



Full wwPDB NMR Structure Validation Report ⓘ

Mar 5, 2026 – 10:00 PM UTC

PDB ID : 2M0V / pdb_00002m0v
BMRB ID : 18826
Title : Complex structure of C-terminal CFTR peptide and extended PDZ2 domain from NHERF1
Authors : Bhattacharya, S.; Ju, J.H.; Cowburn, D.; Bu, Z.
Deposited on : 2012-11-06

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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
wwPDB-RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
wwPDB-ShiftChecker : v1.2
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

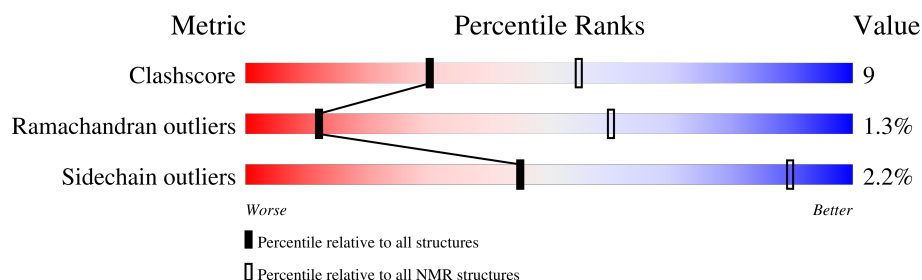
1 Overall quality at a glance

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	229148	14424
Ramachandran outliers	224038	12848
Sidechain outliers	223484	12823

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	128	
2	B	5	

2 Ensemble composition and analysis

This entry contains 20 models. Model 17 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *fewest violations*.

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:171, A:176-A:256, B:2-B:5 (107)	0.79	17

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 2 clusters and 1 single-model cluster was found.

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

3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2059 atoms, of which 1028 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Na(+)/H(+) exchange regulatory cofactor NHE-RF1.

Mol	Chain	Residues	Atoms						Trace
1	A	128	Total	C	H	N	O	S	0
			1970	611	983	180	190	6	

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	143	GLY	-	expression tag	UNP O14745
A	144	ILE	-	expression tag	UNP O14745
A	145	ASP	-	expression tag	UNP O14745
A	146	PRO	-	expression tag	UNP O14745
A	147	PHE	-	expression tag	UNP O14745
A	148	THR	-	expression tag	UNP O14745
A	149	MET	-	expression tag	UNP O14745

- Molecule 2 is a protein called C-terminal CFTR peptide.

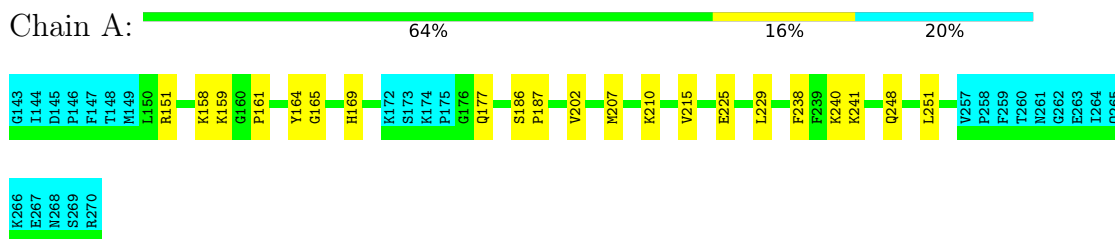
Mol	Chain	Residues	Atoms						Trace
2	B	5	Total	C	H	N	O		0
			89	25	45	9	10		

4 Residue-property plots

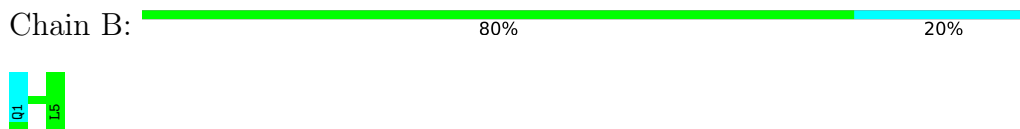
4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA, DNA and oligosaccharide 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: Na(+)/H(+) exchange regulatory cofactor NHE-RF1



- Molecule 2: C-terminal CFTR peptide

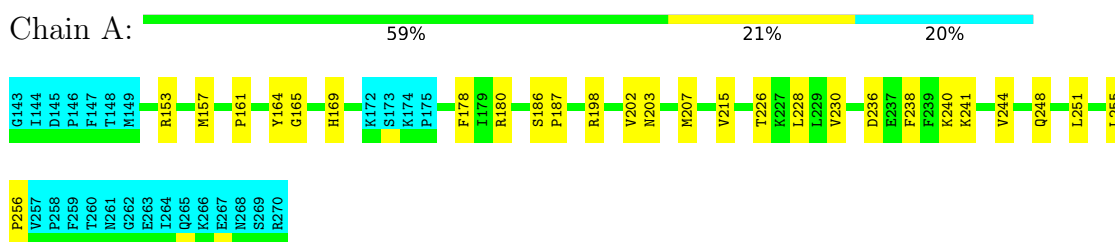


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

- Molecule 1: Na(+)/H(+) exchange regulatory cofactor NHE-RF1



- Molecule 2: C-terminal CFTR peptide

Chain B:  80% 20%



4.2.2 Score per residue for model 2

- Molecule 1: Na(+)/H(+) exchange regulatory cofactor NHE-RF1

Chain A:  61% 20% 20%



- Molecule 2: C-terminal CFTR peptide

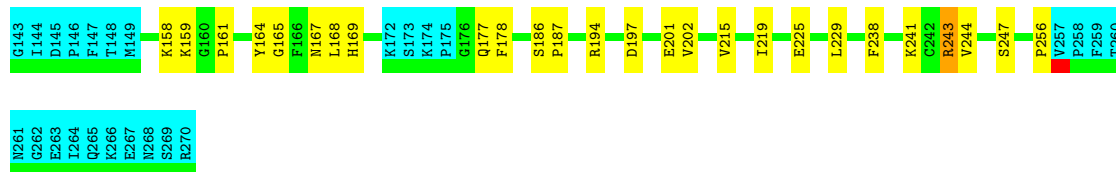
Chain B:  60% 20% 20%



4.2.3 Score per residue for model 3

- Molecule 1: Na(+)/H(+) exchange regulatory cofactor NHE-RF1

Chain A:  60% 20% 20%



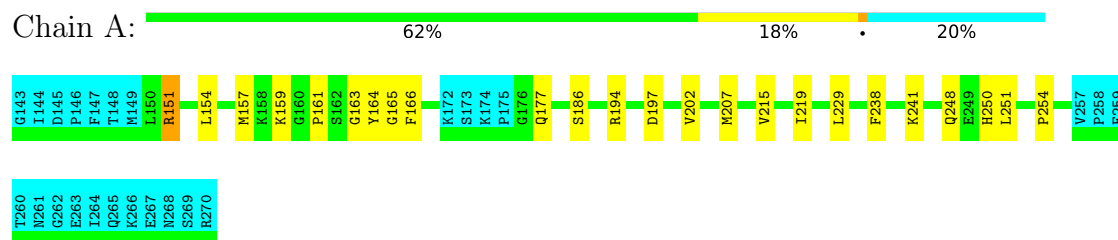
- Molecule 2: C-terminal CFTR peptide

Chain B:  40% 40% 20%



4.2.4 Score per residue for model 4

- Molecule 1: Na(+)/H(+) exchange regulatory cofactor NHE-RF1

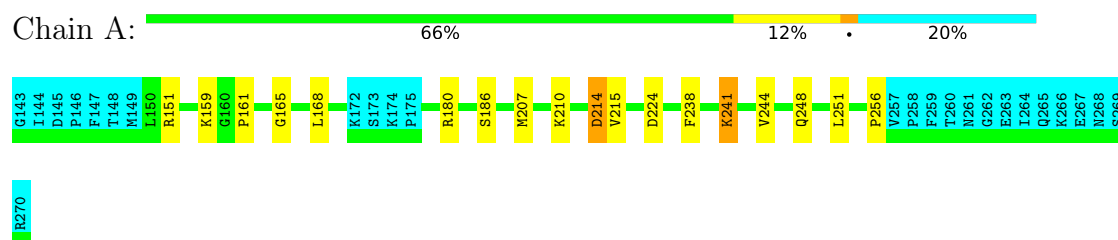


- Molecule 2: C-terminal CFTR peptide



4.2.5 Score per residue for model 5

- Molecule 1: Na(+)/H(+) exchange regulatory cofactor NHE-RF1

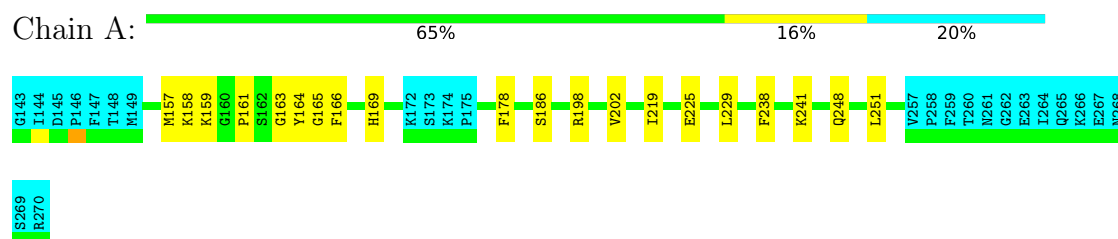


- Molecule 2: C-terminal CFTR peptide



4.2.6 Score per residue for model 6

- Molecule 1: Na(+)/H(+) exchange regulatory cofactor NHE-RF1

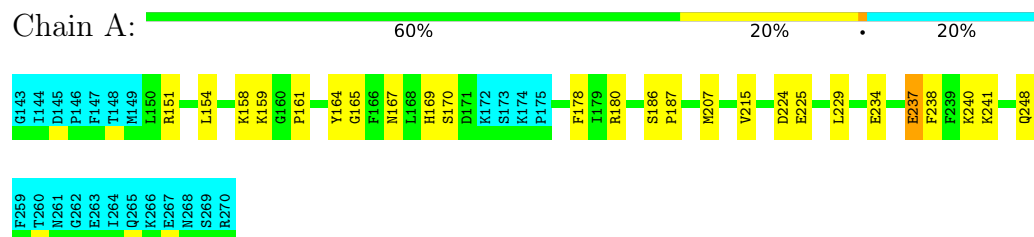


- Molecule 2: C-terminal CFTR peptide



4.2.7 Score per residue for model 7

- Molecule 1: Na(+)/H(+) exchange regulatory cofactor NHE-RF1

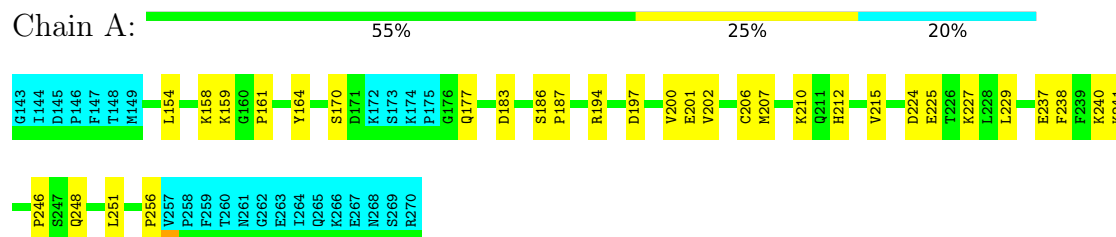


- Molecule 2: C-terminal CFTR peptide

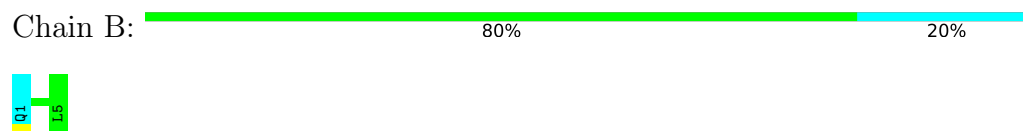


4.2.8 Score per residue for model 8

- Molecule 1: Na(+)/H(+) exchange regulatory cofactor NHE-RF1



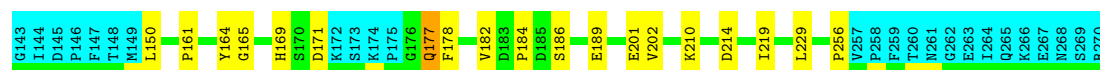
- Molecule 2: C-terminal CFTR peptide



4.2.9 Score per residue for model 9

- Molecule 1: Na(+)/H(+) exchange regulatory cofactor NHE-RF1

Chain A: 



- Molecule 2: C-terminal CFTR peptide

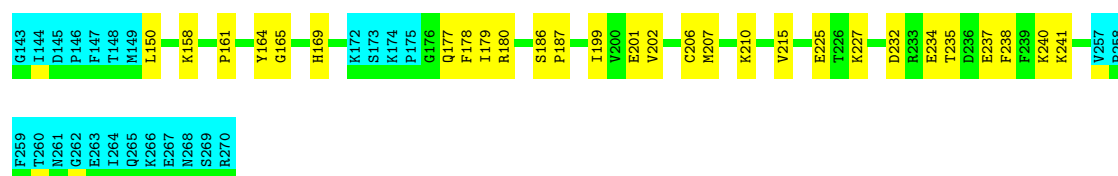
Chain B: 



4.2.10 Score per residue for model 10

- Molecule 1: Na(+)/H(+) exchange regulatory cofactor NHE-RF1

Chain A: 



- Molecule 2: C-terminal CFTR peptide

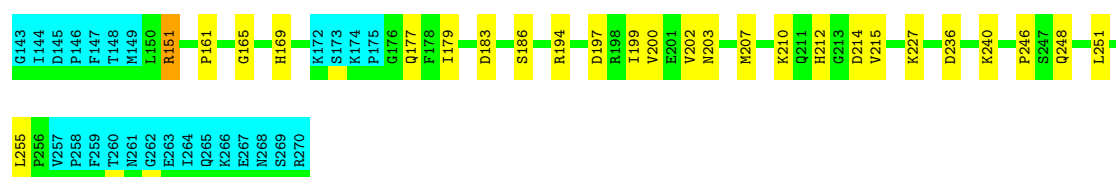
Chain B: 



4.2.11 Score per residue for model 11

- Molecule 1: Na(+)/H(+) exchange regulatory cofactor NHE-RF1

Chain A: 



- Molecule 2: C-terminal CFTR peptide

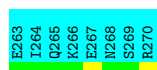
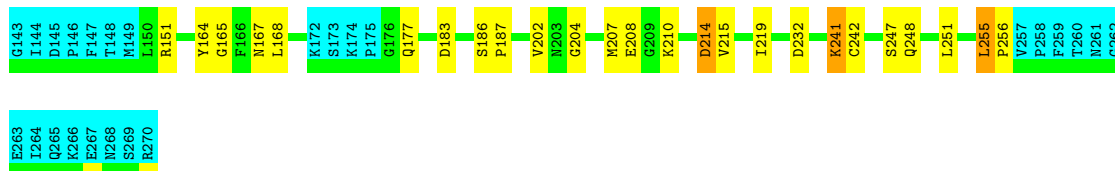
Chain B: 



4.2.12 Score per residue for model 12

- Molecule 1: Na(+)/H(+) exchange regulatory cofactor NHE-RF1

Chain A: 61% 17% 20%



- Molecule 2: C-terminal CFTR peptide

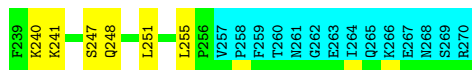
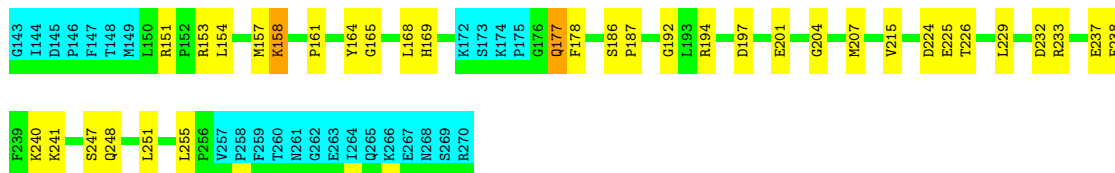
Chain B: 60% 20% 20%



4.2.13 Score per residue for model 13

- Molecule 1: Na(+)/H(+) exchange regulatory cofactor NHE-RF1

Chain A: 53% 26% 20%



- Molecule 2: C-terminal CFTR peptide

Chain B: 60% 20% 20%



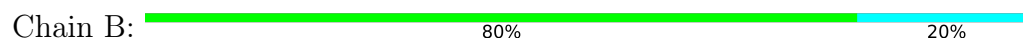
4.2.14 Score per residue for model 14

- Molecule 1: Na(+)/H(+) exchange regulatory cofactor NHE-RF1

Chain A: 59% 21% 20%

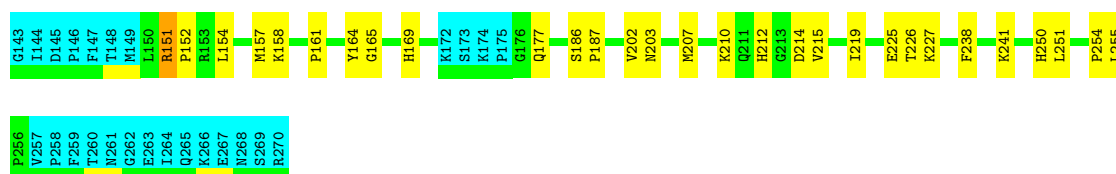


- Molecule 2: C-terminal CFTR peptide



4.2.15 Score per residue for model 15

- Molecule 1: Na(+)/H(+) exchange regulatory cofactor NHE-RF1

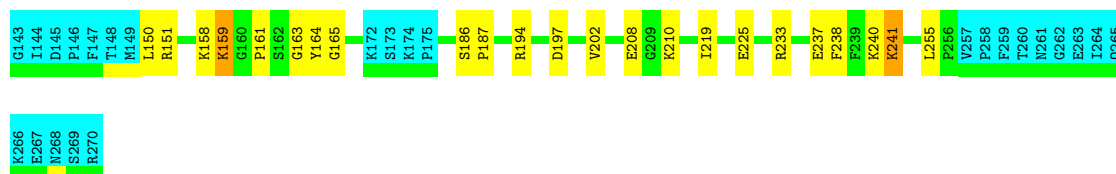


- Molecule 2: C-terminal CFTR peptide

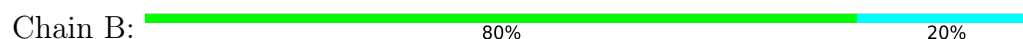


4.2.16 Score per residue for model 16

- Molecule 1: Na(+)/H(+) exchange regulatory cofactor NHE-RF1



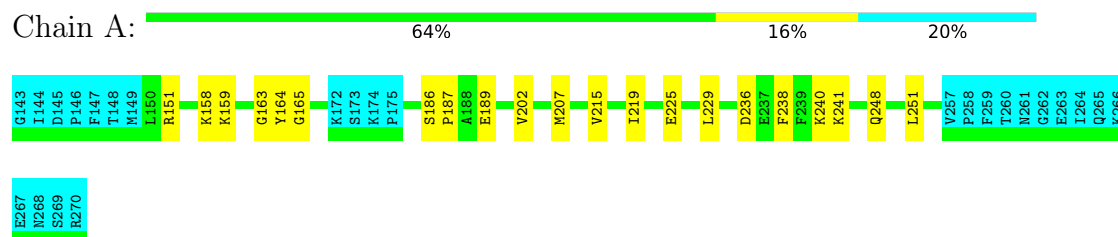
- Molecule 2: C-terminal CFTR peptide





4.2.17 Score per residue for model 17 (medoid)

- Molecule 1: Na(+)/H(+) exchange regulatory cofactor NHE-RF1

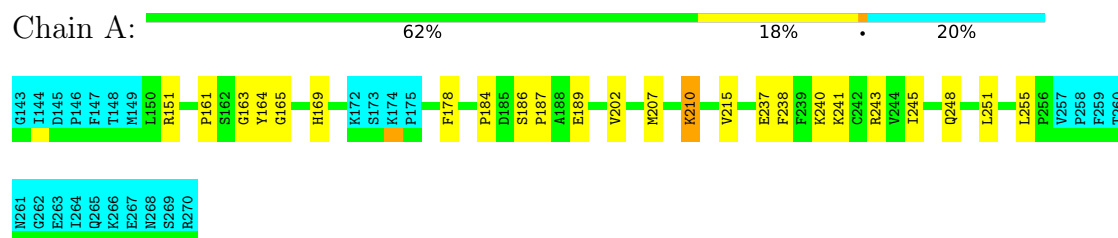


- Molecule 2: C-terminal CFTR peptide

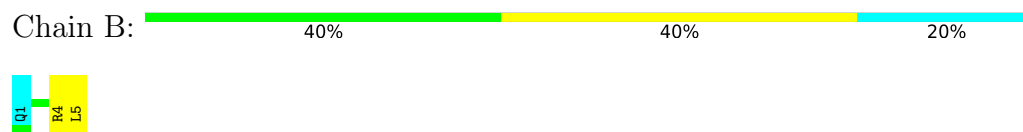


4.2.18 Score per residue for model 18

- Molecule 1: Na(+)/H(+) exchange regulatory cofactor NHE-RF1



- Molecule 2: C-terminal CFTR peptide



4.2.19 Score per residue for model 19

- Molecule 1: Na(+)/H(+) exchange regulatory cofactor NHE-RF1



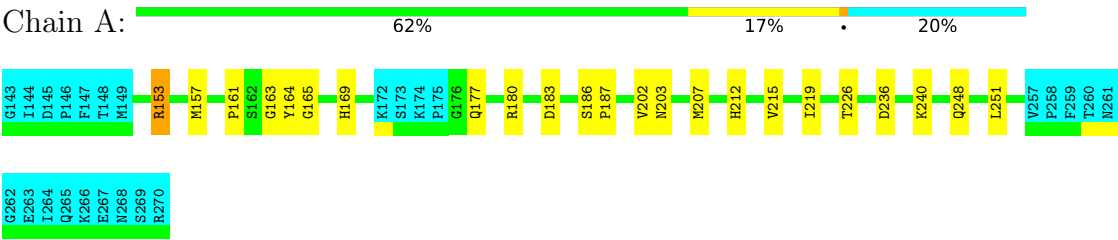


- Molecule 2: C-terminal CFTR peptide



4.2.20 Score per residue for model 20

- Molecule 1: Na(+)/H(+) exchange regulatory cofactor NHE-RF1



- Molecule 2: C-terminal CFTR peptide



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)	working_cs.cif
Number of chemical shift lists	1
Total number of shifts	1534
Number of shifts mapped to atoms	1534
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	87%

6 Model quality [i](#)

6.1 Standard geometry [i](#)

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 [i](#)

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	789	784	781	15±3
2	B	35	35	35	1±1
All	All	16480	16380	16320	296

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:165:GLY:HA3	1:A:186:SER:HB2	0.78	1.56	17	18
1:A:183:ASP:HB3	1:A:186:SER:HB3	0.77	1.56	8	3
1:A:177:GLN:HG3	1:A:215:VAL:HG11	0.74	1.56	11	5
1:A:165:GLY:HA3	1:A:186:SER:HB3	0.73	1.59	14	1
1:A:158:LYS:HB3	1:A:225:GLU:HG2	0.70	1.64	16	9
1:A:210:LYS:HE3	1:A:214:ASP:HB3	0.68	1.64	9	2
1:A:204:GLY:HA2	1:A:248:GLN:HE22	0.67	1.49	12	1
1:A:177:GLN:HG3	1:A:215:VAL:HG21	0.66	1.65	15	3
1:A:202:VAL:HG12	1:A:207:MET:HE3	0.66	1.68	19	4
1:A:207:MET:SD	1:A:215:VAL:HG12	0.64	2.32	15	13
1:A:200:VAL:HB	1:A:229:LEU:HD12	0.64	1.67	19	1
1:A:238:PHE:HA	1:A:241:LYS:HE2	0.63	1.69	5	2
1:A:210:LYS:HD2	1:A:214:ASP:HB3	0.61	1.70	12	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:177:GLN:HA	1:A:177:GLN:HE21	0.61	1.53	13	1
1:A:210:LYS:HE2	1:A:210:LYS:HA	0.61	1.71	18	1
1:A:151:ARG:HG3	1:A:255:LEU:HD21	0.61	1.72	13	1
1:A:238:PHE:O	1:A:241:LYS:HG2	0.59	1.97	18	12
1:A:151:ARG:HG2	1:A:255:LEU:HD21	0.59	1.74	14	5
1:A:233:ARG:HD2	1:A:234:GLU:N	0.59	2.13	19	2
1:A:243:ARG:HA	1:A:243:ARG:HE	0.59	1.57	18	2
1:A:201:GLU:HG2	1:A:229:LEU:HD12	0.59	1.73	13	2
1:A:202:VAL:HB	1:A:207:MET:HE3	0.58	1.75	8	3
1:A:184:PRO:HA	1:A:189:GLU:HG2	0.57	1.74	14	2
1:A:237:GLU:HA	1:A:240:LYS:CD	0.57	2.30	2	2
1:A:202:VAL:HA	1:A:227:LYS:O	0.57	1.99	10	3
1:A:169:HIS:HB3	1:A:178:PHE:CE2	0.57	2.34	1	7
1:A:248:GLN:O	1:A:251:LEU:HG	0.57	2.00	17	15
1:A:158:LYS:HG2	1:A:225:GLU:HG2	0.55	1.79	19	2
1:A:163:GLY:HA3	2:B:5:LEU:O	0.55	2.01	20	1
1:A:167:ASN:HB2	2:B:4:ARG:HG3	0.55	1.77	7	1
1:A:201:GLU:HB2	1:A:229:LEU:HD12	0.55	1.79	2	2
2:B:4:ARG:HD2	2:B:4:ARG:H	0.55	1.61	15	2
1:A:201:GLU:OE2	1:A:206:CYS:HA	0.54	2.03	8	1
1:A:207:MET:HA	1:A:210:LYS:HG3	0.54	1.78	10	1
1:A:168:LEU:O	2:B:2:ASP:HB2	0.53	2.03	5	1
1:A:177:GLN:N	1:A:177:GLN:HE21	0.53	2.01	9	1
1:A:236:ASP:O	1:A:240:LYS:HG3	0.53	2.04	17	3
1:A:207:MET:HA	1:A:210:LYS:CG	0.53	2.33	10	1
1:A:200:VAL:HG21	1:A:246:PRO:HG2	0.53	1.80	8	2
1:A:151:ARG:HG3	1:A:251:LEU:HA	0.52	1.81	7	1
1:A:183:ASP:HB2	1:A:186:SER:HB3	0.52	1.80	11	1
1:A:201:GLU:HG2	1:A:206:CYS:HA	0.52	1.81	10	2
1:A:157:MET:HG3	1:A:164:TYR:HB3	0.52	1.80	6	2
1:A:203:ASN:ND2	1:A:226:THR:HA	0.52	2.20	1	1
1:A:237:GLU:O	1:A:241:LYS:HG3	0.51	2.05	7	2
1:A:200:VAL:O	1:A:207:MET:HB2	0.51	2.06	8	2
1:A:179:ILE:HD11	1:A:199:ILE:HD11	0.51	1.83	11	3
1:A:236:ASP:O	1:A:240:LYS:HG2	0.51	2.06	11	1
1:A:244:VAL:HG11	1:A:256:PRO:HG3	0.51	1.82	3	1
1:A:201:GLU:HA	1:A:207:MET:HB2	0.51	1.83	13	1
1:A:237:GLU:O	1:A:240:LYS:HG2	0.51	2.06	7	3
1:A:169:HIS:HA	2:B:2:ASP:OD1	0.51	2.06	15	2
1:A:151:ARG:HD2	1:A:255:LEU:HD21	0.51	1.82	12	1
1:A:244:VAL:HG21	1:A:256:PRO:HG3	0.50	1.82	1	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:194:ARG:HB3	1:A:197:ASP:OD1	0.50	2.06	4	2
1:A:153:ARG:NE	1:A:153:ARG:HA	0.50	2.22	20	1
1:A:194:ARG:HB3	1:A:197:ASP:OD2	0.50	2.07	3	2
1:A:159:LYS:HA	1:A:163:GLY:O	0.49	2.06	4	5
1:A:159:LYS:HD2	1:A:224:ASP:HA	0.49	1.83	5	1
1:A:194:ARG:HB2	1:A:197:ASP:OD2	0.49	2.08	16	3
1:A:255:LEU:HB2	1:A:256:PRO:HD3	0.48	1.84	12	1
1:A:183:ASP:HB2	1:A:186:SER:OG	0.48	2.08	14	1
1:A:202:VAL:HG11	1:A:219:ILE:CG1	0.48	2.38	9	8
1:A:232:ASP:OD1	1:A:233:ARG:HD3	0.48	2.07	13	1
1:A:163:GLY:HA3	2:B:5:LEU:OXT	0.48	2.09	6	3
1:A:212:HIS:O	1:A:215:VAL:HG22	0.48	2.08	8	4
1:A:157:MET:CG	1:A:164:TYR:HB3	0.47	2.39	4	3
1:A:165:GLY:HA3	1:A:186:SER:CB	0.47	2.38	14	2
1:A:152:PRO:HD2	1:A:251:LEU:HB3	0.47	1.86	15	1
1:A:200:VAL:HG21	1:A:246:PRO:HD2	0.47	1.85	11	1
1:A:202:VAL:HG12	1:A:203:ASN:ND2	0.47	2.25	11	1
1:A:151:ARG:HG2	1:A:255:LEU:HD11	0.47	1.85	18	1
1:A:168:LEU:O	2:B:2:ASP:HB3	0.46	2.10	13	1
1:A:164:TYR:O	1:A:187:PRO:HG2	0.46	2.10	8	14
1:A:204:GLY:HA2	1:A:248:GLN:NE2	0.46	2.22	12	1
1:A:177:GLN:HE21	1:A:177:GLN:CA	0.46	2.23	13	1
1:A:210:LYS:HD2	1:A:214:ASP:CB	0.46	2.40	12	1
1:A:169:HIS:HB2	1:A:180:ARG:HB2	0.46	1.88	20	3
1:A:159:LYS:HD3	1:A:224:ASP:HA	0.46	1.86	8	1
1:A:236:ASP:OD1	1:A:240:LYS:HD2	0.45	2.12	1	1
1:A:151:ARG:HG2	1:A:251:LEU:HA	0.45	1.86	5	1
1:A:201:GLU:HB3	1:A:229:LEU:HD12	0.45	1.88	9	1
1:A:237:GLU:HA	1:A:240:LYS:HG2	0.45	1.89	10	3
1:A:234:GLU:O	1:A:237:GLU:HG3	0.45	2.11	14	1
1:A:203:ASN:ND2	1:A:219:ILE:HA	0.45	2.26	19	2
1:A:157:MET:SD	1:A:226:THR:HG23	0.45	2.51	13	2
1:A:167:ASN:HD22	1:A:168:LEU:N	0.45	2.10	12	2
1:A:157:MET:HB2	1:A:187:PRO:HB2	0.44	1.88	1	1
1:A:169:HIS:HB3	1:A:178:PHE:CZ	0.44	2.47	1	1
1:A:201:GLU:HG3	1:A:247:SER:HA	0.44	1.89	2	1
1:A:164:TYR:H	2:B:5:LEU:C	0.44	2.20	3	5
1:A:150:LEU:HG	1:A:235:THR:HG23	0.44	1.89	10	1
1:A:242:CYS:SG	1:A:256:PRO:HB3	0.44	2.53	12	1
1:A:158:LYS:CB	1:A:225:GLU:HG2	0.44	2.37	6	1
1:A:177:GLN:CG	1:A:215:VAL:HG11	0.44	2.42	15	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:238:PHE:HA	1:A:241:LYS:HE3	0.44	1.88	15	1
1:A:164:TYR:HB2	1:A:166:PHE:CE1	0.43	2.48	6	2
1:A:151:ARG:CD	1:A:255:LEU:HD21	0.43	2.44	12	1
1:A:232:ASP:OD2	1:A:234:GLU:HG2	0.43	2.13	10	1
1:A:203:ASN:OD1	1:A:226:THR:HA	0.43	2.13	15	2
1:A:154:LEU:HD23	1:A:229:LEU:HD13	0.43	1.90	4	1
1:A:159:LYS:HE3	1:A:224:ASP:HA	0.43	1.90	14	1
1:A:169:HIS:HD2	1:A:178:PHE:CZ	0.43	2.31	2	1
1:A:198:ARG:O	1:A:230:VAL:HA	0.43	2.14	1	1
1:A:250:HIS:HA	1:A:254:PRO:O	0.42	2.14	15	2
1:A:154:LEU:HD21	1:A:227:LYS:HE3	0.42	1.90	8	1
1:A:177:GLN:HG2	1:A:215:VAL:HG21	0.42	1.90	10	1
1:A:153:ARG:NH2	1:A:192:GLY:HA3	0.42	2.29	13	1
1:A:177:GLN:HG3	1:A:215:VAL:CG2	0.42	2.44	14	1
1:A:157:MET:SD	1:A:228:LEU:HD23	0.42	2.54	1	1
1:A:244:VAL:HG11	1:A:256:PRO:CG	0.42	2.44	5	1
1:A:154:LEU:HD13	1:A:229:LEU:HD13	0.42	1.90	7	1
1:A:177:GLN:HG2	1:A:215:VAL:HG11	0.42	1.90	12	1
2:B:4:ARG:HD2	2:B:4:ARG:N	0.42	2.28	17	2
1:A:159:LYS:CD	1:A:224:ASP:HA	0.42	2.44	7	1
1:A:202:VAL:CG1	1:A:207:MET:HE3	0.42	2.43	20	1
1:A:237:GLU:HA	1:A:240:LYS:HD3	0.41	1.91	2	1
1:A:241:LYS:HB2	1:A:241:LYS:NZ	0.41	2.30	12	1
1:A:159:LYS:HB3	1:A:164:TYR:CE2	0.41	2.50	3	1
1:A:184:PRO:HA	1:A:189:GLU:OE2	0.41	2.15	18	1
1:A:152:PRO:HB2	1:A:229:LEU:HD21	0.41	1.91	19	1
1:A:195:ALA:O	1:A:196:GLN:HB2	0.41	2.16	14	1
1:A:210:LYS:H	1:A:210:LYS:CD	0.41	2.28	19	1
1:A:237:GLU:HA	1:A:240:LYS:HE2	0.41	1.93	14	2
1:A:210:LYS:HG3	1:A:214:ASP:HB3	0.41	1.93	15	1
1:A:169:HIS:HB3	1:A:178:PHE:CE1	0.41	2.51	10	1
1:A:207:MET:HE2	1:A:207:MET:HB3	0.41	1.79	10	1
1:A:167:ASN:HA	2:B:4:ARG:HA	0.41	1.92	19	1
1:A:202:VAL:HG12	1:A:207:MET:CE	0.40	2.44	18	1
1:A:159:LYS:HG2	1:A:224:ASP:HA	0.40	1.94	14	1
1:A:151:ARG:HD2	1:A:251:LEU:HA	0.40	1.93	4	1
1:A:229:LEU:HD21	1:A:251:LEU:CD2	0.40	2.46	6	1
1:A:234:GLU:HA	1:A:237:GLU:HG2	0.40	1.91	7	1
1:A:229:LEU:HD11	1:A:248:GLN:HG3	0.40	1.93	14	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	103/128 (80%)	96±2 (93±2%)	6±2 (6±2%)	1±1 (1±1%)	12	60
2	B	3/5 (60%)	2±0 (83±17%)	0±0 (15±17%)	0±0 (2±7%)	9	53
All	All	2120/2660 (80%)	1964 (93%)	128 (6%)	28 (1%)	12	60

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	161	PRO	17
1	A	151	ARG	4
1	A	150	LEU	2
2	B	2	ASP	1
1	A	256	PRO	1
1	A	255	LEU	1
1	A	204	GLY	1
1	A	245	ILE	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	87/110 (79%)	85±2 (98±2%)	2±2 (2±2%)	46	90
2	B	4/5 (80%)	4±0 (95±10%)	0±0 (5±10%)	23	74
All	All	1820/2300 (79%)	1780 (98%)	40 (2%)	45	90

All 23 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	210	LYS	4
2	B	4	ARG	4
1	A	247	SER	3
1	A	241	LYS	3
1	A	154	LEU	3
1	A	153	ARG	2
1	A	180	ARG	2
1	A	214	ASP	2
1	A	177	GLN	2
1	A	208	GLU	2
1	A	255	LEU	1
1	A	243	ARG	1
1	A	198	ARG	1
1	A	237	GLU	1
1	A	182	VAL	1
1	A	232	ASP	1
1	A	158	LYS	1
1	A	224	ASP	1
1	A	194	ARG	1
1	A	159	LYS	1
1	A	233	ARG	1
1	A	189	GLU	1
1	A	229	LEU	1

6.3.3 RNA [i](#)

There are no RNA molecules in this entry.

6.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.6 Ligand geometry [i](#)

There are no ligands in this entry.

6.7 Other polymers [i](#)

There are no such molecules in this entry.

6.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

7 Chemical shift validation [i](#)

The completeness of assignment taking into account all chemical shift lists is 87% for the well-defined parts and 86% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *assigned_chem_shift_list_1*

7.1.1 Bookkeeping [i](#)

The following table shows the results of parsing the chemical shift list and reports the number of nuclei with statistically unusual chemical shifts.

Total number of shifts	1534
Number of shifts mapped to atoms	1534
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	3

7.1.2 Chemical shift referencing [i](#)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	127	0.21 ± 0.19	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	114	0.18 ± 0.17	None needed (< 0.5 ppm)
$^{13}\text{C}'$	114	0.11 ± 0.17	None needed (< 0.5 ppm)
^{15}N	117	-0.14 ± 0.33	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. 1243 atoms were assigned a chemical shift out of a possible 1431. 0 out of 18 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	506/532 (95%)	216/218 (99%)	195/214 (91%)	95/100 (95%)
Sidechain	693/826 (84%)	482/532 (91%)	199/254 (78%)	12/40 (30%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	44/73 (60%)	27/36 (75%)	17/31 (55%)	0/6 (0%)
Overall	1243/1431 (87%)	725/786 (92%)	411/499 (82%)	107/146 (73%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 86%, i.e. 1529 atoms were assigned a chemical shift out of a possible 1783. 0 out of 19 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	621/658 (94%)	263/269 (98%)	241/266 (91%)	117/123 (95%)
Sidechain	856/1032 (83%)	593/663 (89%)	248/319 (78%)	15/50 (30%)
Aromatic	52/93 (56%)	33/46 (72%)	19/41 (46%)	0/6 (0%)
Overall	1529/1783 (86%)	889/978 (91%)	508/626 (81%)	132/179 (74%)

7.1.4 Statistically unusual chemical shifts ⓘ

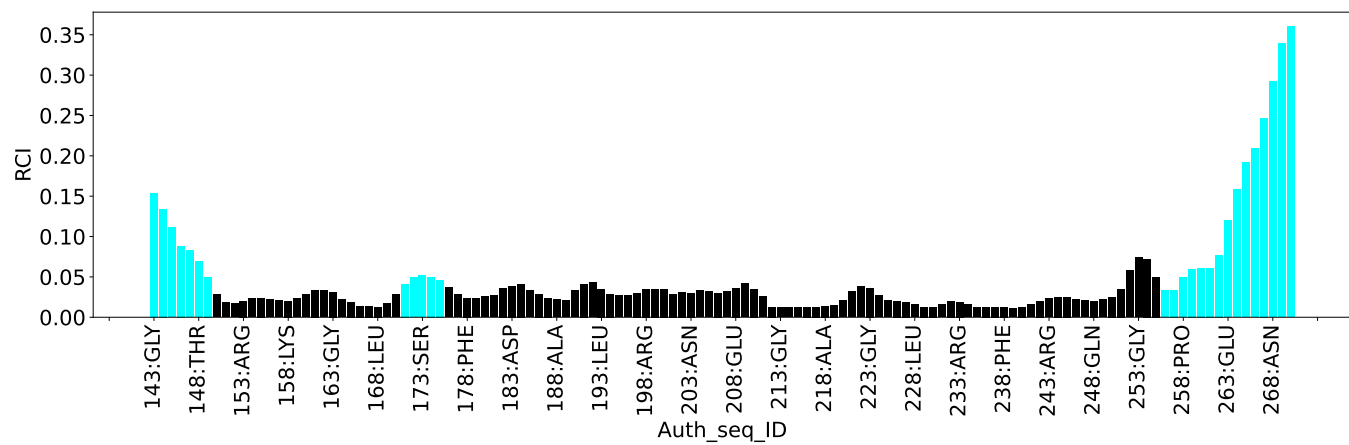
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	235	THR	HG1	6.09	0.08 – 2.19	23.4
1	A	226	THR	HG1	4.09	0.08 – 2.19	14.0
1	A	198	ARG	HG2	0.13	0.26 – 2.87	-5.5

7.1.5 Random Coil Index (RCI) plots ⓘ

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. If well-defined core and ill-defined regions are not identified then it is shown as gray bars.

Random coil index (RCI) for chain A:



Random coil index (RCI) for chain B:

