Full wwPDB NMR Structure Validation Report (i)

May 29, 2020 – 01:31 am BST

PDB ID	:	2V9H
Title	:	Solution Structure of an Escherichia coli YaeT tandem POTRA domain
Authors	:	Knowles, T.J.; Jeeves, M.; Bobat, S.; Dancea, F.; Mcclelland, D.M.; Palmer, T.; Overduin, M.; Henderson, I.R.
Deposited on	:	2007-08-23

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 (i) symbol.

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

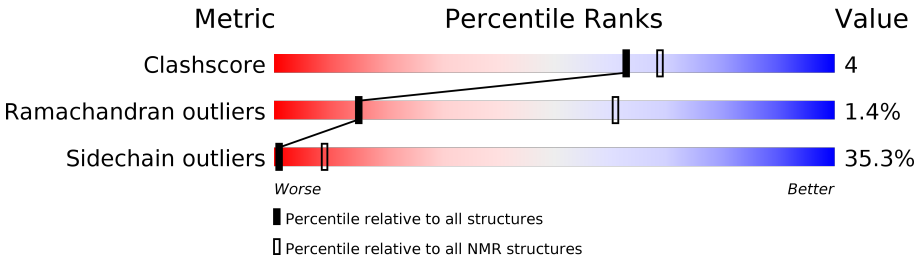
Cyrange	:	Kirchner and Güntert (2011)
NmrClust	:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	2.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 91%.

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	158937	12864
Ramachandran outliers	154571	11451
Sidechain outliers	154315	11428

The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. A cyan segment indicates the fraction of residues that are not part of the well-defined cores, and a grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5%

Mol	Chain	Length	Quality of chain
1	A	164	54% 32% • 7% 6%

2 Ensemble composition and analysis

This entry contains 20 models. Model 9 is the overall representative, medoid model (most similar to other models). The authors have identified model 3 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:23-A:33, A:38-A:89 (63)	0.29	2
2	A:92-A:170 (79)	0.40	9

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

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 2383 atoms, of which 1200 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called OUTER MEMBRANE PROTEIN ASSEMBLY FACTOR YAET.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	154	2383	742	1200	205	234	2	0

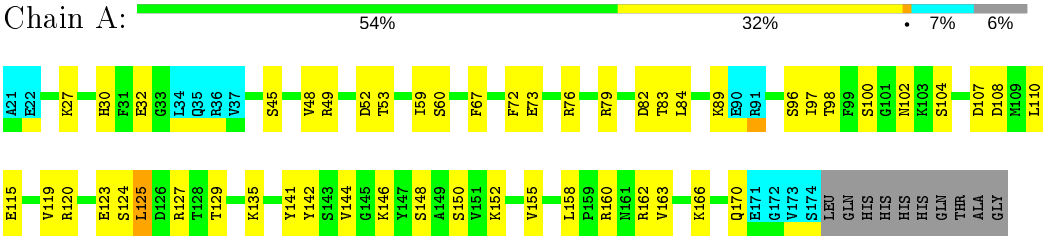
4 Residue-property plots

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: OUTER MEMBRANE PROTEIN ASSEMBLY FACTOR YAET

Chain A:



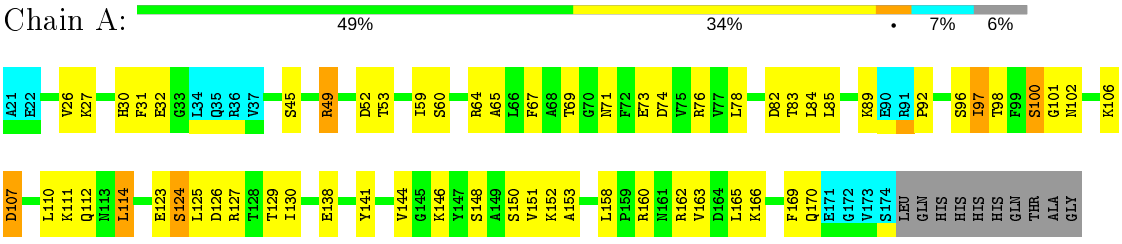
4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

• Molecule 1: OUTER MEMBRANE PROTEIN ASSEMBLY FACTOR YAET

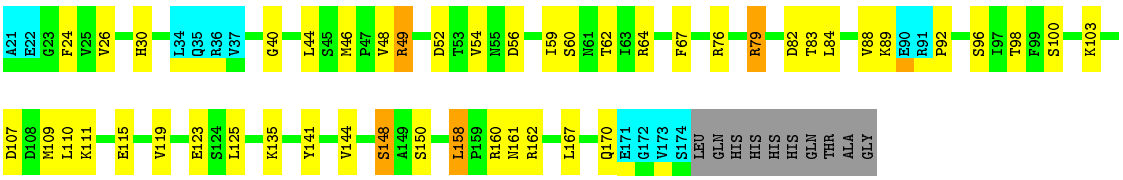
Chain A:



4.2.2 Score per residue for model 2

• Molecule 1: OUTER MEMBRANE PROTEIN ASSEMBLY FACTOR YAET

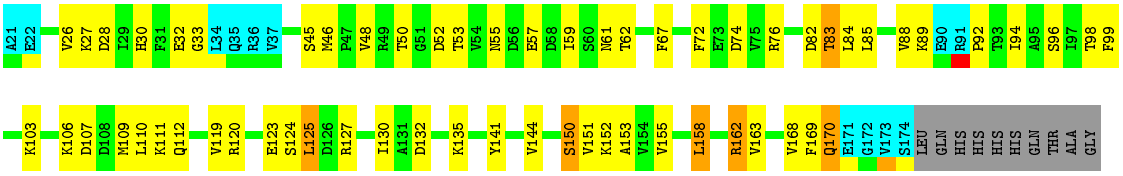
Chain A:



4.2.3 Score per residue for model 3

• Molecule 1: OUTER MEMBRANE PROTEIN ASSEMBLY FACTOR YAET

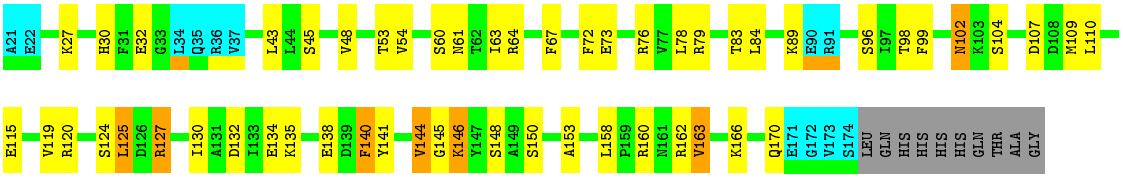
Chain A:



4.2.4 Score per residue for model 4

• Molecule 1: OUTER MEMBRANE PROTEIN ASSEMBLY FACTOR YAET

Chain A:



4.2.5 Score per residue for model 5

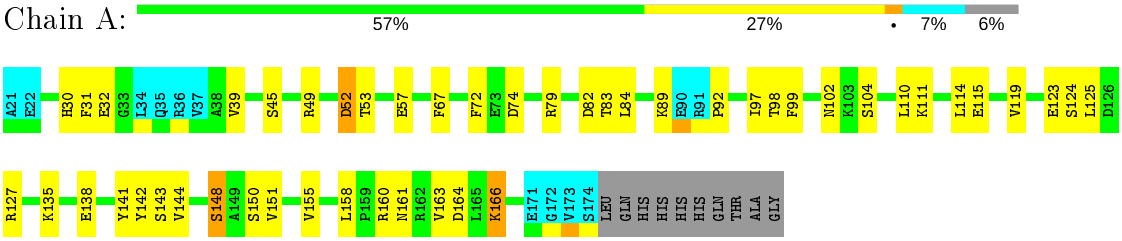
• Molecule 1: OUTER MEMBRANE PROTEIN ASSEMBLY FACTOR YAET

Chain A:

4.2.6 Score per residue for model 6

• Molecule 1: OUTER MEMBRANE PROTEIN ASSEMBLY FACTOR YAET

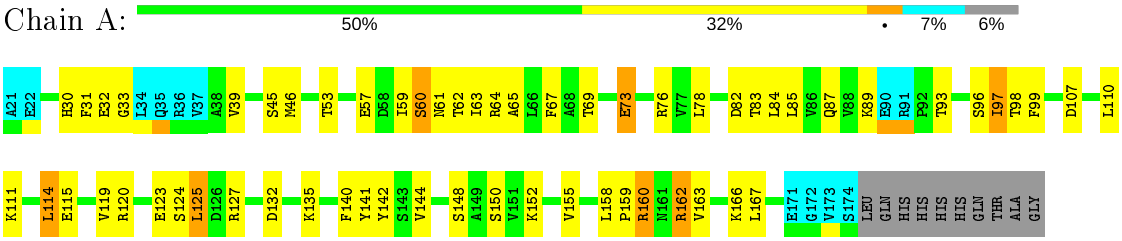
Chain A:



4.2.7 Score per residue for model 7

• Molecule 1: OUTER MEMBRANE PROTEIN ASSEMBLY FACTOR YAET

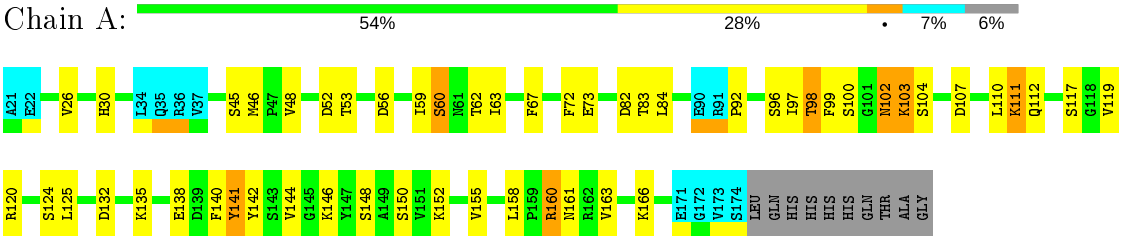
Chain A:



4.2.8 Score per residue for model 8

• Molecule 1: OUTER MEMBRANE PROTEIN ASSEMBLY FACTOR YAET

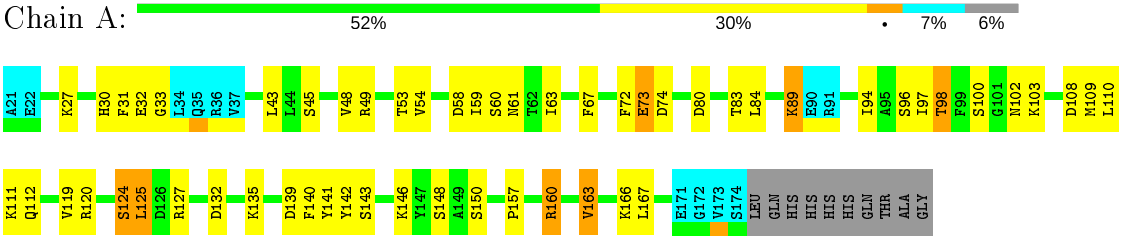
Chain A:



4.2.9 Score per residue for model 9 (medoid)

• Molecule 1: OUTER MEMBRANE PROTEIN ASSEMBLY FACTOR YAET

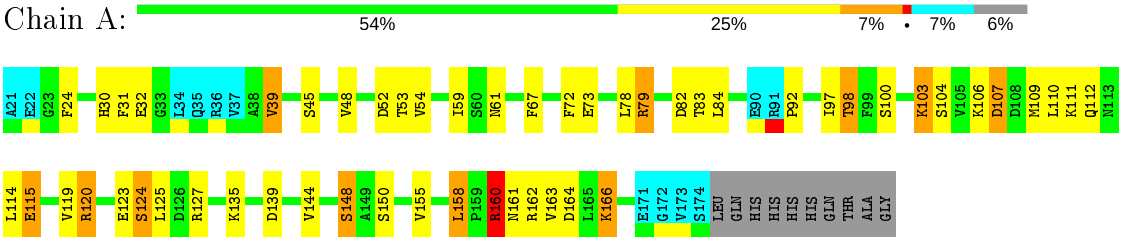
Chain A:



4.2.10 Score per residue for model 10

• Molecule 1: OUTER MEMBRANE PROTEIN ASSEMBLY FACTOR YAET

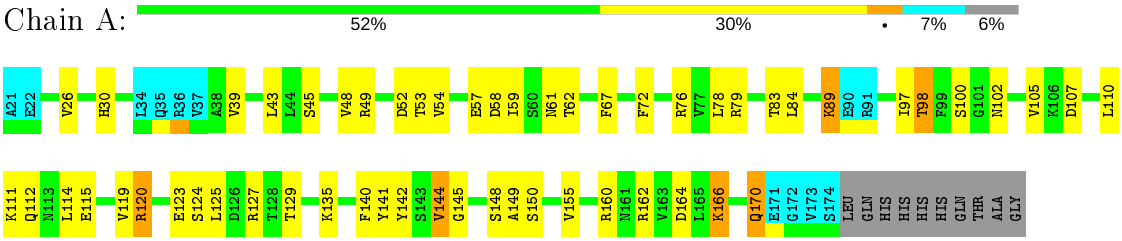
Chain A:



4.2.11 Score per residue for model 11

• Molecule 1: OUTER MEMBRANE PROTEIN ASSEMBLY FACTOR YAET

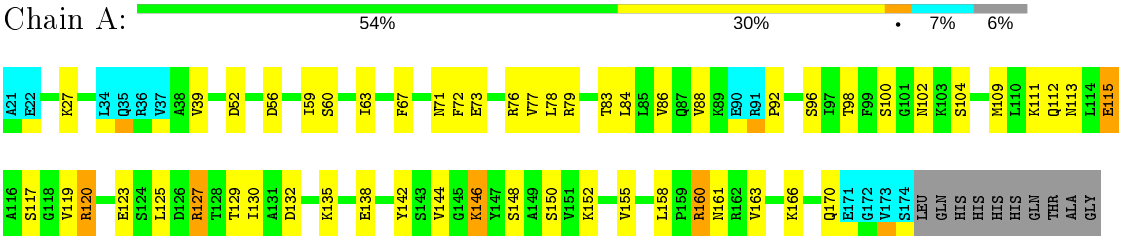
Chain A:



4.2.12 Score per residue for model 12

• Molecule 1: OUTER MEMBRANE PROTEIN ASSEMBLY FACTOR YAET

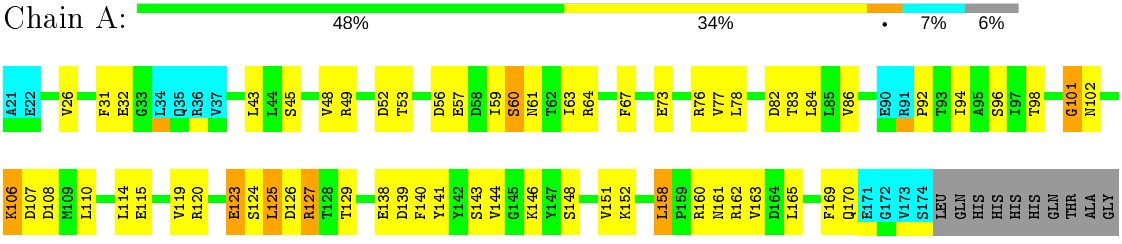
Chain A:



4.2.13 Score per residue for model 13

• Molecule 1: OUTER MEMBRANE PROTEIN ASSEMBLY FACTOR YAET

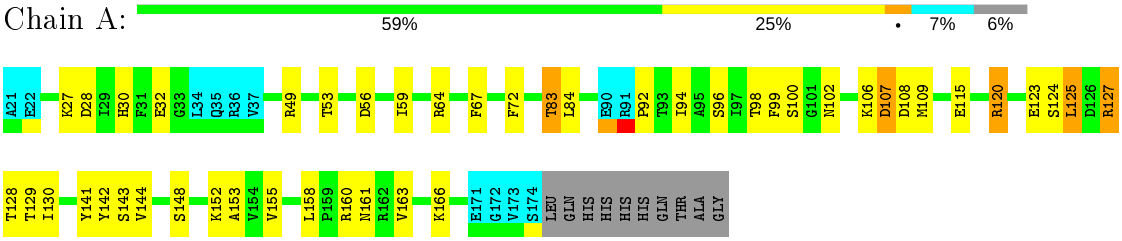
Chain A:



4.2.14 Score per residue for model 14

• Molecule 1: OUTER MEMBRANE PROTEIN ASSEMBLY FACTOR YAET

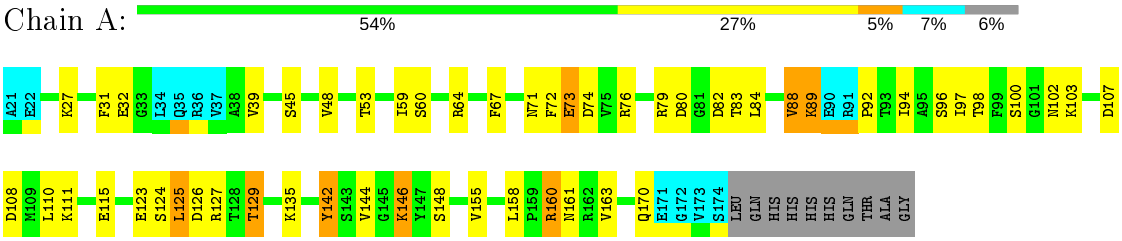
Chain A:



4.2.15 Score per residue for model 15

• Molecule 1: OUTER MEMBRANE PROTEIN ASSEMBLY FACTOR YAET

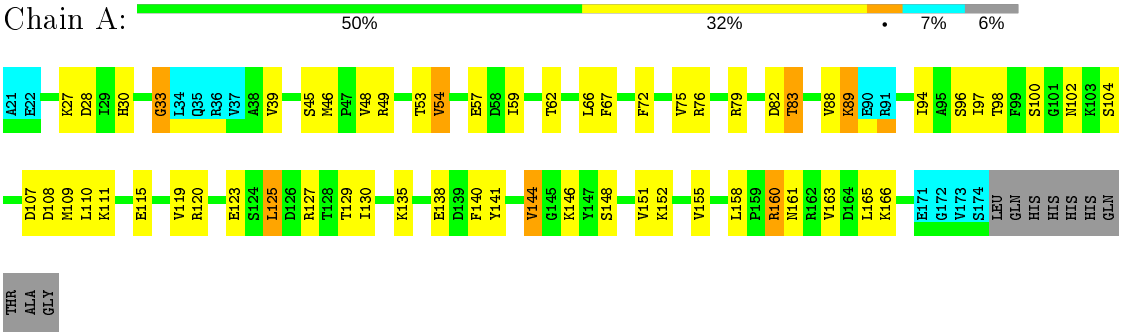
Chain A:



4.2.16 Score per residue for model 16

• Molecule 1: OUTER MEMBRANE PROTEIN ASSEMBLY FACTOR YAET

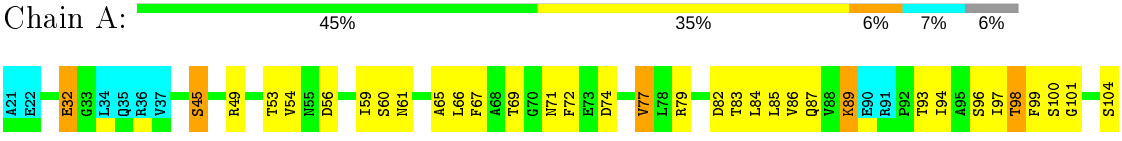
Chain A:

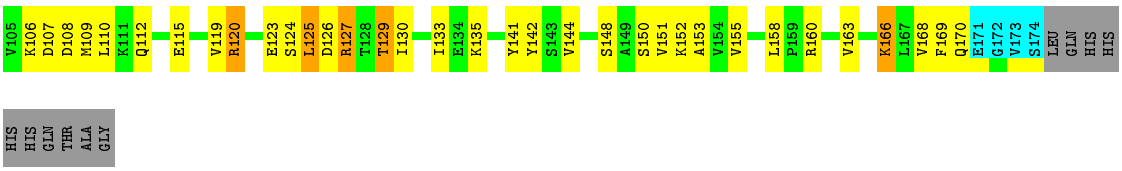


4.2.17 Score per residue for model 17

• Molecule 1: OUTER MEMBRANE PROTEIN ASSEMBLY FACTOR YAET

Chain A:

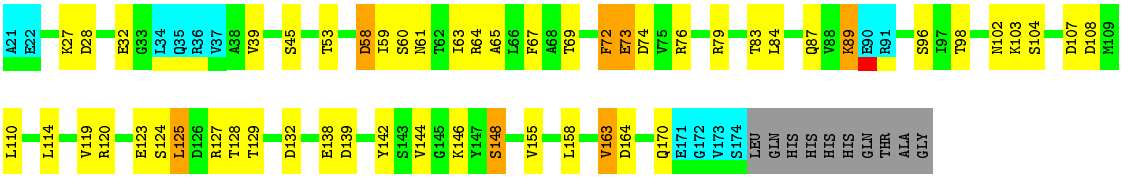




4.2.18 Score per residue for model 18

- Molecule 1: OUTER MEMBRANE PROTEIN ASSEMBLY FACTOR YAET

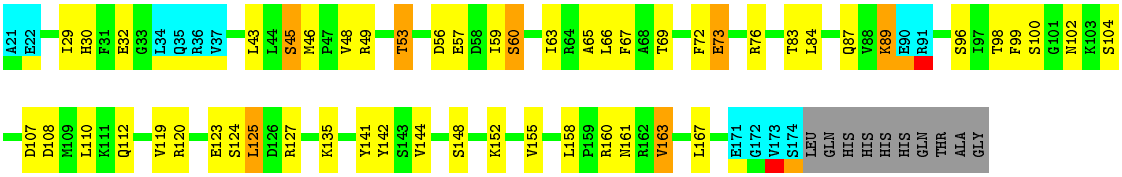
Chain A:



4.2.19 Score per residue for model 19

- Molecule 1: OUTER MEMBRANE PROTEIN ASSEMBLY FACTOR YAET

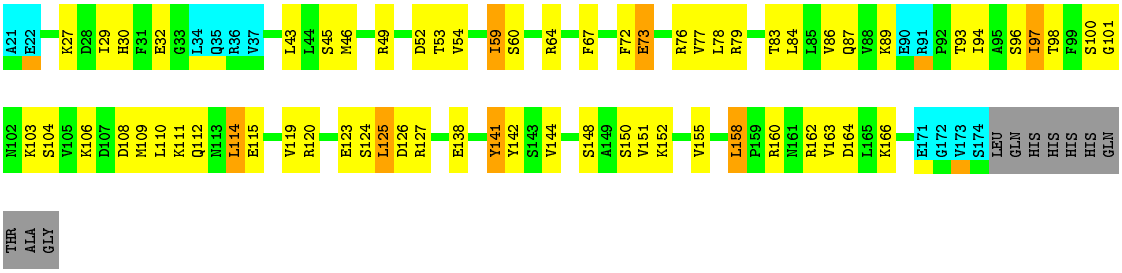
Chain A:



4.2.20 Score per residue for model 20

- Molecule 1: OUTER MEMBRANE PROTEIN ASSEMBLY FACTOR YAET

Chain A:



5 Refinement protocol and experimental data overview

The models were refined using the following method: *distance geometry*.

Of the 450 calculated structures, 20 were deposited, based on the following criterion: *LEAST RESTRAINT VIOLATIONS*.

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

Software name	Classification	Version
ARIA	refinement	
NMRPipe	structure solution	
Sparky	structure solution	
VNMR	structure solution	
CYANA	structure solution	
CNS	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)	input_cs.cif
Number of chemical shift lists	1
Total number of shifts	1906
Number of shifts mapped to atoms	1906
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	91%

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	1088	1104	1103	10±4
All	All	21760	22080	22060	194

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 4.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:59:ILE:HD11	1:A:79:ARG:HD3	0.70	1.61	20	1
1:A:108:ASP:HA	1:A:111:LYS:HE2	0.69	1.62	5	1
1:A:138:GLU:HG3	1:A:151:VAL:HG23	0.68	1.66	20	4
1:A:93:THR:HB	1:A:162:ARG:HG3	0.68	1.64	7	1
1:A:74:ASP:HB3	1:A:89:LYS:HB2	0.66	1.68	18	6
1:A:115:GLU:HG2	1:A:120:ARG:HG3	0.63	1.69	20	1
1:A:107:ASP:HA	1:A:110:LEU:HD12	0.63	1.68	10	2
1:A:98:THR:HB	1:A:166:LYS:HG3	0.62	1.70	8	2
1:A:125:LEU:HD22	1:A:163:VAL:HG11	0.61	1.71	19	2
1:A:73:GLU:HB3	1:A:124:SER:HB3	0.59	1.74	1	1
1:A:73:GLU:HB3	1:A:124:SER:HB2	0.58	1.75	9	1
1:A:45:SER:HB3	1:A:69:THR:HG21	0.58	1.76	7	3
1:A:115:GLU:HA	1:A:120:ARG:HB3	0.58	1.75	17	1
1:A:58:ASP:HA	1:A:61:ASN:HB2	0.58	1.74	18	4

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:93:THR:HB	1:A:162:ARG:HD2	0.58	1.75	20	1
1:A:46:MET:HG2	1:A:62:THR:HG23	0.57	1.76	3	5
1:A:125:LEU:HD22	1:A:163:VAL:HG21	0.57	1.76	5	3
1:A:60:SER:HA	1:A:63:ILE:HD12	0.56	1.76	18	8
1:A:97:ILE:HG21	1:A:114:LEU:HD22	0.56	1.76	1	4
1:A:142:TYR:HA	1:A:146:LYS:HA	0.56	1.76	12	3
1:A:43:LEU:HD22	1:A:49:ARG:HG2	0.56	1.77	19	1
1:A:24:PHE:CE1	1:A:79:ARG:HD2	0.55	2.36	2	2
1:A:32:GLU:HB2	1:A:87:GLN:HG2	0.55	1.76	20	2
1:A:138:GLU:HG3	1:A:151:VAL:HG12	0.55	1.78	13	1
1:A:92:PRO:HA	1:A:161:ASN:O	0.55	2.02	8	6
1:A:31:PHE:HD2	1:A:39:VAL:HG12	0.55	1.62	10	2
1:A:93:THR:HA	1:A:124:SER:HA	0.55	1.78	17	1
1:A:99:PHE:HE1	1:A:111:LYS:HG3	0.54	1.62	6	4
1:A:66:LEU:HB3	1:A:75:VAL:HG21	0.54	1.78	16	1
1:A:108:ASP:HA	1:A:111:LYS:CE	0.54	2.32	5	1
1:A:33:GLY:HA3	1:A:88:VAL:H	0.54	1.59	3	1
1:A:101:GLY:HA3	1:A:169:PHE:HB2	0.54	1.78	1	3
1:A:65:ALA:O	1:A:69:THR:HG23	0.54	2.03	7	5
1:A:103:LYS:H	1:A:103:LYS:HD2	0.53	1.63	8	1
1:A:32:GLU:HB3	1:A:87:GLN:HG2	0.53	1.78	17	2
1:A:28:ASP:HB3	1:A:83:THR:HG23	0.53	1.79	3	3
1:A:66:LEU:HD22	1:A:72:PHE:HE2	0.53	1.63	17	1
1:A:33:GLY:HA3	1:A:88:VAL:HG22	0.53	1.79	16	1
1:A:48:VAL:HG12	1:A:54:VAL:HG11	0.52	1.79	4	1
1:A:73:GLU:HG2	1:A:124:SER:HB2	0.52	1.80	10	2
1:A:125:LEU:HD11	1:A:130:ILE:HD11	0.52	1.81	16	1
1:A:158:LEU:HD11	1:A:162:ARG:HB2	0.51	1.82	20	3
1:A:94:ILE:HG13	1:A:125:LEU:HB2	0.51	1.81	13	1
1:A:115:GLU:HG2	1:A:120:ARG:HB3	0.51	1.82	12	3
1:A:98:THR:HB	1:A:166:LYS:HG2	0.51	1.83	6	2
1:A:130:ILE:HG23	1:A:153:ALA:HB3	0.51	1.83	14	5
1:A:49:ARG:HD2	1:A:52:ASP:HB2	0.51	1.83	2	1
1:A:29:ILE:HD13	1:A:43:LEU:HD21	0.51	1.82	19	1
1:A:41:ALA:HA	1:A:44:LEU:HD12	0.51	1.81	5	1
1:A:48:VAL:HG11	1:A:54:VAL:HG13	0.50	1.83	16	1
1:A:45:SER:HB2	1:A:66:LEU:HD23	0.50	1.82	17	2
1:A:94:ILE:HD11	1:A:125:LEU:HB2	0.49	1.85	15	6
1:A:150:SER:H	1:A:170:GLN:HB2	0.48	1.68	3	1
1:A:77:VAL:HB	1:A:86:VAL:HG22	0.48	1.84	17	1
1:A:126:ASP:HB3	1:A:129:THR:OG1	0.47	2.09	15	4

