	VAL	20
1	A	84	ILE	20
1	A	30	LEU	20
1	A	9	VAL	16
1	A	63	VAL	14
1	A	104	GLN	13
1	A	153	LEU	12
1	A	11	GLN	12
1	A	118	LEU	11
1	A	14	THR	9
1	A	103	ARG	9
1	A	162	ARG	8
1	A	101	ILE	8
1	A	8	GLN	8
1	A	111	PHE	8

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Mol	Chain	Res	Type	Models (Total)
1	A	25	SER	7
1	A	3	LYS	6
1	A	23	ARG	4
1	A	106	ASN	4
1	A	65	ILE	4
1	A	80	LYS	4
1	A	165	ILE	4
1	A	55	TYR	3
1	A	148	LYS	3
1	A	129	ASN	3
1	A	21	ASP	2
1	A	22	PHE	2
1	A	35	SER	2
1	A	71	THR	1
1	A	10	LYS	1
1	A	98	PHE	1
1	A	44	GLN	1
1	A	36	LEU	1
1	A	115	TRP	1
1	A	145	MET	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	IM2	A	1142	1	15,20,20	3.52±0.05	1±0 (6±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	IM2	A	1142	1	16,26,26	2.49±0.06	2±0 (12±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	IM2	A	1142	1	1±0,1,9,10	0±0,17,32,32	0±0,1,1,1

All unique bond outliers are listed below.

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
2	A	1142	IM2	C3-C31	13.53	1.33	1.48	4	20

All unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
2	A	1142	IM2	C31-C3-N4	6.91	126.78	120.42	4	20
2	A	1142	IM2	C5-N4-C3	6.83	101.06	115.64	16	20

All unique chiral outliers are listed below.

Mol	Chain	Res	Type	Atoms	Models (Total)
2	A	1142	IM2	C5	20

There are no torsion outliers.

There are no ring outliers.

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

The completeness of assignment taking into account all chemical shift lists is 90% for the well-defined parts and 78% for the entire structure.

7.1 Chemical shift list 1

File name: BMRB entry 18037

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	1851
Number of shifts mapped to atoms	1851
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	153	-0.12 ± 0.14	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	138	-0.00 ± 0.07	None needed (< 0.5 ppm)
$^{13}\text{C}'$	134	0.14 ± 0.20	None needed (< 0.5 ppm)
^{15}N	137	0.21 ± 0.46	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 90%, i.e. 1478 atoms were assigned a chemical shift out of a possible 1639. 0 out of 21 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	649/665 (98%)	262/264 (99%)	261/274 (95%)	126/127 (99%)
Sidechain	731/863 (85%)	441/504 (88%)	273/322 (85%)	17/37 (46%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	98/111 (88%)	48/57 (84%)	43/47 (91%)	7/7 (100%)
Overall	1478/1639 (90%)	751/825 (91%)	577/643 (90%)	150/171 (88%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 78%, i.e. 1587 atoms were assigned a chemical shift out of a possible 2023. 0 out of 24 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	701/823 (85%)	284/327 (87%)	282/338 (83%)	135/158 (85%)
Sidechain	782/1073 (73%)	470/629 (75%)	294/392 (75%)	18/52 (35%)
Aromatic	104/127 (82%)	50/65 (77%)	45/53 (85%)	9/9 (100%)
Overall	1587/2023 (78%)	804/1021 (79%)	621/783 (79%)	162/219 (74%)

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:

