



Full wwPDB NMR Structure Validation Report ⓘ

Feb 18, 2018 – 09:30 am GMT

PDB ID : 2L6E
Title : NMR Structure of the monomeric mutant C-terminal domain of HIV-1 Capsid
in complex with stapled peptide Inhibitor
Authors : Bhattacharya, S.; Zhang, H.; Debnath, A.K.; Cowburn, D.
Deposited on : 2010-11-18

This is a Full wwPDB NMR Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/NMRValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

Cyrange	:	Kirchner and Güntert (2011)
NmrClust	:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Mogul	:	1.7.3 (157068), CSD as539be (2018)
Percentile statistics	:	20171227.v01 (using entries in the PDB archive December 27th 2017)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	trunk30686
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk30686

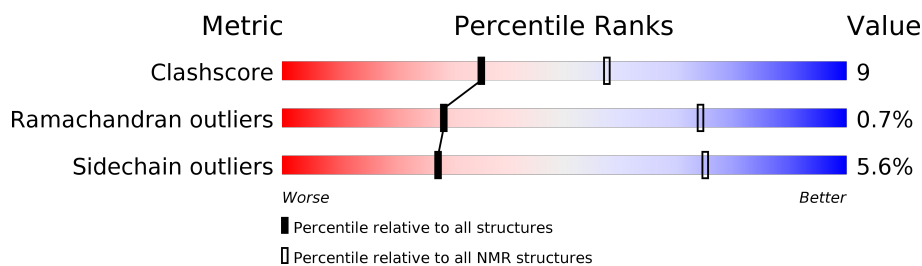
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 87%.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	NMR archive (#Entries)
Clashscore	136279	12091
Ramachandran outliers	132675	10835
Sidechain outliers	132484	10811

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

Mol	Chain	Length	Quality of chain
1	A	105	
2	B	14	

2 Ensemble composition and analysis

This entry contains 20 models. Model 7 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *lowest energy*.

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

Well-defined (core) protein residues			
Well-defined core	Residue range (total)	Backbone RMSD (Å)	Medoid model
1	A:150-A:218, B:2-B:3, B:5-B:7, B:9-B:10 (76)	0.34	7

Ill-defined regions of proteins are excluded from the global statistics.

Ligands and non-protein polymers are included in the analysis.

The models can be grouped into 3 clusters. No single-model clusters were found.

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

3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 1711 atoms, of which 874 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Capsid protein p24.

Mol	Chain	Residues	Atoms						Trace
1	A	94	Total	C	H	N	O	S	0
			1449	442	736	130	136	5	

There are 23 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	127	MET	-	INITIATING METHIONINE	UNP P35963
A	128	GLY	-	EXPRESSION TAG	UNP P35963
A	129	SER	-	EXPRESSION TAG	UNP P35963
A	130	SER	-	EXPRESSION TAG	UNP P35963
A	131	HIS	-	EXPRESSION TAG	UNP P35963
A	132	HIS	-	EXPRESSION TAG	UNP P35963
A	133	HIS	-	EXPRESSION TAG	UNP P35963
A	134	HIS	-	EXPRESSION TAG	UNP P35963
A	135	HIS	-	EXPRESSION TAG	UNP P35963
A	136	HIS	-	EXPRESSION TAG	UNP P35963
A	137	SER	-	EXPRESSION TAG	UNP P35963
A	138	SER	-	EXPRESSION TAG	UNP P35963
A	139	GLY	-	EXPRESSION TAG	UNP P35963
A	140	LEU	-	EXPRESSION TAG	UNP P35963
A	141	VAL	-	EXPRESSION TAG	UNP P35963
A	142	PRO	-	EXPRESSION TAG	UNP P35963
A	143	ARG	-	EXPRESSION TAG	UNP P35963
A	144	GLY	-	EXPRESSION TAG	UNP P35963
A	145	SER	-	EXPRESSION TAG	UNP P35963
A	146	HIS	-	EXPRESSION TAG	UNP P35963
A	147	MET	-	EXPRESSION TAG	UNP P35963
A	184	ALA	TRP	ENGINEERED MUTATION	UNP P35963
A	185	ALA	MET	ENGINEERED MUTATION	UNP P35963

- Molecule 2 is a protein called NYAD-13 stapled peptide inhibitor.

Mol	Chain	Residues	Atoms						Trace
2	B	14	Total	C	H	N	O		0
			262	87	138	17	20		

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: Capsid protein p24

Chain A: 



- Molecule 2: NYAD-13 stapled peptide inhibitor

Chain B: 



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: Capsid protein p24

Chain A: 

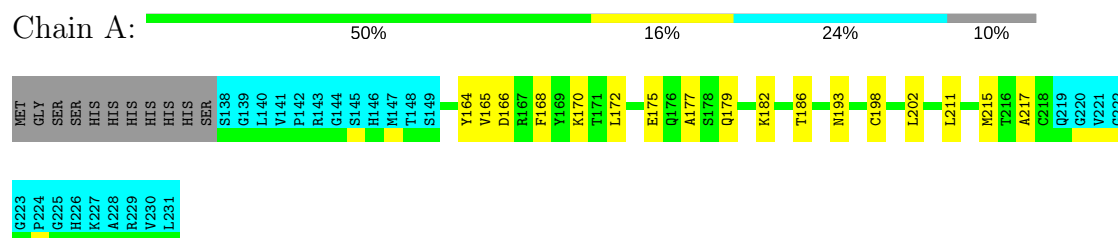


- Molecule 2: NYAD-13 stapled peptide inhibitor

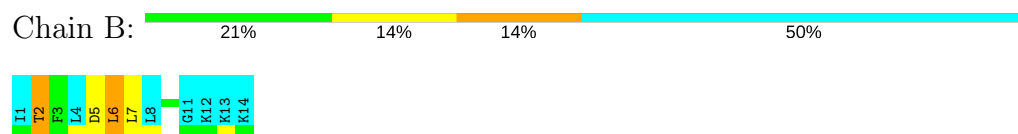
Chain B: 

4.2.2 Score per residue for model 2

- Molecule 1: Capsid protein p24

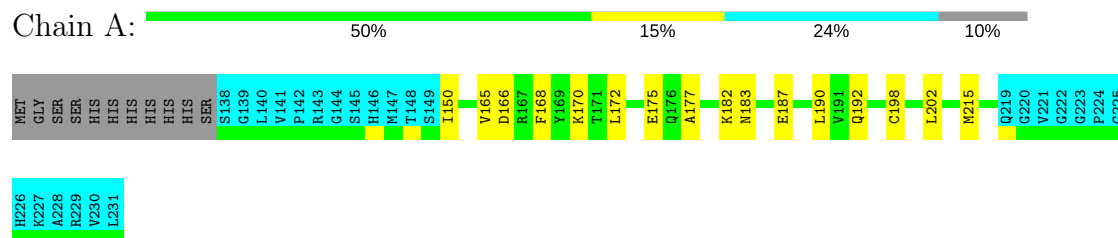


- Molecule 2: NYAD-13 stapled peptide inhibitor

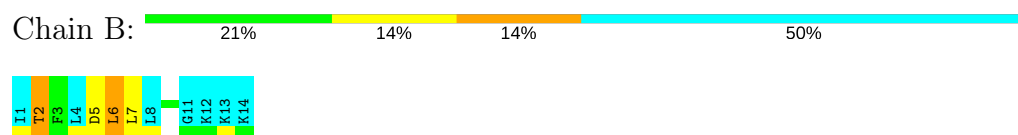


4.2.3 Score per residue for model 3

- Molecule 1: Capsid protein p24



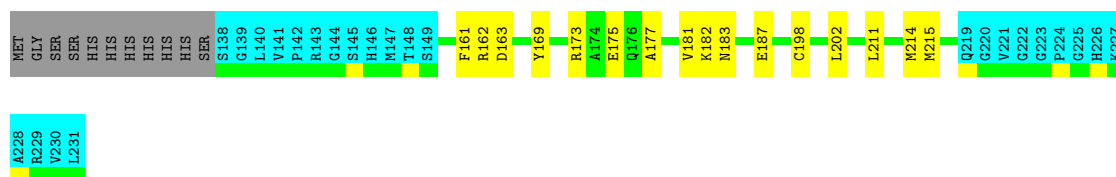
- Molecule 2: NYAD-13 stapled peptide inhibitor