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:127:ARG:H	1:A:127:ARG:HD2	0.47	1.68	17	1
1:A:29:ILE:HG21	1:A:46:MET:HE1	0.47	1.84	20	1
1:A:99:PHE:HB3	1:A:102:ASN:HD21	0.47	1.70	4	1
1:A:130:ILE:HA	1:A:133:ILE:HD12	0.47	1.86	17	1
1:A:48:VAL:HB	1:A:54:VAL:HG11	0.47	1.87	9	1
1:A:77:VAL:HG22	1:A:86:VAL:HG13	0.46	1.86	12	3
1:A:151:VAL:HA	1:A:168:VAL:O	0.46	2.10	17	2
1:A:145:GLY:O	1:A:146:LYS:HG2	0.46	2.10	4	1
1:A:30:HIS:O	1:A:85:LEU:HA	0.46	2.11	5	1
1:A:43:LEU:HD22	1:A:49:ARG:HD2	0.46	1.87	13	2
1:A:72:PHE:CD1	1:A:88:VAL:HG21	0.45	2.47	15	1
1:A:32:GLU:HG3	1:A:85:LEU:HD11	0.45	1.87	3	1
1:A:73:GLU:HG2	1:A:89:LYS:HD2	0.45	1.88	15	1
1:A:115:GLU:HG2	1:A:120:ARG:HB2	0.45	1.89	14	1
1:A:100:SER:OG	1:A:166:LYS:HE3	0.44	2.12	1	1
1:A:40:GLY:O	1:A:44:LEU:HG	0.44	2.12	2	1
1:A:117:SER:HB2	1:A:133:ILE:HG12	0.44	1.89	5	1
1:A:77:VAL:O	1:A:78:LEU:HD13	0.43	2.13	20	1
1:A:99:PHE:HD1	1:A:107:ASP:HB2	0.43	1.73	17	2
1:A:127:ARG:HA	1:A:130:ILE:HG12	0.43	1.90	12	2
1:A:106:LYS:O	1:A:110:LEU:HG	0.43	2.13	13	1
1:A:102:ASN:HA	1:A:141:TYR:OH	0.43	2.14	8	1
1:A:98:THR:HB	1:A:166:LYS:HE3	0.43	1.91	11	1
1:A:158:LEU:HD12	1:A:160:ARG:HB2	0.43	1.91	13	1
1:A:119:VAL:HG21	1:A:133:ILE:HD11	0.42	1.91	17	1
1:A:134:GLU:O	1:A:138:GLU:HG2	0.42	2.13	4	1
1:A:102:ASN:HB2	1:A:105:VAL:O	0.42	2.14	11	2
1:A:157:PRO:HA	1:A:163:VAL:HG12	0.42	1.91	9	1
1:A:48:VAL:HG23	1:A:52:ASP:HB3	0.42	1.91	10	1
1:A:73:GLU:O	1:A:126:ASP:HB2	0.42	2.13	20	1
1:A:49:ARG:O	1:A:52:ASP:HB2	0.42	2.15	6	2
1:A:158:LEU:HG	1:A:162:ARG:O	0.42	2.14	5	3
1:A:32:GLU:O	1:A:87:GLN:HA	0.42	2.15	5	1
1:A:160:ARG:HD2	1:A:160:ARG:HA	0.42	1.63	10	1
1:A:127:ARG:HD3	1:A:128:THR:HG23	0.42	1.91	14	1
1:A:140:PHE:O	1:A:144:VAL:HG23	0.42	2.14	4	2
1:A:123:GLU:HG3	1:A:124:SER:N	0.42	2.30	13	1
1:A:137:LEU:HD22	1:A:169:PHE:HZ	0.42	1.75	5	1
1:A:126:ASP:HA	1:A:127:ARG:NH1	0.42	2.30	13	1
1:A:103:LYS:HD2	1:A:103:LYS:HA	0.42	1.67	10	1
1:A:103:LYS:CD	1:A:103:LYS:H	0.41	2.27	8	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:27:LYS:HB2	1:A:82:ASP:HB3	0.41	1.93	5	1
1:A:144:VAL:HG13	1:A:145:GLY:H	0.41	1.74	11	1
1:A:74:ASP:HB3	1:A:89:LYS:HB3	0.41	1.92	3	1
1:A:73:GLU:HG3	1:A:73:GLU:H	0.41	1.55	19	1
1:A:98:THR:HB	1:A:166:LYS:HD3	0.41	1.93	10	1
1:A:97:ILE:HG21	1:A:114:LEU:CD1	0.41	2.46	10	1
1:A:73:GLU:OE1	1:A:89:LYS:HE2	0.41	2.16	19	1
1:A:120:ARG:HG3	1:A:123:GLU:HB2	0.41	1.92	5	1
1:A:99:PHE:HE2	1:A:167:LEU:HD13	0.41	1.76	19	1
1:A:29:ILE:HD12	1:A:43:LEU:HD21	0.40	1.92	5	1
1:A:94:ILE:CD1	1:A:125:LEU:HB2	0.40	2.47	14	1
1:A:149:ALA:HA	1:A:170:GLN:O	0.40	2.16	11	1
1:A:104:SER:HB2	1:A:141:TYR:CE1	0.40	2.52	20	1
1:A:94:ILE:CD1	1:A:119:VAL:HG12	0.40	2.46	17	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	142/164 (87%)	136±2 (96±1%)	4±2 (3±1%)	2±1 (1±1%)	15	61
All	All	2840/3280 (87%)	2728 (96%)	73 (3%)	39 (1%)	15	61

All 7 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	144	VAL	19
1	A	160	ARG	9
1	A	161	ASN	4
1	A	33	GLY	3
1	A	148	SER	2
1	A	159	PRO	1
1	A	101	GLY	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	121/139 (87%)	78±3 (65±3%)	43±3 (35±3%)	1 9
All	All	2420/2780 (87%)	1566 (65%)	854 (35%)	1 9

All 91 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	125	LEU	20
1	A	83	THR	20
1	A	67	PHE	20
1	A	84	LEU	19
1	A	98	THR	19
1	A	53	THR	18
1	A	148	SER	18
1	A	158	LEU	18
1	A	59	ILE	18
1	A	127	ARG	18
1	A	96	SER	17
1	A	45	SER	16
1	A	160	ARG	16
1	A	141	TYR	16
1	A	119	VAL	16
1	A	123	GLU	16
1	A	163	VAL	16
1	A	30	HIS	15
1	A	120	ARG	15
1	A	107	ASP	15
1	A	135	LYS	15
1	A	110	LEU	15
1	A	155	VAL	15
1	A	100	SER	14
1	A	72	PHE	14
1	A	124	SER	14
1	A	76	ARG	14
1	A	150	SER	14
1	A	89	LYS	12

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Mol	Chain	Res	Type	Models (Total)
1	A	102	ASN	12
1	A	152	LYS	12
1	A	142	TYR	11
1	A	32	GLU	11
1	A	112	GLN	11
1	A	166	LYS	11
1	A	79	ARG	11
1	A	82	ASP	11
1	A	170	GLN	10
1	A	111	LYS	10
1	A	27	LYS	10
1	A	104	SER	10
1	A	60	SER	10
1	A	108	ASP	10
1	A	109	MET	10
1	A	73	GLU	9
1	A	129	THR	9
1	A	64	ARG	9
1	A	146	LYS	9
1	A	115	GLU	9
1	A	97	ILE	9
1	A	39	VAL	8
1	A	48	VAL	8
1	A	56	ASP	8
1	A	52	ASP	8
1	A	78	LEU	7
1	A	103	LYS	7
1	A	49	ARG	7
1	A	26	VAL	7
1	A	106	LYS	7
1	A	132	ASP	7
1	A	57	GLU	7
1	A	61	ASN	6
1	A	54	VAL	6
1	A	140	PHE	6
1	A	162	ARG	6
1	A	114	LEU	6
1	A	164	ASP	5
1	A	71	ASN	4
1	A	143	SER	4
1	A	139	ASP	4
1	A	117	SER	3

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Mol	Chain	Res	Type	Models (Total)
1	A	43	LEU	3
1	A	138	GLU	3
1	A	85	LEU	3
1	A	80	ASP	3
1	A	165	LEU	3
1	A	167	LEU	3
1	A	113	ASN	2
1	A	88	VAL	2
1	A	31	PHE	2
1	A	50	THR	2
1	A	128	THR	1
1	A	77	VAL	1
1	A	62	THR	1
1	A	168	VAL	1
1	A	55	ASN	1
1	A	58	ASP	1
1	A	87	GLN	1
1	A	169	PHE	1
1	A	46	MET	1
1	A	28	ASP	1

6.3.3 RNA

There are no RNA molecules in this entry.

6.4 Non-standard residues in protein, DNA, RNA chains

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

6.5 Carbohydrates

There are no carbohydrates in this entry.

6.6 Ligand geometry

There are no ligands in this entry.

6.7 Other polymers

There are no such molecules in this entry.

6.8 Polymer linkage issues

There are no chain breaks in this entry.

7 Chemical shift validation

The completeness of assignment taking into account all chemical shift lists is 91% for the well-defined parts and 89% for the entire structure.

7.1 Chemical shift list 1

File name: input_cs.cif

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	1906
Number of shifts mapped to atoms	1906
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	4

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	154	-0.31 ± 0.15	None needed (< 0.5 ppm)
$^{13}C_{\beta}$	141	-0.11 ± 0.08	None needed (< 0.5 ppm)
$^{13}C'$	150	-0.23 ± 0.10	None needed (< 0.5 ppm)
^{15}N	149	-0.35 ± 0.32	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 91%, i.e. 1542 atoms were assigned a chemical shift out of a possible 1694. 0 out of 31 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	699/702 (100%)	280/280 (100%)	281/284 (99%)	138/138 (100%)
Sidechain	763/897 (85%)	464/516 (90%)	290/339 (86%)	9/42 (21%)

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	Total	^{1}H	^{13}C	^{15}N
Aromatic	80/95 (84%)	42/51 (82%)	38/42 (90%)	0/2 (0%)
Overall	1542/1694 (91%)	786/847 (93%)	609/665 (92%)	147/182 (81%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 89%, i.e. 1653 atoms were assigned a chemical shift out of a possible 1847. 0 out of 34 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	750/762 (98%)	300/304 (99%)	302/308 (98%)	148/150 (99%)
Sidechain	823/990 (83%)	501/570 (88%)	312/371 (84%)	10/49 (20%)
Aromatic	80/95 (84%)	42/51 (82%)	38/42 (90%)	0/2 (0%)
Overall	1653/1847 (89%)	843/925 (91%)	652/721 (90%)	158/201 (79%)

7.1.4 Statistically unusual chemical shifts (i)

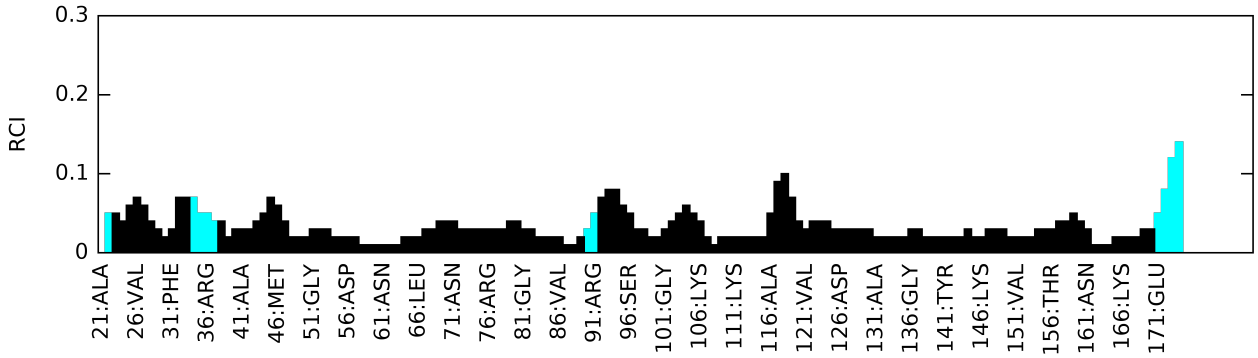
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

Mol	Chain	Res	Type	Atom	Shift, *ppm*	Expected range, *ppm*	Z-score
1	A	71	ASN	HB3	0.84	4.41 – 1.11	-5.8
1	A	36	ARG	H	11.50	11.29 – 5.19	5.3
1	A	90	GLU	HB2	3.12	3.08 – 0.98	5.2
1	A	90	GLU	HB3	3.10	3.10 – 0.90	5.0

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:


RCI
0.3
0.2
0.1
0
21:ALA
26:VAL
31:PHE
36:ARG
41:ALA
46:MET
51:GLY
56:ASP
61:ASN
66:LEU
71:ASN
76:ARG
81:GLY
86:VAL
91:ARG
96:SER
101:GLY
106:LYS
111:LYS
116:ALA
121:VAL
126:ASP
131:ALA
136:GLY
141:TYR
146:LYS
151:VAL
156:THR
161:ASN
166:LYS
171:GLU