



Full wwPDB NMR Structure Validation Report ⓘ

Mar 6, 2026 – 01:30 AM UTC

PDB ID : 1QMC / pdb_00001qmc
Title : C-terminal DNA-binding domain of HIV-1 integrase, NMR, 42 structures
Authors : Eijkelenboom, A.P.A.M.; Sprangers, R.; Hard, K.; Puras Lutzke, R.A.; Plas-
terk, R.H.A.; Boelens, R.; Kaptein, R.
Deposited on : 1999-09-27

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

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

A user guide is available at

<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

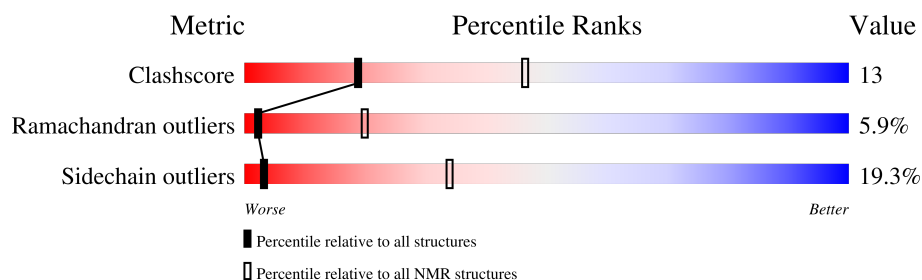
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment was not calculated.

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	52	 58% 37% . .
1	B	52	 62% 35% .

2 Ensemble composition and analysis

This entry contains 42 models. Model 1 is the overall representative, medoid model (most similar to other models).

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

Well-defined (core) protein residues			
Well-defined core	Residue range (total)	Backbone RMSD (Å)	Medoid model
1	A:220-A:270, B:219-B:270 (103)	0.54	1

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

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

The models can be grouped into 4 clusters and 1 single-model cluster was found.

Cluster number	Models
1	1, 3, 4, 5, 6, 7, 8, 9, 11, 12, 21, 24, 28, 34, 38
2	2, 13, 16, 17, 18, 30, 32, 35, 36, 40, 41
3	10, 14, 15, 19, 20, 25, 26, 29, 37
4	22, 23, 27, 33, 39, 42
Single-model clusters	31

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 1778 atoms, of which 910 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called HIV-1 INTEGRASE.

Mol	Chain	Residues	Atoms						Trace
1	A	52	Total	C	H	N	O	S	0
			889	278	455	83	72	1	
1	B	52	Total	C	H	N	O	S	0
			889	278	455	83	72	1	

There are 2 discrepancies between the modelled and reference sequences:

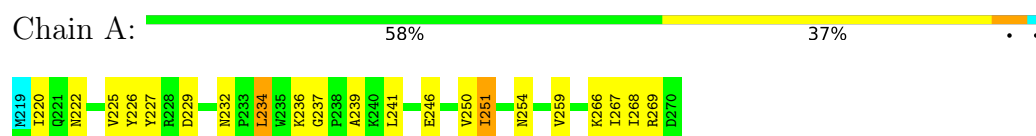
Chain	Residue	Modelled	Actual	Comment	Reference
A	219	MET	-	cloning artifact	UNP P03366
B	219	MET	-	cloning artifact	UNP P03366

4 Residue-property plots [i](#)

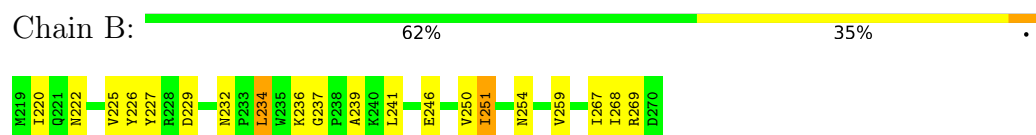
4.1 Average score per residue in the NMR ensemble

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: HIV-1 INTEGRASE



• Molecule 1: HIV-1 INTEGRASE

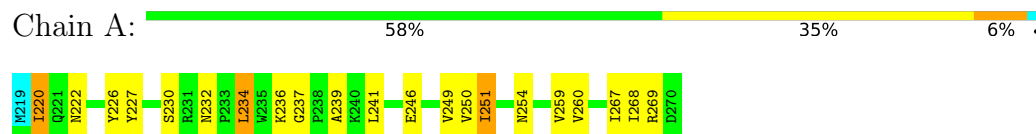


4.2 Scores per residue for each member of the ensemble

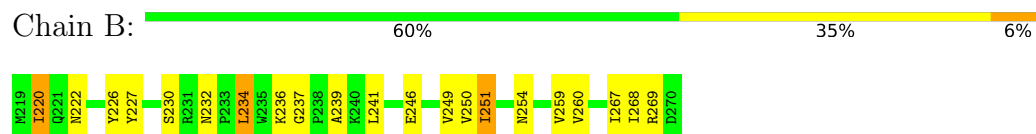
Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1 (medoid)

• Molecule 1: HIV-1 INTEGRASE

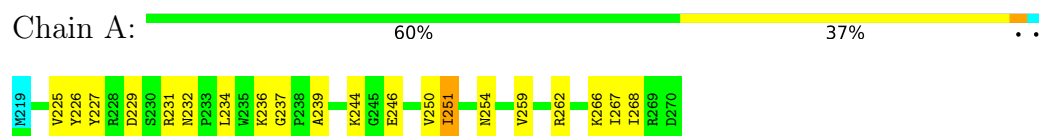


• Molecule 1: HIV-1 INTEGRASE

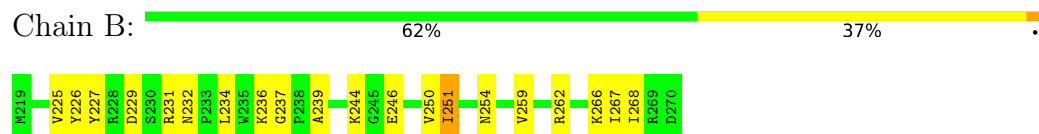


4.2.2 Score per residue for model 2

- Molecule 1: HIV-1 INTEGRASE

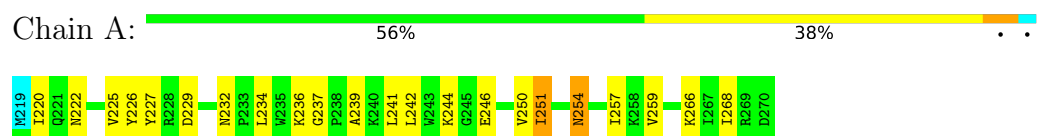


- Molecule 1: HIV-1 INTEGRASE

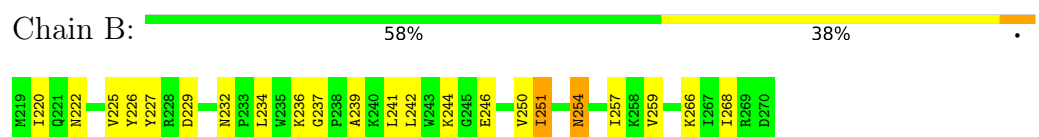


4.2.3 Score per residue for model 3

- Molecule 1: HIV-1 INTEGRASE

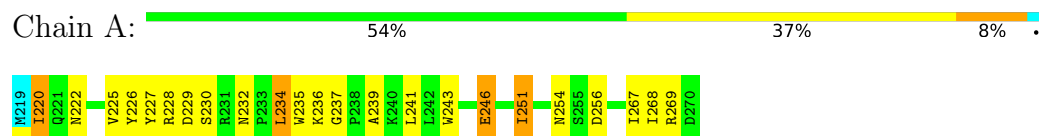


- Molecule 1: HIV-1 INTEGRASE

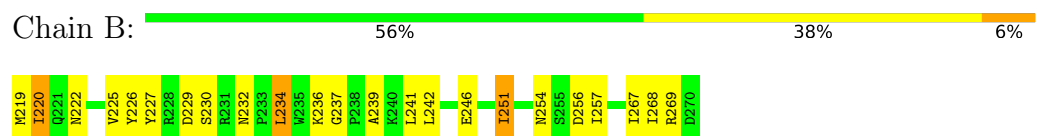


4.2.4 Score per residue for model 4

- Molecule 1: HIV-1 INTEGRASE

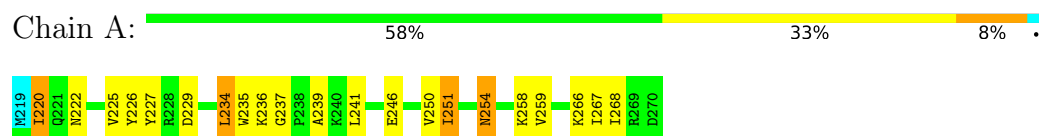


- Molecule 1: HIV-1 INTEGRASE

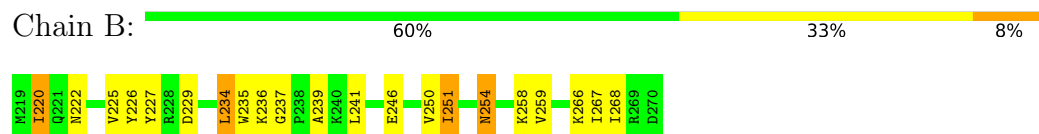


4.2.5 Score per residue for model 5

- Molecule 1: HIV-1 INTEGRASE

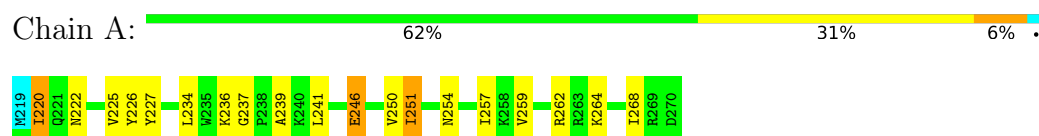


- Molecule 1: HIV-1 INTEGRASE

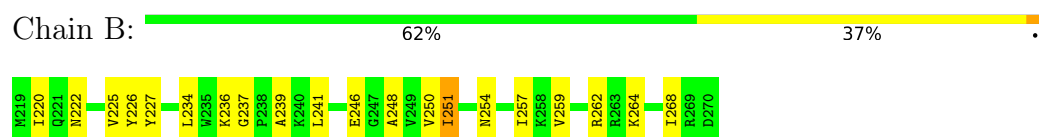


4.2.6 Score per residue for model 6

- Molecule 1: HIV-1 INTEGRASE

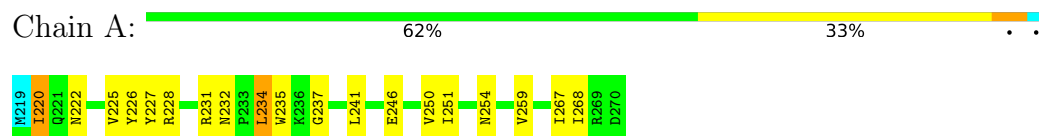


- Molecule 1: HIV-1 INTEGRASE

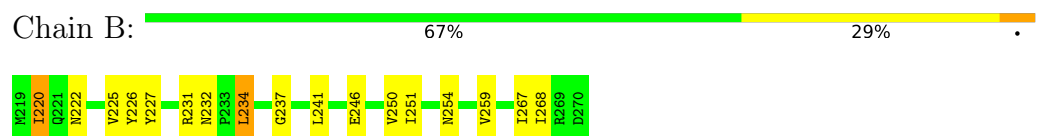


4.2.7 Score per residue for model 7

- Molecule 1: HIV-1 INTEGRASE

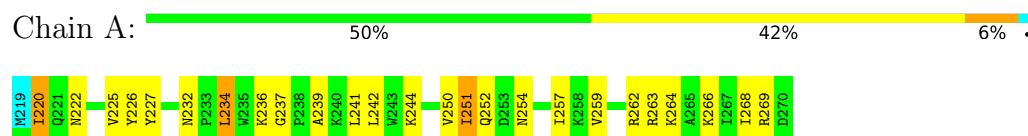


- Molecule 1: HIV-1 INTEGRASE

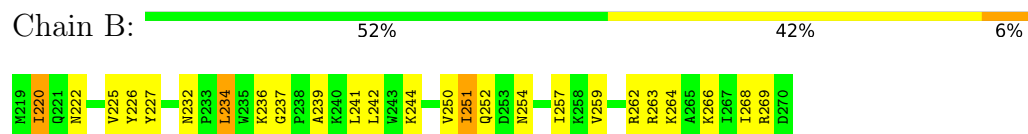


4.2.8 Score per residue for model 8

- Molecule 1: HIV-1 INTEGRASE

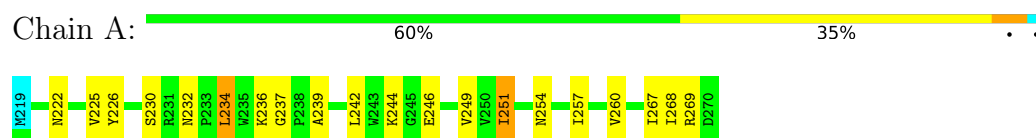


- Molecule 1: HIV-1 INTEGRASE

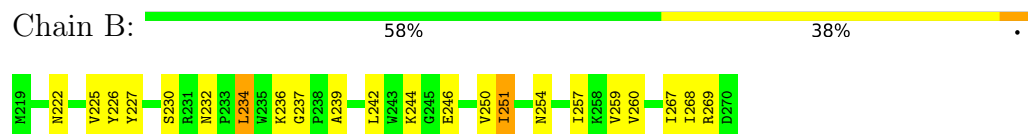


4.2.9 Score per residue for model 9

- Molecule 1: HIV-1 INTEGRASE

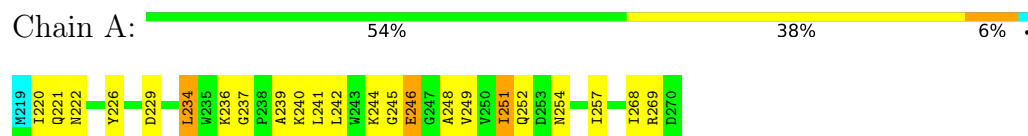


- Molecule 1: HIV-1 INTEGRASE

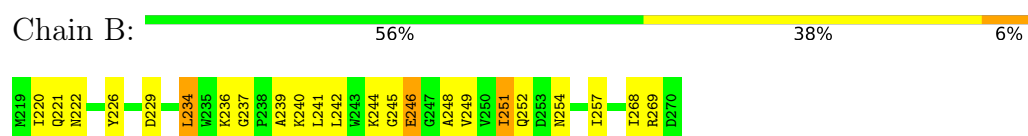


4.2.10 Score per residue for model 10

- Molecule 1: HIV-1 INTEGRASE

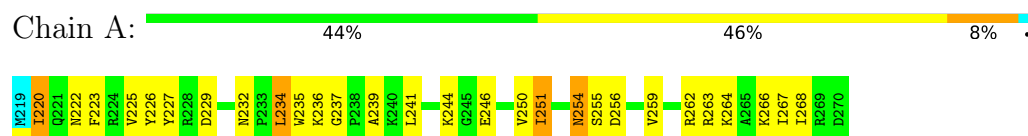


- Molecule 1: HIV-1 INTEGRASE

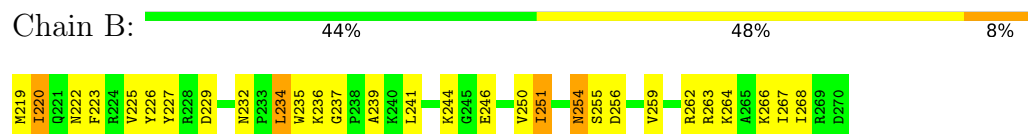


4.2.11 Score per residue for model 11

- Molecule 1: HIV-1 INTEGRASE

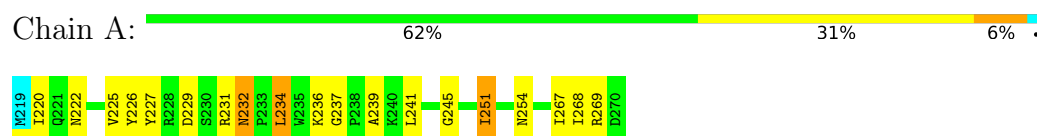


- Molecule 1: HIV-1 INTEGRASE

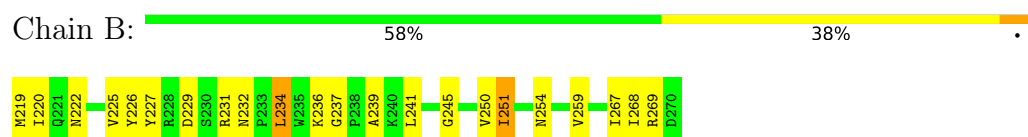


4.2.12 Score per residue for model 12

- Molecule 1: HIV-1 INTEGRASE

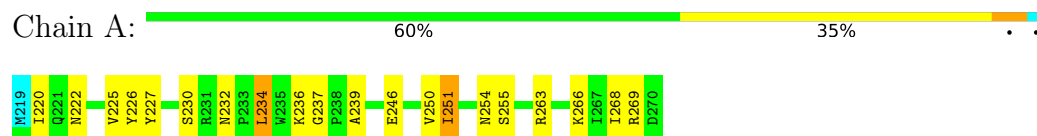


- Molecule 1: HIV-1 INTEGRASE

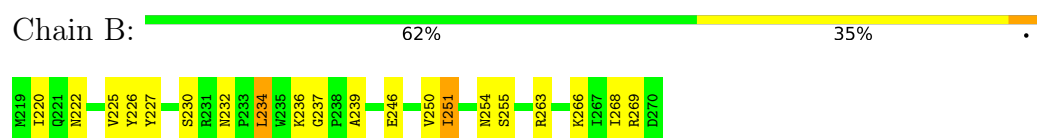


4.2.13 Score per residue for model 13

- Molecule 1: HIV-1 INTEGRASE

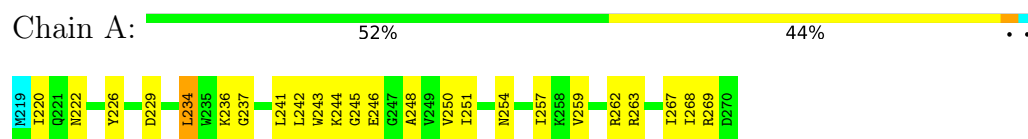


- Molecule 1: HIV-1 INTEGRASE

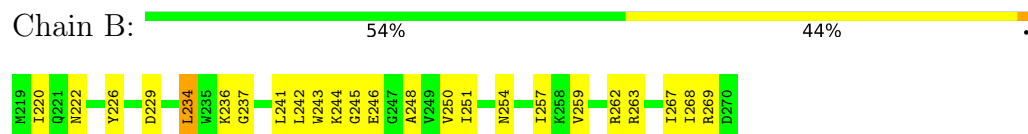


4.2.14 Score per residue for model 14

- Molecule 1: HIV-1 INTEGRASE

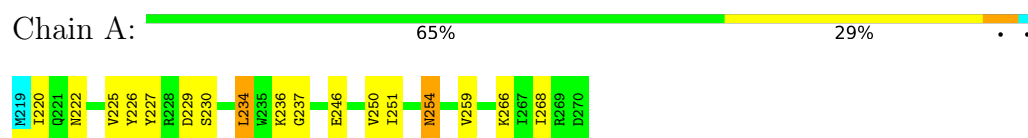


- Molecule 1: HIV-1 INTEGRASE

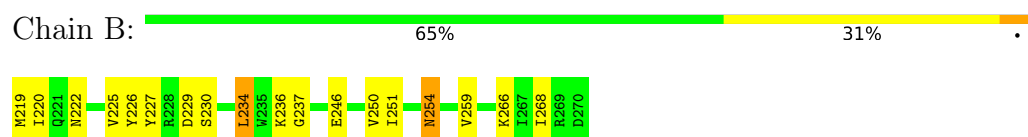


4.2.15 Score per residue for model 15

- Molecule 1: HIV-1 INTEGRASE

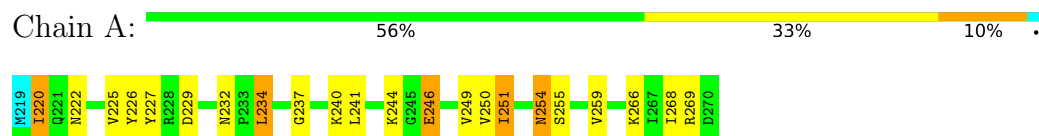


- Molecule 1: HIV-1 INTEGRASE

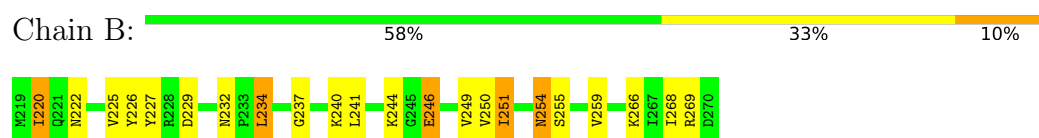


4.2.16 Score per residue for model 16

- Molecule 1: HIV-1 INTEGRASE

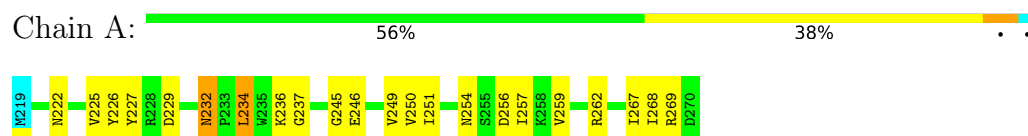


- Molecule 1: HIV-1 INTEGRASE

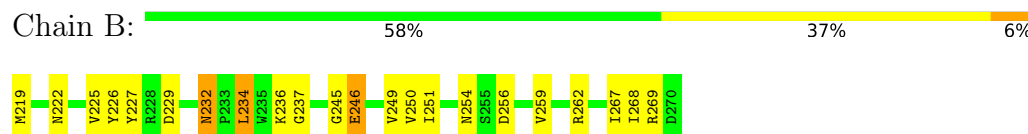


4.2.17 Score per residue for model 17

- Molecule 1: HIV-1 INTEGRASE

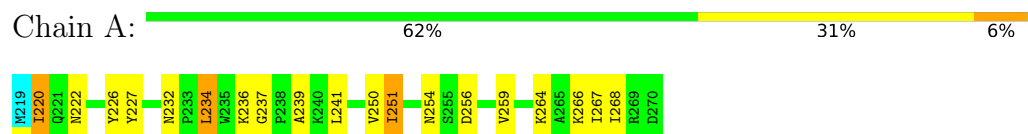


- Molecule 1: HIV-1 INTEGRASE

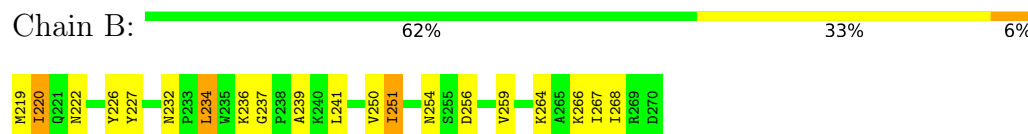


4.2.18 Score per residue for model 18

- Molecule 1: HIV-1 INTEGRASE

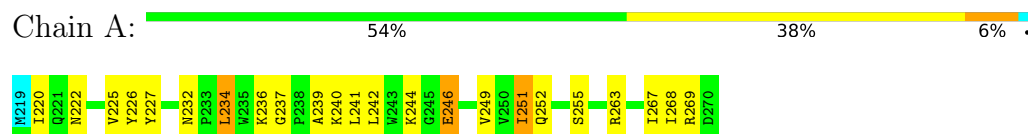


- Molecule 1: HIV-1 INTEGRASE

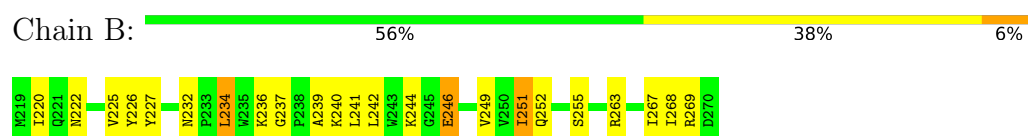


4.2.19 Score per residue for model 19

- Molecule 1: HIV-1 INTEGRASE

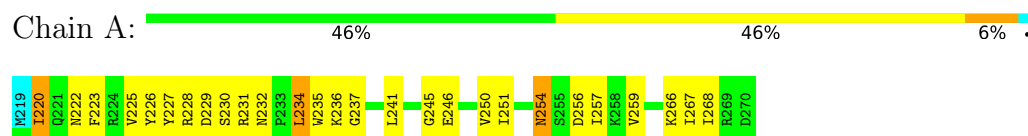


- Molecule 1: HIV-1 INTEGRASE

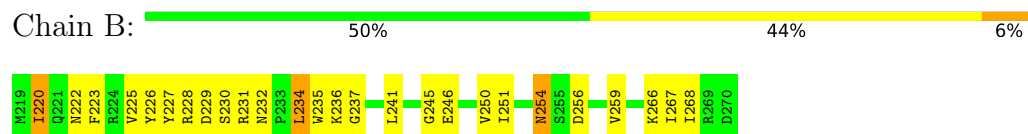


4.2.20 Score per residue for model 20

- Molecule 1: HIV-1 INTEGRASE

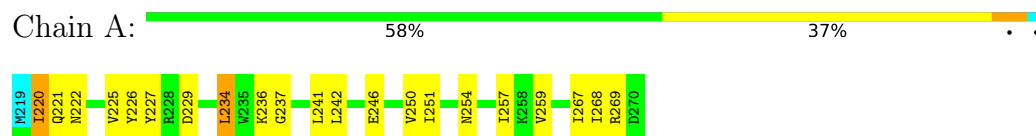


- Molecule 1: HIV-1 INTEGRASE

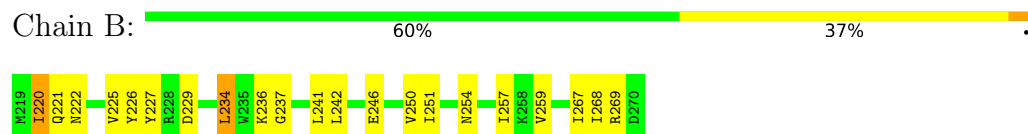


4.2.21 Score per residue for model 21

- Molecule 1: HIV-1 INTEGRASE

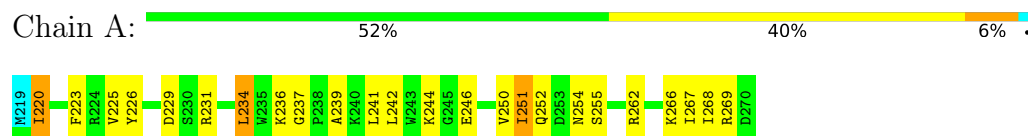


- Molecule 1: HIV-1 INTEGRASE

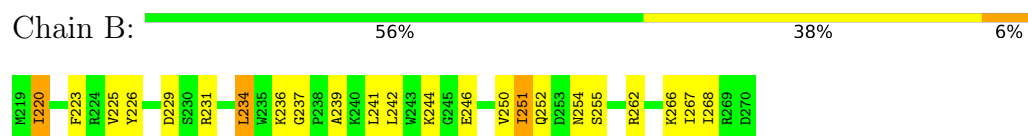


4.2.22 Score per residue for model 22

- Molecule 1: HIV-1 INTEGRASE

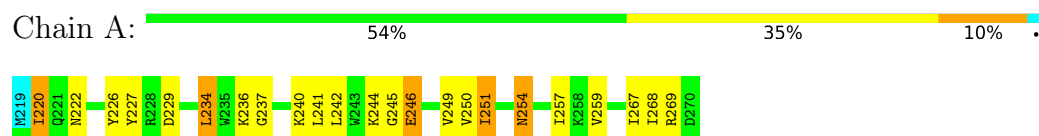


- Molecule 1: HIV-1 INTEGRASE

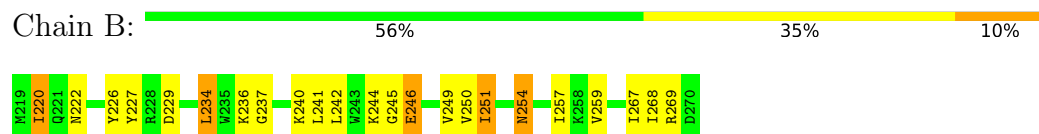


4.2.23 Score per residue for model 23

- Molecule 1: HIV-1 INTEGRASE

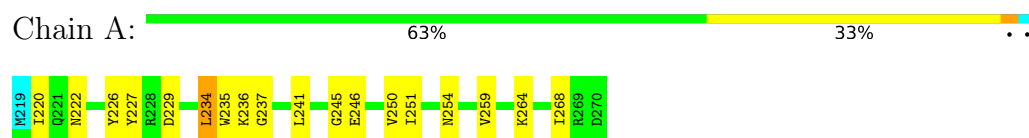


- Molecule 1: HIV-1 INTEGRASE

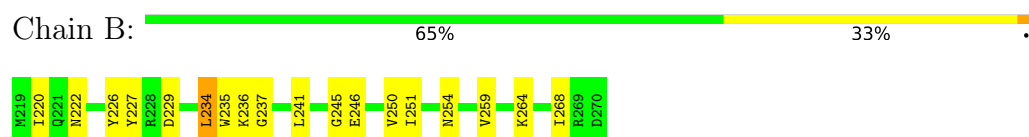


4.2.24 Score per residue for model 24

- Molecule 1: HIV-1 INTEGRASE

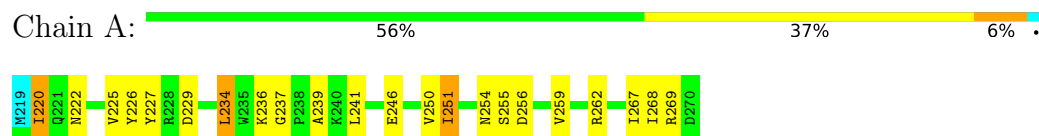


- Molecule 1: HIV-1 INTEGRASE



4.2.25 Score per residue for model 25

- Molecule 1: HIV-1 INTEGRASE

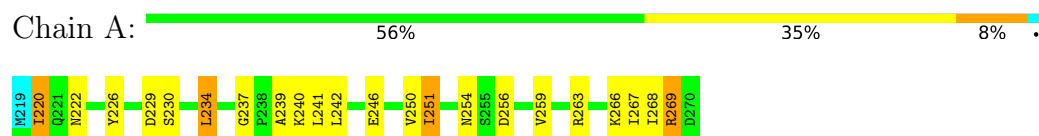


- Molecule 1: HIV-1 INTEGRASE

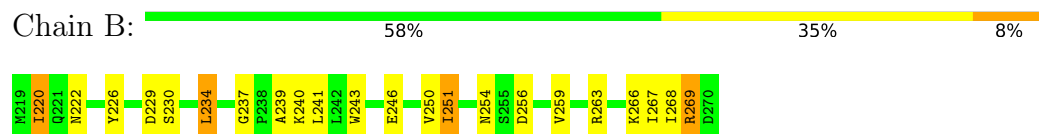


4.2.26 Score per residue for model 26

- Molecule 1: HIV-1 INTEGRASE

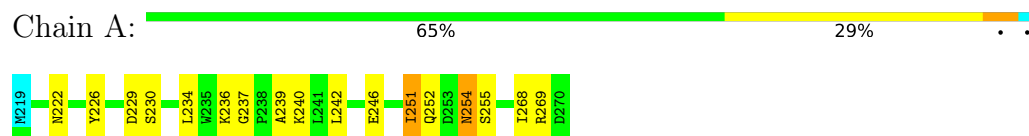


- Molecule 1: HIV-1 INTEGRASE

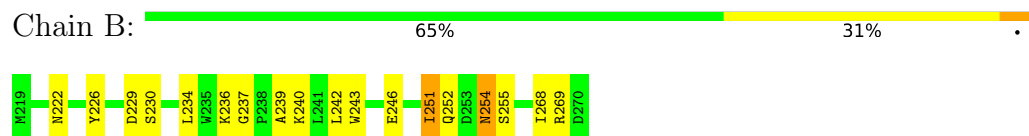


4.2.27 Score per residue for model 27

- Molecule 1: HIV-1 INTEGRASE

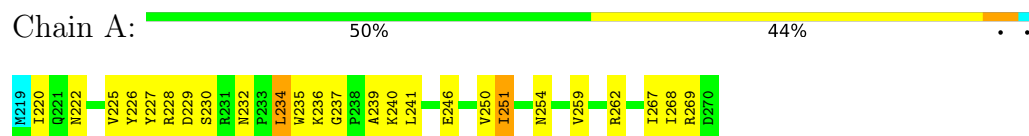


- Molecule 1: HIV-1 INTEGRASE

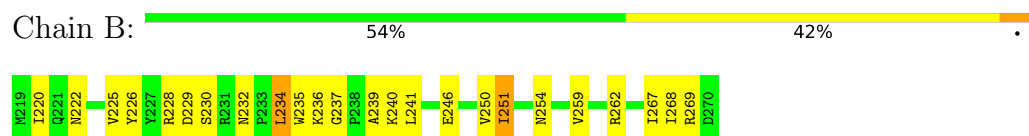


4.2.28 Score per residue for model 28

- Molecule 1: HIV-1 INTEGRASE

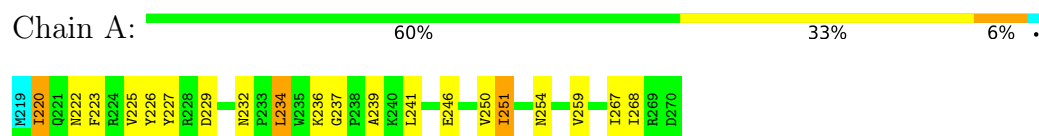


- Molecule 1: HIV-1 INTEGRASE

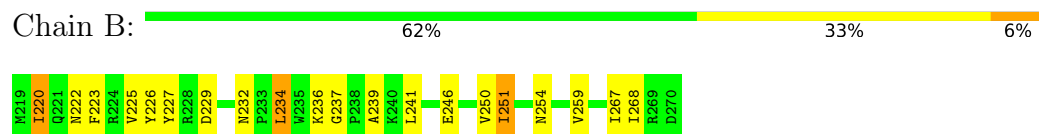


4.2.29 Score per residue for model 29

- Molecule 1: HIV-1 INTEGRASE

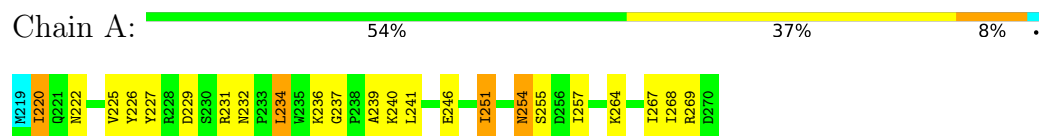


- Molecule 1: HIV-1 INTEGRASE

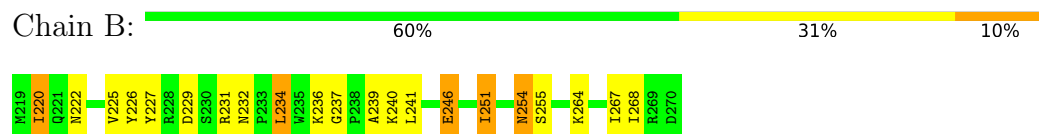


4.2.30 Score per residue for model 30

- Molecule 1: HIV-1 INTEGRASE

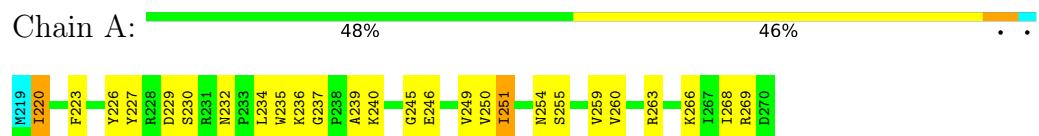


- Molecule 1: HIV-1 INTEGRASE

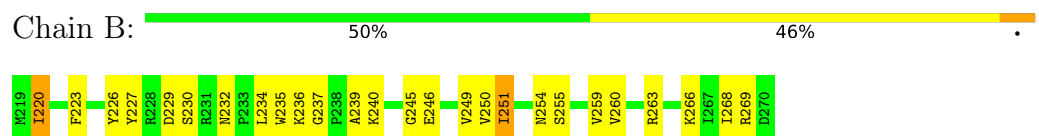


4.2.31 Score per residue for model 31

- Molecule 1: HIV-1 INTEGRASE

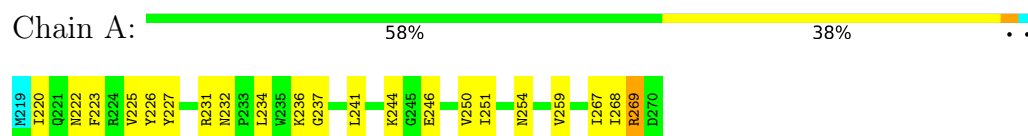


- Molecule 1: HIV-1 INTEGRASE

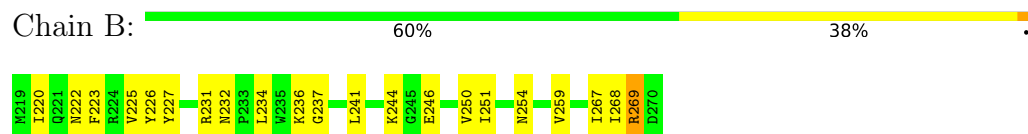


4.2.32 Score per residue for model 32

- Molecule 1: HIV-1 INTEGRASE

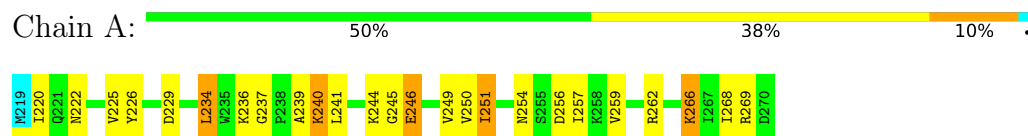


- Molecule 1: HIV-1 INTEGRASE

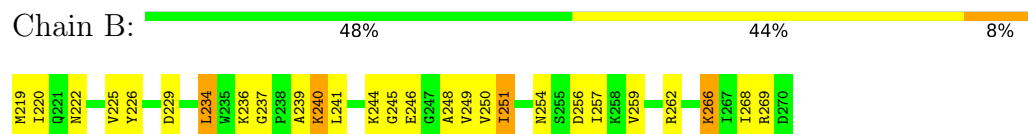


4.2.33 Score per residue for model 33

- Molecule 1: HIV-1 INTEGRASE

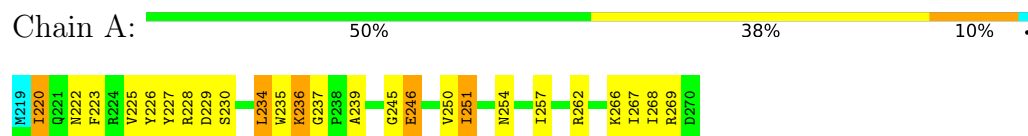


- Molecule 1: HIV-1 INTEGRASE

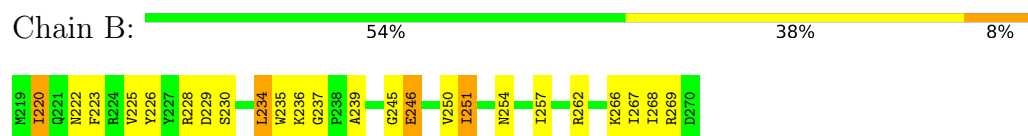


4.2.34 Score per residue for model 34

- Molecule 1: HIV-1 INTEGRASE

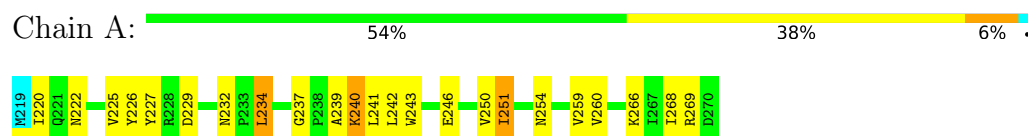


- Molecule 1: HIV-1 INTEGRASE

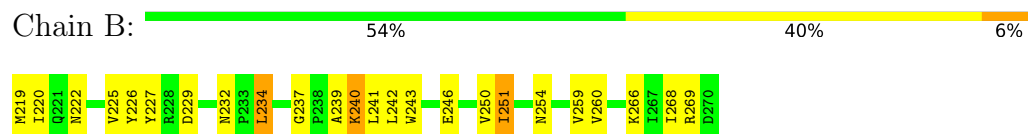


4.2.35 Score per residue for model 35

- Molecule 1: HIV-1 INTEGRASE

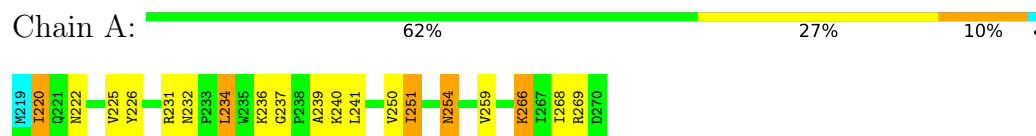


- Molecule 1: HIV-1 INTEGRASE

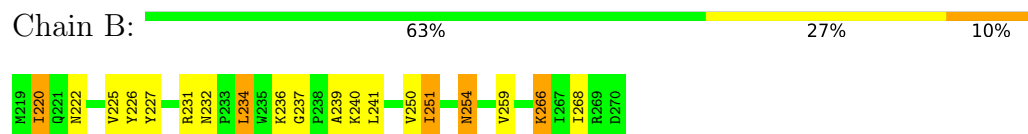


4.2.36 Score per residue for model 36

- Molecule 1: HIV-1 INTEGRASE

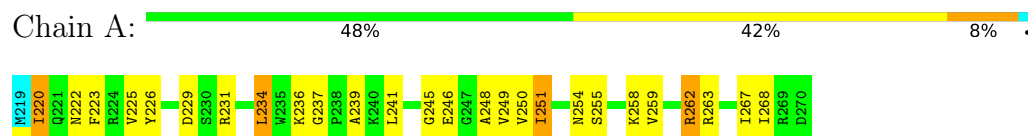


- Molecule 1: HIV-1 INTEGRASE

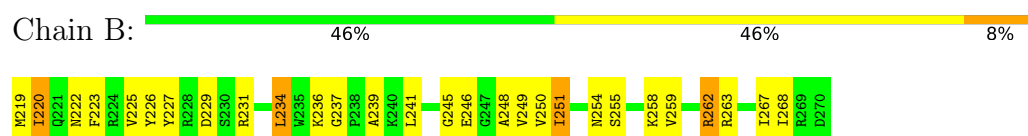


4.2.37 Score per residue for model 37

- Molecule 1: HIV-1 INTEGRASE

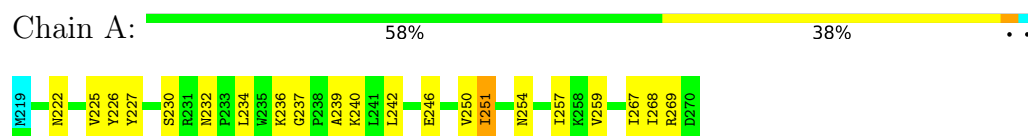


- Molecule 1: HIV-1 INTEGRASE

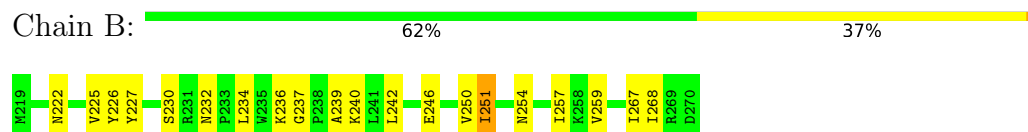


4.2.38 Score per residue for model 38

- Molecule 1: HIV-1 INTEGRASE

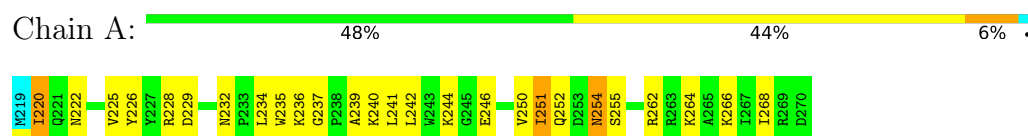


- Molecule 1: HIV-1 INTEGRASE

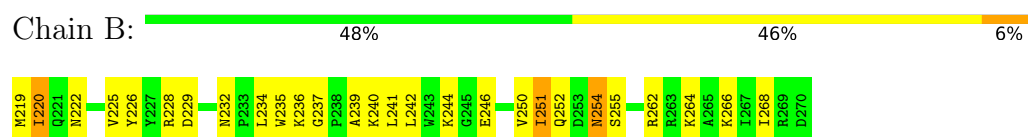


4.2.39 Score per residue for model 39

- Molecule 1: HIV-1 INTEGRASE

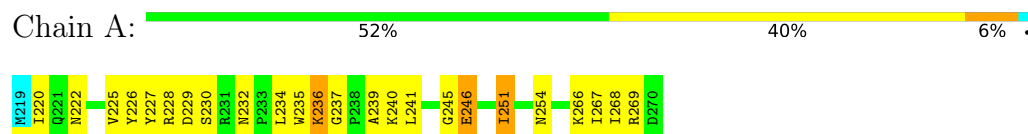


- Molecule 1: HIV-1 INTEGRASE

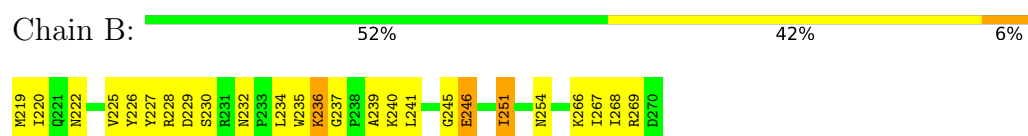


4.2.40 Score per residue for model 40

- Molecule 1: HIV-1 INTEGRASE



- Molecule 1: HIV-1 INTEGRASE



4.2.41 Score per residue for model 41

- Molecule 1: HIV-1 INTEGRASE

Chain A:  63% 29% 6% .



- Molecule 1: HIV-1 INTEGRASE

Chain B:  63% 31% 6%



4.2.42 Score per residue for model 42

- Molecule 1: HIV-1 INTEGRASE

Chain A:  58% 38% . .



- Molecule 1: HIV-1 INTEGRASE

Chain B:  60% 38% .



5 Refinement protocol and experimental data overview

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

Of the 50 calculated structures, 42 were deposited, based on the following criterion: *LOW OVERALL ENERGY*.

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

Software name	Classification	Version
X-PLOR	refinement	3.851
X-PLOR	structure solution	3.851

No chemical shift data was provided.

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	426	444	447	12±2
1	B	434	455	455	12±2
All	All	36120	37758	37884	952

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 13.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:250:VAL:HG21	1:B:250:VAL:HG21	0.91	1.41	16	30
1:A:241:LEU:HD22	1:A:267:ILE:HD11	0.87	1.47	23	9
1:A:220:ILE:HG22	1:A:223:PHE:CE1	0.87	2.05	31	7
1:B:220:ILE:HG22	1:B:223:PHE:CE1	0.86	2.05	31	7
1:B:241:LEU:HD22	1:B:267:ILE:HD11	0.85	1.47	23	9
1:B:225:VAL:HG21	1:B:241:LEU:HD13	0.83	1.50	39	4
1:A:225:VAL:HG21	1:A:241:LEU:HD13	0.83	1.50	39	5
1:B:241:LEU:HD13	1:B:267:ILE:HD12	0.81	1.53	23	1
1:A:241:LEU:HD13	1:A:267:ILE:HD12	0.80	1.53	23	1
1:B:226:TYR:CE1	1:B:268:ILE:HD12	0.72	2.19	3	24
1:A:226:TYR:CE1	1:A:268:ILE:HD12	0.72	2.19	30	24
1:B:220:ILE:HG21	1:B:241:LEU:CD2	0.71	2.16	35	26
1:A:220:ILE:HG21	1:A:241:LEU:CD2	0.70	2.16	35	26

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:239:ALA:CB	1:B:251:ILE:HD13	0.69	2.18	28	30
1:A:239:ALA:CB	1:A:251:ILE:HD13	0.68	2.17	10	30
1:A:234:LEU:HD13	1:A:234:LEU:O	0.68	1.88	41	4
1:B:234:LEU:HD13	1:B:234:LEU:O	0.68	1.88	41	4
1:B:225:VAL:HG13	1:B:266:LYS:O	0.67	1.90	16	10
1:A:225:VAL:HG13	1:A:266:LYS:O	0.66	1.90	16	10
1:B:225:VAL:HG13	1:B:267:ILE:HD13	0.66	1.68	9	17
1:A:225:VAL:HG13	1:A:267:ILE:HD13	0.65	1.68	22	17
1:A:241:LEU:HD13	1:A:267:ILE:CD1	0.64	2.21	23	1
1:B:241:LEU:HD13	1:B:267:ILE:CD1	0.64	2.22	23	1
1:A:249:VAL:HG13	1:A:262:ARG:HG2	0.63	1.71	33	3
1:B:242:LEU:HD11	1:B:252:GLN:HG3	0.63	1.71	10	2
1:B:249:VAL:HG13	1:B:262:ARG:HG2	0.63	1.71	33	3
1:B:226:TYR:CE2	1:B:268:ILE:HD12	0.62	2.29	37	18
1:B:241:LEU:HD22	1:B:267:ILE:CD1	0.62	2.23	23	9
1:A:250:VAL:HG22	1:A:259:VAL:HG22	0.62	1.71	26	26
1:B:250:VAL:HG22	1:B:259:VAL:HG22	0.62	1.71	26	29
1:A:220:ILE:HD13	1:A:241:LEU:HD23	0.61	1.72	11	5
1:B:242:LEU:HD11	1:B:252:GLN:CG	0.61	2.26	8	3
1:A:226:TYR:CE2	1:A:268:ILE:HD12	0.61	2.29	37	18
1:A:242:LEU:HD11	1:A:252:GLN:HG3	0.61	1.71	10	2
1:A:240:LYS:O	1:A:251:ILE:HG22	0.61	1.95	19	10
1:B:240:LYS:O	1:B:251:ILE:HG22	0.61	1.95	19	10
1:A:241:LEU:HD22	1:A:267:ILE:CD1	0.61	2.23	23	9
1:A:242:LEU:HD11	1:A:252:GLN:CG	0.60	2.26	8	3
1:A:220:ILE:HG21	1:A:241:LEU:HD21	0.60	1.74	42	5
1:B:220:ILE:HD13	1:B:241:LEU:HD23	0.60	1.74	8	4
1:B:220:ILE:HG21	1:B:241:LEU:HD21	0.59	1.74	42	6
1:A:242:LEU:HD22	1:B:243:TRP:CZ2	0.59	2.33	35	3
1:A:220:ILE:HG22	1:A:223:PHE:CD1	0.58	2.33	31	1
1:A:225:VAL:CG2	1:A:241:LEU:HD13	0.58	2.27	39	1
1:B:220:ILE:HG22	1:B:223:PHE:CD1	0.57	2.33	31	1
1:B:234:LEU:HD22	1:B:234:LEU:C	0.57	2.25	17	8
1:A:234:LEU:C	1:A:234:LEU:HD22	0.57	2.25	17	31
1:B:234:LEU:C	1:B:234:LEU:HD22	0.57	2.25	29	23
1:A:257:ILE:HD11	1:B:246:GLU:HG2	0.57	1.77	17	1
1:B:225:VAL:CG2	1:B:241:LEU:HD13	0.56	2.27	39	1
1:A:249:VAL:HG22	1:A:260:VAL:O	0.56	2.01	31	3
1:A:243:TRP:CZ2	1:B:242:LEU:HD22	0.55	2.36	35	3
1:B:249:VAL:HG22	1:B:260:VAL:O	0.55	2.01	31	2
1:B:226:TYR:HE1	1:B:268:ILE:HD12	0.55	1.62	36	22

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:239:ALA:HB3	1:B:251:ILE:HD13	0.55	1.79	27	15
1:A:239:ALA:HB3	1:A:251:ILE:HD13	0.55	1.78	26	16
1:A:226:TYR:HE2	1:A:268:ILE:HD12	0.55	1.62	20	18
1:A:226:TYR:HE1	1:A:268:ILE:HD12	0.54	1.62	12	22
1:B:226:TYR:HE2	1:B:268:ILE:HD12	0.54	1.62	20	18
1:A:234:LEU:C	1:A:234:LEU:HD23	0.54	2.28	20	2
1:B:234:LEU:C	1:B:234:LEU:HD23	0.54	2.28	20	2
1:A:257:ILE:HD13	1:B:248:ALA:HB3	0.53	1.79	33	1
1:A:248:ALA:HB3	1:B:257:ILE:HD12	0.53	1.79	14	2
1:A:232:ASN:OD1	1:A:234:LEU:HD11	0.52	2.04	17	1
1:A:220:ILE:HD13	1:A:241:LEU:CD2	0.52	2.35	25	4
1:B:220:ILE:HD13	1:B:241:LEU:CD2	0.52	2.35	25	2
1:A:257:ILE:HD11	1:B:246:GLU:CD	0.51	2.30	10	3
1:B:232:ASN:OD1	1:B:234:LEU:HD11	0.51	2.04	17	1
1:A:246:GLU:CD	1:B:257:ILE:HD11	0.51	2.31	10	2
1:B:248:ALA:HB1	1:B:259:VAL:HG12	0.50	1.82	37	1
1:A:248:ALA:HB1	1:A:259:VAL:HG12	0.49	1.83	37	1
1:A:242:LEU:HD13	1:A:257:ILE:HG23	0.49	1.84	38	1
1:A:242:LEU:HD12	1:A:257:ILE:HG23	0.49	1.84	23	4
1:A:257:ILE:HD11	1:B:246:GLU:OE1	0.49	2.08	34	1
1:B:242:LEU:HD12	1:B:257:ILE:HG23	0.49	1.84	23	4
1:A:246:GLU:CG	1:B:257:ILE:HD11	0.49	2.38	10	1
1:B:225:VAL:HB	1:B:251:ILE:HG21	0.49	1.85	2	3
1:A:225:VAL:HB	1:A:251:ILE:HG21	0.48	1.84	41	3
1:A:220:ILE:HD12	1:A:220:ILE:O	0.48	2.09	31	2
1:A:257:ILE:HD12	1:B:248:ALA:HB3	0.48	1.85	14	3
1:A:223:PHE:CZ	1:A:269:ARG:CG	0.48	2.96	34	1
1:B:223:PHE:CZ	1:B:269:ARG:CG	0.48	2.96	34	1
1:B:220:ILE:HD12	1:B:220:ILE:O	0.48	2.09	31	2
1:B:242:LEU:HD13	1:B:257:ILE:HG23	0.48	1.84	38	1
1:A:257:ILE:HD11	1:B:246:GLU:CG	0.48	2.38	17	2
1:B:225:VAL:HG22	1:B:267:ILE:HG13	0.47	1.86	4	1
1:A:225:VAL:HG22	1:A:267:ILE:HG13	0.47	1.86	4	1
1:B:220:ILE:HG13	1:B:241:LEU:HD23	0.47	1.86	5	1
1:A:246:GLU:HB2	1:B:257:ILE:HD11	0.47	1.85	33	2
1:A:228:ARG:NH1	1:A:235:TRP:CZ2	0.47	2.83	28	1
1:A:232:ASN:ND2	1:A:234:LEU:HD13	0.46	2.25	29	1
1:B:232:ASN:ND2	1:B:234:LEU:HD13	0.46	2.25	29	1
1:A:235:TRP:CH2	1:A:266:LYS:CD	0.46	2.99	39	2
1:B:228:ARG:NH1	1:B:235:TRP:CZ2	0.46	2.83	28	1
1:A:246:GLU:OE1	1:B:257:ILE:HD11	0.46	2.11	34	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:220:ILE:HD13	1:A:220:ILE:N	0.46	2.26	1	1
1:A:220:ILE:HG13	1:A:241:LEU:HD23	0.46	1.86	5	1
1:B:220:ILE:N	1:B:220:ILE:HD13	0.46	2.26	1	1
1:B:235:TRP:CH2	1:B:266:LYS:CD	0.46	2.99	39	2
1:A:242:LEU:HD11	1:A:252:GLN:HB2	0.46	1.88	22	2
1:B:225:VAL:HG21	1:B:241:LEU:CD1	0.46	2.35	39	1
1:B:244:LYS:HG3	1:B:249:VAL:HG12	0.46	1.88	19	2
1:B:228:ARG:CG	1:B:235:TRP:CE2	0.45	2.99	40	2
1:A:228:ARG:CG	1:A:235:TRP:CD2	0.45	3.00	34	5
1:A:234:LEU:HD13	1:A:234:LEU:C	0.45	2.36	24	2
1:B:242:LEU:HD11	1:B:252:GLN:HB2	0.45	1.88	22	2
1:A:227:TYR:N	1:A:227:TYR:CD1	0.45	2.84	42	10
1:B:234:LEU:HD13	1:B:234:LEU:C	0.45	2.36	5	2
1:B:227:TYR:CD1	1:B:227:TYR:N	0.45	2.85	17	19
1:B:266:LYS:O	1:B:267:ILE:HD13	0.45	2.12	5	1
1:A:228:ARG:CG	1:A:235:TRP:CE2	0.45	2.99	40	2
1:A:242:LEU:CD1	1:A:257:ILE:HG23	0.45	2.42	3	2
1:B:227:TYR:N	1:B:227:TYR:CD1	0.45	2.84	42	11
1:A:266:LYS:O	1:A:267:ILE:HD13	0.45	2.11	5	1
1:B:232:ASN:OD1	1:B:234:LEU:HD22	0.45	2.12	20	1
1:B:228:ARG:CG	1:B:235:TRP:CD2	0.45	2.99	34	4
1:A:235:TRP:CH2	1:A:266:LYS:CG	0.45	3.00	20	2
1:A:225:VAL:CG1	1:A:267:ILE:HD13	0.45	2.41	9	1
1:B:235:TRP:CH2	1:B:266:LYS:CG	0.45	3.00	20	2
1:A:227:TYR:CD1	1:A:227:TYR:N	0.44	2.84	7	19
1:A:268:ILE:HG22	1:A:269:ARG:N	0.44	2.28	4	29
1:B:242:LEU:CD1	1:B:257:ILE:HG23	0.44	2.42	38	2
1:A:246:GLU:HG2	1:B:257:ILE:HD11	0.44	1.88	4	1
1:A:244:LYS:HG3	1:A:249:VAL:HG12	0.44	1.88	19	2
1:A:234:LEU:HD22	1:A:235:TRP:N	0.44	2.27	5	1
1:B:220:ILE:HG21	1:B:241:LEU:HD23	0.44	1.90	16	3
1:B:225:VAL:CB	1:B:251:ILE:HG21	0.44	2.43	2	3
1:A:232:ASN:OD1	1:A:234:LEU:HD22	0.44	2.12	20	1
1:A:225:VAL:CB	1:A:251:ILE:HG21	0.44	2.43	2	2
1:B:234:LEU:HD22	1:B:235:TRP:N	0.44	2.27	5	1
1:A:220:ILE:CD1	1:A:241:LEU:HD23	0.44	2.43	35	1
1:B:234:LEU:HD22	1:B:235:TRP:O	0.44	2.13	41	3
1:A:220:ILE:HG21	1:A:241:LEU:HD23	0.44	1.90	33	3
1:B:268:ILE:HG22	1:B:269:ARG:N	0.43	2.28	1	25
1:A:259:VAL:HG21	1:B:259:VAL:CG2	0.43	2.43	21	5
1:A:259:VAL:CG2	1:B:259:VAL:HG21	0.43	2.44	14	5

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:227:TYR:CZ	1:B:236:LYS:HB3	0.43	2.49	40	1
1:B:220:ILE:CD1	1:B:241:LEU:HD23	0.42	2.43	35	1
1:A:234:LEU:HD22	1:A:235:TRP:O	0.42	2.13	41	3
1:B:235:TRP:CZ3	1:B:264:LYS:O	0.42	2.73	42	3
1:B:228:ARG:HG2	1:B:235:TRP:CD2	0.42	2.50	34	2
1:A:223:PHE:CZ	1:A:269:ARG:HG2	0.42	2.50	34	1
1:B:235:TRP:CZ3	1:B:266:LYS:CG	0.42	3.03	20	1
1:A:227:TYR:CZ	1:A:236:LYS:HB3	0.42	2.49	40	1
1:B:227:TYR:HB2	1:B:260:VAL:HG11	0.41	1.93	35	2
1:A:235:TRP:CZ3	1:A:264:LYS:O	0.41	2.73	39	3
1:A:234:LEU:N	1:A:234:LEU:CD1	0.41	2.83	13	4
1:A:250:VAL:O	1:A:251:ILE:HG23	0.41	2.16	3	1
1:A:228:ARG:HG2	1:A:235:TRP:CD2	0.41	2.50	34	3
1:A:232:ASN:CG	1:A:234:LEU:HD22	0.41	2.41	20	1
1:B:223:PHE:CZ	1:B:269:ARG:HG2	0.41	2.50	34	1
1:B:225:VAL:CG1	1:B:267:ILE:HD13	0.41	2.41	9	1
1:A:244:LYS:CG	1:A:249:VAL:HG12	0.41	2.46	16	2
1:B:244:LYS:CG	1:B:249:VAL:HG12	0.41	2.46	23	2
1:A:235:TRP:CZ3	1:A:266:LYS:CG	0.41	3.04	20	1
1:B:234:LEU:N	1:B:234:LEU:CD1	0.41	2.83	13	3
1:A:227:TYR:HB2	1:A:260:VAL:HG11	0.41	1.92	35	1
1:A:232:ASN:ND2	1:A:234:LEU:HD12	0.40	2.31	12	1
1:A:235:TRP:CH2	1:A:266:LYS:HG2	0.40	2.52	20	3
1:B:232:ASN:CG	1:B:234:LEU:HD22	0.40	2.41	20	1
1:A:227:TYR:O	1:A:236:LYS:N	0.40	2.54	34	2
1:B:250:VAL:O	1:B:251:ILE:HG23	0.40	2.16	3	1
1:A:259:VAL:CG2	1:B:259:VAL:CG2	0.40	3.00	21	2
1:A:242:LEU:HD13	1:B:243:TRP:CZ2	0.40	2.51	27	1
1:A:250:VAL:CG1	1:A:257:ILE:CG2	0.40	3.00	21	2
1:A:223:PHE:CE2	1:A:269:ARG:HB3	0.40	2.51	32	1
1:B:223:PHE:CE2	1:B:269:ARG:HB3	0.40	2.51	32	1

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	50/52 (96%)	40±1 (81±2%)	7±1 (14±2%)	3±1 (6±1%)	2	20
1	B	50/52 (96%)	40±1 (81±2%)	7±1 (14±2%)	3±1 (6±1%)	2	20
All	All	4200/4368 (96%)	3386 (81%)	568 (14%)	246 (6%)	2	20

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	237	GLY	42
1	B	237	GLY	42
1	A	254	ASN	37
1	B	254	ASN	37
1	A	246	GLU	32
1	B	246	GLU	32
1	A	245	GLY	12
1	B	245	GLY	12

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	45/46 (98%)	36±2 (81±4%)	9±2 (19±4%)	3	34
1	B	46/46 (100%)	37±2 (81±4%)	9±2 (19±4%)	3	34
All	All	3822/3864 (99%)	3085 (81%)	737 (19%)	3	34

All 45 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	234	LEU	42
1	A	251	ILE	42
1	B	234	LEU	42
1	B	251	ILE	42
1	A	222	ASN	37
1	A	236	LYS	37
1	B	222	ASN	37
1	B	236	LYS	37

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Mol	Chain	Res	Type	Models (Total)
1	A	229	ASP	29
1	B	229	ASP	29
1	A	220	ILE	28
1	B	220	ILE	28
1	A	232	ASN	25
1	B	232	ASN	25
1	A	230	SER	15
1	A	254	ASN	15
1	B	230	SER	15
1	B	254	ASN	15
1	B	219	MET	13
1	A	262	ARG	11
1	B	262	ARG	11
1	A	255	SER	11
1	B	255	SER	11
1	A	244	LYS	10
1	B	244	LYS	10
1	A	246	GLU	10
1	B	246	GLU	10
1	A	231	ARG	9
1	B	231	ARG	9
1	A	256	ASP	8
1	B	256	ASP	8
1	A	263	ARG	8
1	B	263	ARG	8
1	A	266	LYS	7
1	B	266	LYS	7
1	A	240	LYS	7
1	B	240	LYS	7
1	A	264	LYS	5
1	B	264	LYS	5
1	A	258	LYS	2
1	B	258	LYS	2
1	A	221	GLN	2
1	B	221	GLN	2
1	A	269	ARG	2
1	B	269	ARG	2

6.3.3 RNA ⓘ

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

No chemical shift data were provided