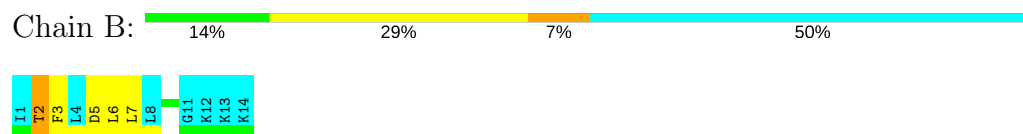
4.2.4 Score per residue for model 4

- Molecule 1: Capsid protein p24



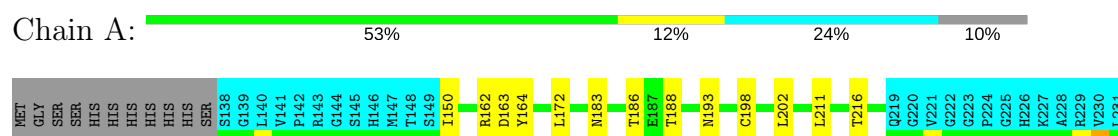


- Molecule 2: NYAD-13 stapled peptide inhibitor

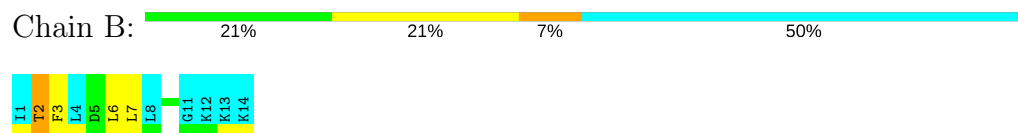


4.2.5 Score per residue for model 5

- Molecule 1: Capsid protein p24

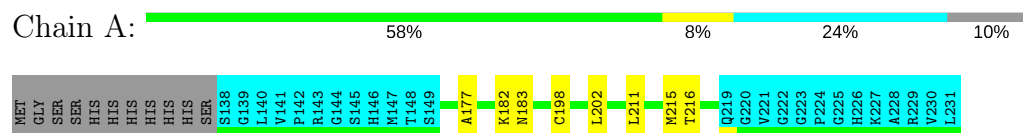


- Molecule 2: NYAD-13 stapled peptide inhibitor

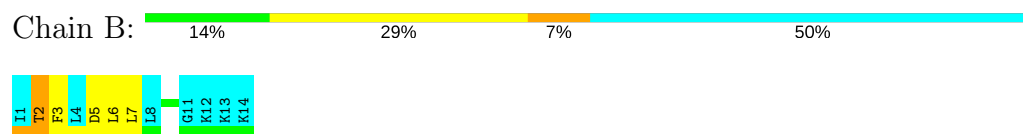


4.2.6 Score per residue for model 6

- Molecule 1: Capsid protein p24

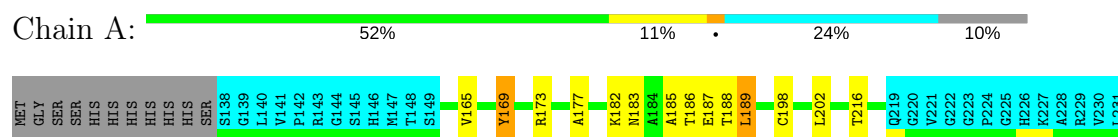


- Molecule 2: NYAD-13 stapled peptide inhibitor

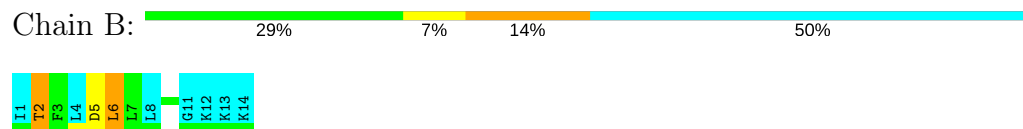


4.2.7 Score per residue for model 7 (medoid)

- Molecule 1: Capsid protein p24

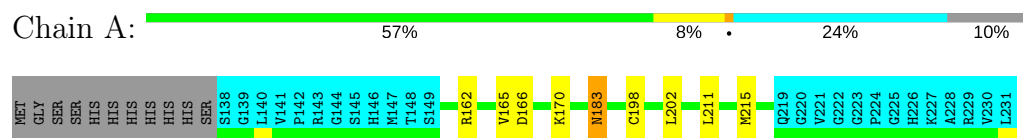


- Molecule 2: NYAD-13 stapled peptide inhibitor

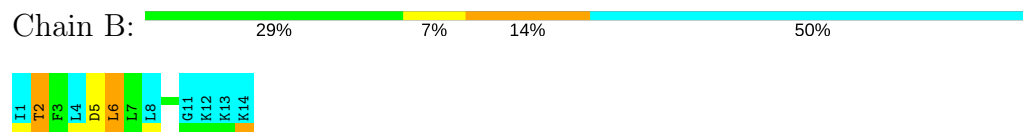


4.2.8 Score per residue for model 8

- Molecule 1: Capsid protein p24

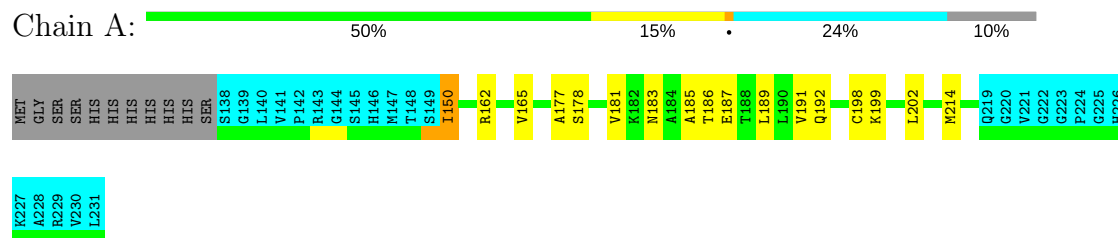


- Molecule 2: NYAD-13 stapled peptide inhibitor

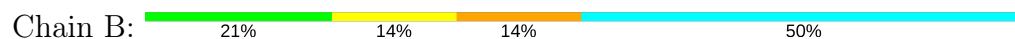


4.2.9 Score per residue for model 9

- Molecule 1: Capsid protein p24



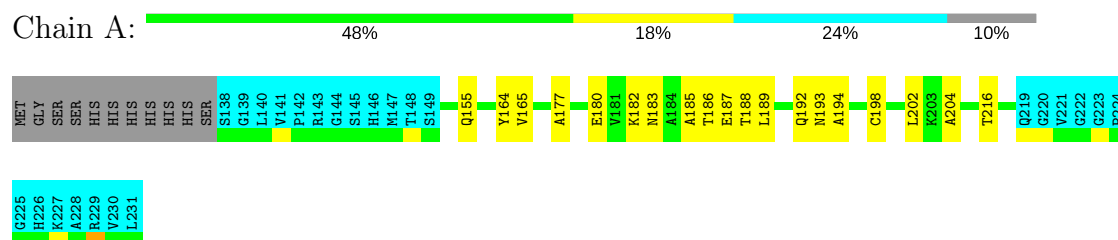
- Molecule 2: NYAD-13 stapled peptide inhibitor



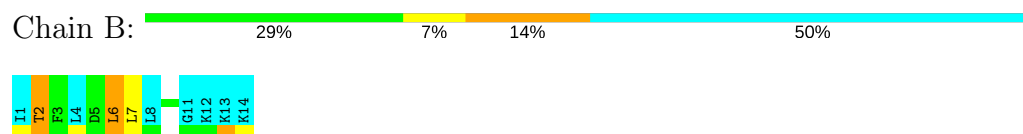


4.2.10 Score per residue for model 10

- Molecule 1: Capsid protein p24

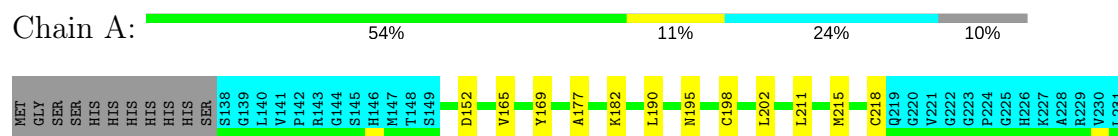


- Molecule 2: NYAD-13 stapled peptide inhibitor

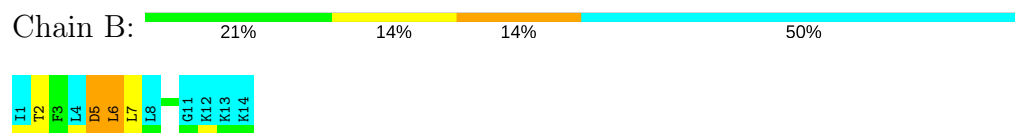


4.2.11 Score per residue for model 11

- Molecule 1: Capsid protein p24

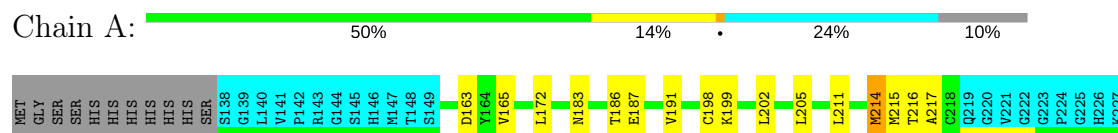


- Molecule 2: NYAD-13 stapled peptide inhibitor



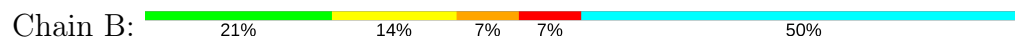
4.2.12 Score per residue for model 12

- Molecule 1: Capsid protein p24



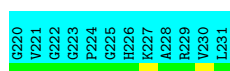
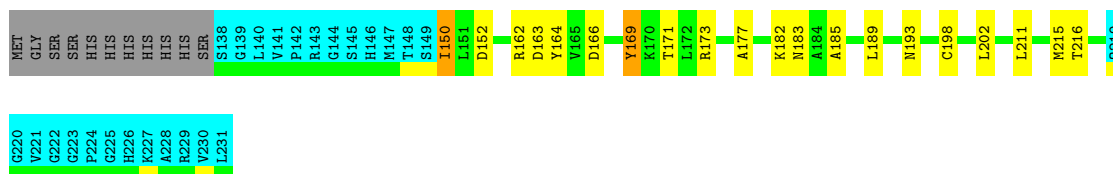


- Molecule 2: NYAD-13 stapled peptide inhibitor



4.2.13 Score per residue for model 13

- Molecule 1: Capsid protein p24



- Molecule 2: NYAD-13 stapled peptide inhibitor

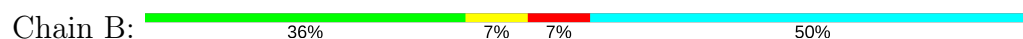


4.2.14 Score per residue for model 14

- Molecule 1: Capsid protein p24

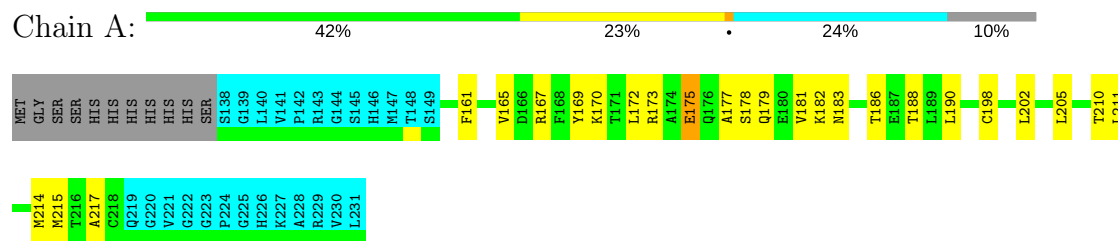


- Molecule 2: NYAD-13 stapled peptide inhibitor

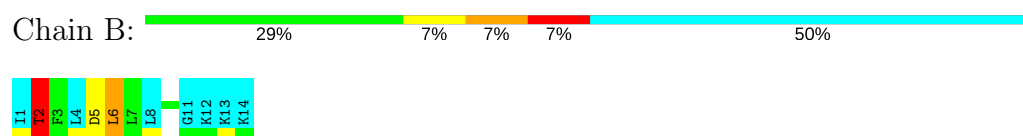


4.2.15 Score per residue for model 15

- Molecule 1: Capsid protein p24

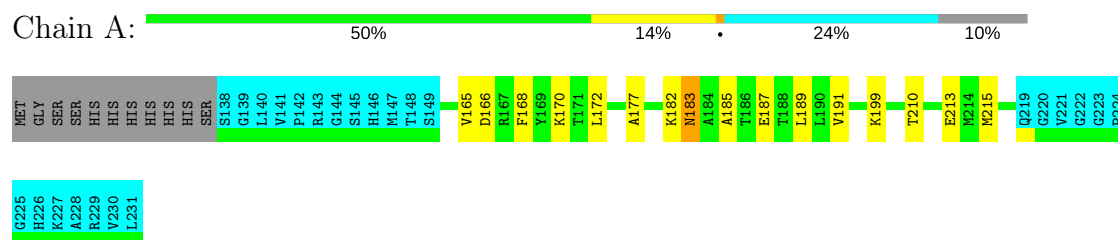


- Molecule 2: NYAD-13 stapled peptide inhibitor

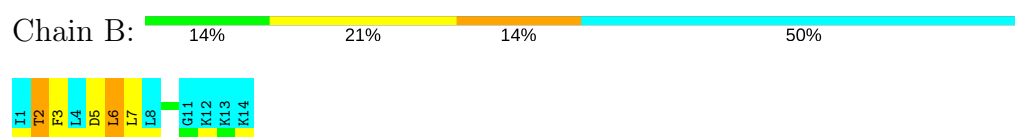


4.2.16 Score per residue for model 16

- Molecule 1: Capsid protein p24

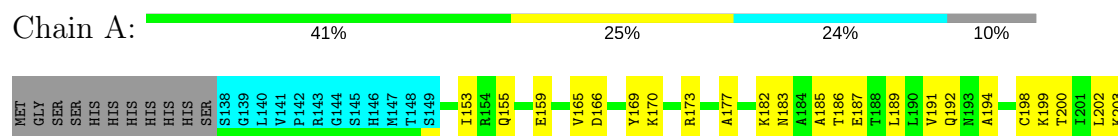


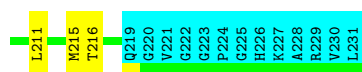
- Molecule 2: NYAD-13 stapled peptide inhibitor



4.2.17 Score per residue for model 17

- Molecule 1: Capsid protein p24



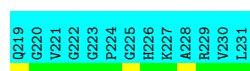


- Molecule 2: NYAD-13 stapled peptide inhibitor

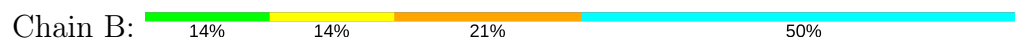


4.2.18 Score per residue for model 18

- Molecule 1: Capsid protein p24

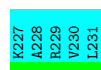


- Molecule 2: NYAD-13 stapled peptide inhibitor



4.2.19 Score per residue for model 19

- Molecule 1: Capsid protein p24

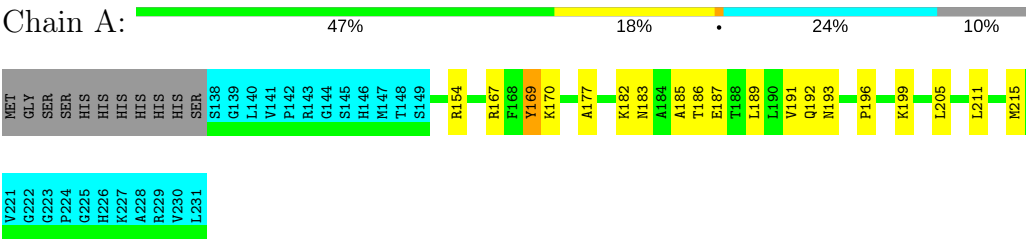


- Molecule 2: NYAD-13 stapled peptide inhibitor

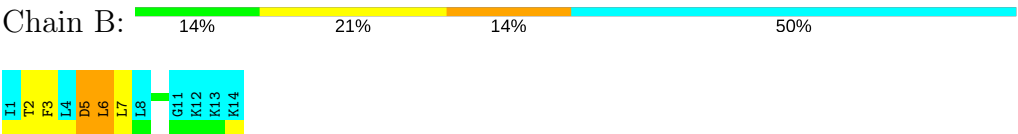


4.2.20 Score per residue for model 20

- Molecule 1: Capsid protein p24



- Molecule 2: NYAD-13 stapled peptide inhibitor



5 Refinement protocol and experimental data overview

The models were refined using the following method: *simulated annealing*.

Of the 1000 calculated structures, 20 were deposited, based on the following criterion: *structures with the lowest energy*.

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

Software name	Classification	Version
CYANA	structure solution	2.1
ARIA	refinement	2.2

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 17307
Number of chemical shift lists	1
Total number of shifts	1184
Number of shifts mapped to atoms	1182
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	2
Assignment completeness (well-defined parts)	87%

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: MK8

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	539	556	546	11±3
2	B	66	61	60	4±2
All	All	12100	12340	12120	228

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 9.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:167:ARG:HA	1:A:170:LYS:HE2	0.83	1.48	20	3
1:A:186:THR:HA	1:A:189:LEU:HD11	0.75	1.59	7	2
1:A:166:ASP:O	1:A:170:LYS:HG2	0.70	1.86	16	2
1:A:183:ASN:O	1:A:187:GLU:HG3	0.66	1.88	17	8
1:A:185:ALA:O	1:A:189:LEU:HG	0.66	1.89	16	8
1:A:177:ALA:HB1	1:A:181:VAL:CG1	0.66	2.20	9	3
1:A:165:VAL:HG13	2:B:6:LEU:HD11	0.65	1.69	2	14
1:A:186:THR:HA	1:A:189:LEU:CD1	0.64	2.21	7	4
1:A:182:LYS:HA	1:A:182:LYS:HE2	0.61	1.71	6	1
2:B:6:LEU:HD13	2:B:6:LEU:H	0.61	1.56	13	2
1:A:183:ASN:HB3	2:B:2:THR:OG1	0.60	1.96	15	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:211:LEU:HB2	2:B:5:ASP:OD1	0.59	1.98	20	1
2:B:6:LEU:HD22	2:B:7:LEU:N	0.58	2.14	13	2
1:A:183:ASN:ND2	2:B:3:PHE:HB3	0.58	2.13	6	3
1:A:189:LEU:HA	1:A:192:GLN:HB3	0.57	1.76	10	5
1:A:198:CYS:O	1:A:202:LEU:HG	0.57	2.00	8	18
1:A:183:ASN:HD22	2:B:3:PHE:HB3	0.57	1.59	6	3
1:A:183:ASN:OD1	2:B:3:PHE:HB3	0.57	1.98	19	3
1:A:191:VAL:O	1:A:199:LYS:HE2	0.56	2.00	16	6
2:B:3:PHE:CZ	2:B:7:LEU:HD21	0.56	2.35	19	1
2:B:3:PHE:HA	2:B:6:LEU:HD11	0.56	1.77	13	2
1:A:178:SER:O	1:A:181:VAL:HG12	0.55	2.01	15	2
1:A:167:ARG:CA	1:A:170:LYS:HE2	0.54	2.30	20	1
1:A:169:TYR:HB2	2:B:6:LEU:HD12	0.54	1.79	11	2
1:A:187:GLU:CD	2:B:2:THR:HG22	0.53	2.24	7	4
1:A:177:ALA:HB1	1:A:181:VAL:HG11	0.53	1.80	9	3
1:A:183:ASN:HA	1:A:186:THR:HG22	0.52	1.81	10	2
1:A:183:ASN:HB2	2:B:2:THR:OG1	0.52	2.04	1	1
1:A:211:LEU:O	1:A:215:MET:HG2	0.52	2.04	1	8
1:A:166:ASP:O	1:A:170:LYS:HG3	0.52	2.04	2	2
1:A:177:ALA:O	1:A:182:LYS:HE3	0.52	2.05	17	6
2:B:3:PHE:CD1	2:B:6:LEU:HD21	0.52	2.40	13	2
1:A:172:LEU:O	1:A:175:GLU:HB2	0.51	2.06	15	1
1:A:180:GLU:HA	1:A:183:ASN:ND2	0.51	2.20	1	3
1:A:169:TYR:CZ	1:A:173:ARG:HD3	0.50	2.42	17	2
1:A:211:LEU:HD22	2:B:6:LEU:HD22	0.50	1.83	8	1
1:A:169:TYR:HB2	2:B:6:LEU:CD1	0.50	2.36	11	1
1:A:164:TYR:OH	1:A:193:ASN:HB2	0.49	2.08	5	4
1:A:172:LEU:HD21	1:A:186:THR:OG1	0.49	2.07	14	3
1:A:177:ALA:HB3	1:A:182:LYS:HE3	0.48	1.86	6	1
1:A:177:ALA:CB	1:A:182:LYS:HE2	0.47	2.39	2	1
1:A:211:LEU:HB2	2:B:5:ASP:OD2	0.47	2.09	18	1
1:A:169:TYR:CE1	1:A:173:ARG:HD2	0.47	2.44	13	1
1:A:211:LEU:O	1:A:215:MET:HG3	0.47	2.10	4	5
1:A:211:LEU:HD22	2:B:6:LEU:HB3	0.47	1.86	13	2
1:A:168:PHE:CE1	1:A:186:THR:HG23	0.47	2.44	2	2
1:A:183:ASN:HA	2:B:3:PHE:H	0.47	1.70	16	1
1:A:191:VAL:O	1:A:199:LYS:HD3	0.47	2.10	9	1
1:A:187:GLU:HG2	2:B:2:THR:HG22	0.46	1.86	17	8
1:A:169:TYR:CD1	2:B:6:LEU:HD23	0.46	2.45	13	2
1:A:169:TYR:O	1:A:173:ARG:HG3	0.46	2.11	4	3
1:A:161:PHE:CD2	1:A:215:MET:HA	0.46	2.45	15	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:186:THR:OG1	2:B:3:PHE:HB2	0.46	2.10	5	1
1:A:153:ILE:HG23	1:A:167:ARG:HG3	0.46	1.86	18	1
1:A:211:LEU:HB2	2:B:5:ASP:HB3	0.46	1.87	13	1
1:A:196:PRO:HA	1:A:199:LYS:HB3	0.46	1.87	20	1
1:A:168:PHE:HE1	1:A:172:LEU:HD11	0.46	1.70	2	1
2:B:3:PHE:CE1	2:B:7:LEU:HD21	0.46	2.46	19	1
1:A:177:ALA:HB3	1:A:182:LYS:CG	0.46	2.41	13	2
1:A:189:LEU:HD12	1:A:190:LEU:N	0.45	2.26	18	1
1:A:183:ASN:HD22	1:A:183:ASN:N	0.45	2.09	8	1
1:A:154:ARG:HG2	1:A:155:GLN:N	0.45	2.26	19	1
1:A:168:PHE:CE1	1:A:172:LEU:HD11	0.45	2.47	3	3
1:A:177:ALA:O	1:A:182:LYS:HE2	0.45	2.12	4	2
1:A:162:ARG:HG3	1:A:163:ASP:N	0.45	2.27	4	2
1:A:165:VAL:CG1	2:B:6:LEU:HD11	0.44	2.43	18	3
1:A:205:LEU:HD13	1:A:214:MET:HE3	0.44	1.90	12	1
1:A:183:ASN:O	1:A:186:THR:HG22	0.44	2.13	15	1
1:A:177:ALA:HB3	1:A:182:LYS:HE2	0.43	1.89	2	1
1:A:177:ALA:HB3	1:A:182:LYS:HG3	0.43	1.89	4	2
1:A:187:GLU:HG2	2:B:2:THR:HA	0.43	1.89	14	1
1:A:166:ASP:O	1:A:170:LYS:HE3	0.43	2.14	3	2
1:A:175:GLU:HB3	1:A:182:LYS:HE3	0.43	1.90	2	1
1:A:186:THR:HB	2:B:2:THR:HA	0.43	1.90	12	1
1:A:183:ASN:HB3	2:B:2:THR:HB	0.43	1.89	7	1
1:A:203:LYS:NZ	1:A:203:LYS:HB3	0.43	2.28	1	1
1:A:210:THR:O	1:A:214:MET:HG2	0.43	2.14	15	1
1:A:177:ALA:HB3	1:A:182:LYS:HG2	0.43	1.90	2	1
1:A:198:CYS:SG	1:A:218:CYS:SG	0.42	3.16	11	1
1:A:210:THR:HG22	1:A:213:GLU:OE1	0.42	2.14	16	1
2:B:3:PHE:HA	2:B:6:LEU:CD1	0.42	2.45	20	1
1:A:169:TYR:O	1:A:173:ARG:HG2	0.42	2.13	15	1
1:A:178:SER:O	1:A:182:LYS:HG3	0.42	2.15	18	1
1:A:211:LEU:HG	1:A:215:MET:SD	0.42	2.55	19	1
1:A:205:LEU:HD11	1:A:217:ALA:CB	0.42	2.45	20	2
1:A:211:LEU:HD22	2:B:6:LEU:HA	0.42	1.91	13	1
1:A:200:THR:HA	1:A:203:LYS:HG2	0.41	1.91	17	1
1:A:155:GLN:HB3	1:A:194:ALA:HA	0.41	1.92	17	2
1:A:195:ASN:HB3	1:A:198:CYS:SG	0.41	2.55	11	1
1:A:154:ARG:HA	1:A:193:ASN:HB3	0.41	1.93	20	1
1:A:179:GLN:O	1:A:182:LYS:HG2	0.41	2.15	15	1
1:A:177:ALA:CB	1:A:182:LYS:HE3	0.41	2.46	6	1
1:A:171:THR:O	1:A:175:GLU:HG2	0.41	2.16	19	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:183:ASN:HB3	2:B:2:THR:CB	0.40	2.46	7	1
1:A:162:ARG:HA	1:A:215:MET:CE	0.40	2.47	13	1
1:A:191:VAL:HG12	1:A:199:LYS:HG3	0.40	1.94	17	1
1:A:163:ASP:O	1:A:166:ASP:HB3	0.40	2.16	13	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	69/105 (66%)	68±1 (99±1%)	1±1 (1±1%)	0±0 (0±1%)	40	79
2	B	7/14 (50%)	7±0 (94±7%)	0±0 (1±4%)	0±0 (4±7%)	5	30
All	All	1520/2380 (64%)	1493 (98%)	16 (1%)	11 (1%)	28	74

All 2 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
2	B	2	THR	6
1	A	150	ILE	5

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	58/86 (67%)	57±1 (98±2%)	1±1 (2±2%)	54	92
2	B	7/11 (64%)	5±0 (69±6%)	2±0 (31±6%)	1	14
All	All	1300/1940 (67%)	1227 (94%)	73 (6%)	27	75

All 19 unique residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
2	B	2	THR	20
2	B	6	LEU	20
1	A	188	THR	5
1	A	214	MET	5
2	B	5	ASP	3
1	A	169	TYR	3
1	A	162	ARG	2
1	A	150	ILE	2
1	A	152	ASP	2
1	A	183	ASN	2
2	B	7	LEU	1
1	A	163	ASP	1
1	A	189	LEU	1
1	A	176	GLN	1
1	A	159	GLU	1
1	A	213	GLU	1
1	A	179	GLN	1
1	A	175	GLU	1
1	A	192	GLN	1

6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues are 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	MK8	B	4	2	5,8,9	0.81±0.04	0±0 (0±0%)
2	MK8	B	8	2	5,8,9	1.05±0.11	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	MK8	B	4	2	5,10,12	0.91±0.16	0±0 (0±0%)
2	MK8	B	8	2	5,10,12	0.95±0.07	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	MK8	B	4	2	-	0±0,6,8,11	0±0,0,0,0
2	MK8	B	8	2	-	0±0,6,8,11	0±0,0,0,0

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.

6.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.6 Ligand geometry [i](#)

There are no ligands in this entry.

6.7 Other polymers [i](#)

There are no such molecules in this entry.

6.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

7 Chemical shift validation

The completeness of assignment taking into account all chemical shift lists is 87% for the well-defined parts and 80% for the entire structure.

7.1 Chemical shift list 1

File name: BMRB entry 17307

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	1184
Number of shifts mapped to atoms	1182
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	2
Number of shift outliers (ShiftChecker)	3

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

- No matching atoms found in structure. All 2 occurrences are reported below.

Chain	Res	Type	Atom	Shift Data		
				Value	Uncertainty	Ambiguity
B	4	MK8	H	8.038	0.05	1
B	8	MK8	H	8.396	0.05	1

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	92	-0.33 ± 0.12	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	84	0.14 ± 0.11	None needed (< 0.5 ppm)
$^{13}\text{C}'$	91	-0.07 ± 0.09	None needed (< 0.5 ppm)
^{15}N	85	-0.19 ± 0.38	None needed (< 0.5 ppm)

7.1.3 Completeness of resonance assignments [i](#)

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 87%, i.e. 825 atoms were assigned a chemical shift out of a possible 945. 0 out of 12 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	350/372 (94%)	148/148 (100%)	137/152 (90%)	65/72 (90%)
Sidechain	428/514 (83%)	274/300 (91%)	146/190 (77%)	8/24 (33%)
Aromatic	47/59 (80%)	31/31 (100%)	16/28 (57%)	0/0 (—%)
Overall	825/945 (87%)	453/479 (95%)	299/370 (81%)	73/96 (76%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 80%, i.e. 1039 atoms were assigned a chemical shift out of a possible 1297. 0 out of 17 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	463/518 (89%)	195/206 (95%)	183/212 (86%)	85/100 (85%)
Sidechain	529/704 (75%)	345/414 (83%)	175/255 (69%)	9/35 (26%)
Aromatic	47/75 (63%)	31/39 (79%)	16/32 (50%)	0/4 (0%)
Overall	1039/1297 (80%)	571/659 (87%)	374/499 (75%)	94/139 (68%)

7.1.4 Statistically unusual chemical shifts [i](#)

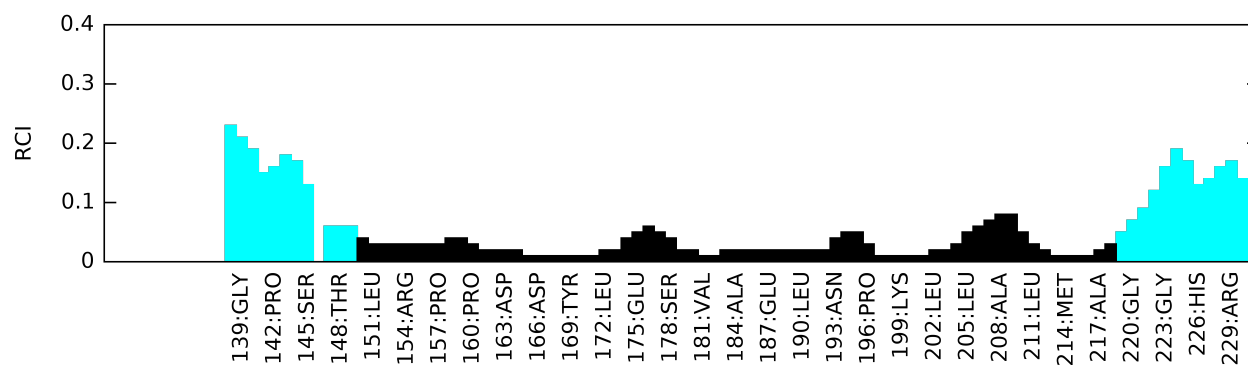
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

Mol	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	167	ARG	NE	110.38	92.63 – 76.73	16.2
1	A	155	GLN	HB2	0.13	3.30 – 0.80	-7.7
1	A	182	LYS	HD2	0.28	2.76 – 0.46	-5.8

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

The images below report *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:



Random coil index (RCI) for chain B:

