



Full wwPDB NMR Structure Validation Report ⓘ

Feb 12, 2017 – 11:25 pm GMT

PDB ID : 2KUI
Title : NMR structure of the PASTA domain of Mycobacterium tuberculosis of PknB
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Deposited on : 2010-02-17

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

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

A user guide is available at

<http://wwpdb.org/validation/2016/NMRValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

Cyrange	:	Kirchner and Güntert (2011)
NmrClust	:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	trunk28760
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	recalc28949

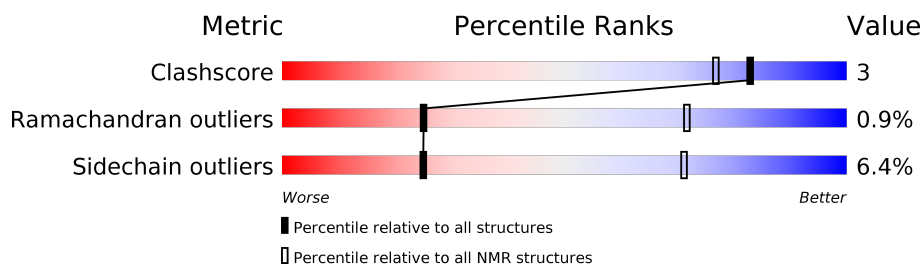
1 Overall quality at a glance

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	125131	11601
Ramachandran outliers	121729	10391
Sidechain outliers	121581	10367

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	275	 90% 7% . .

2 Ensemble composition and analysis

This entry contains 28 models. Model 16 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:359-A:423 (65)	0.52	16
2	A:426-A:490 (65)	0.36	18
3	A:492-A:626 (135)	1.29	16

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. No single-model clusters were found.

Cluster number	Models
1	1, 10, 12, 13, 14, 15, 17, 18, 21, 23, 25, 28
2	2, 3, 8, 11, 16, 19, 20, 22, 26, 27
3	5, 7, 9, 24
4	4, 6

3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 3990 atoms, of which 1988 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Serine/threonine-protein kinase pknB.

Mol	Chain	Residues	Atoms						Trace
1	A	272	Total	C	H	N	O	S	0
			3990	1243	1988	354	402	3	

There are 3 discrepancies between the modelled and reference sequences:

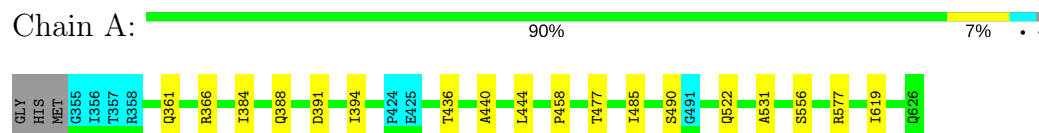
Chain	Residue	Modelled	Actual	Comment	Reference
A	352	GLY	-	EXPRESSION TAG	UNP P0A5S4
A	353	HIS	-	EXPRESSION TAG	UNP P0A5S4
A	354	MET	-	EXPRESSION TAG	UNP P0A5S4

4 Residue-property plots

4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA and DNA chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outliers are shown as green connectors. Residues which are classified as ill-defined in the NMR ensemble, are shown in cyan with an underline colour-coded according to the previous scheme. Residues which were present in the experimental sample, but not modelled in the final structure are shown in grey.

- Molecule 1: Serine/threonine-protein kinase pknB

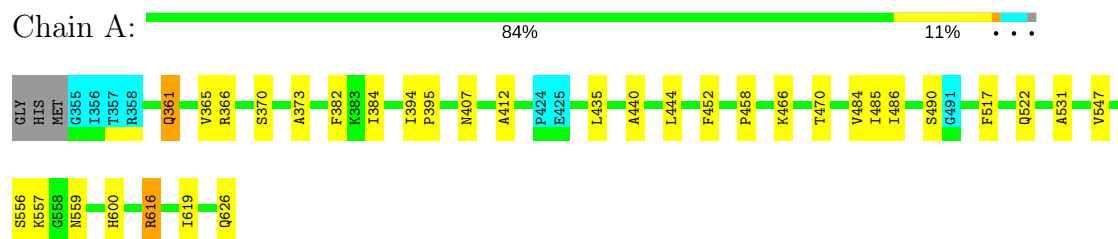


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

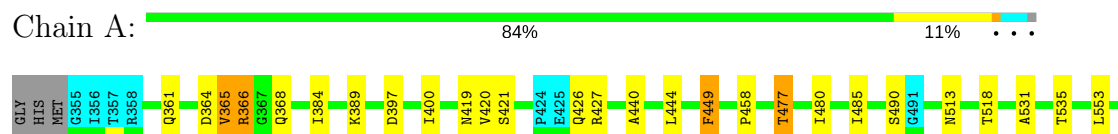
4.2.1 Score per residue for model 1

- Molecule 1: Serine/threonine-protein kinase pknB



4.2.2 Score per residue for model 2

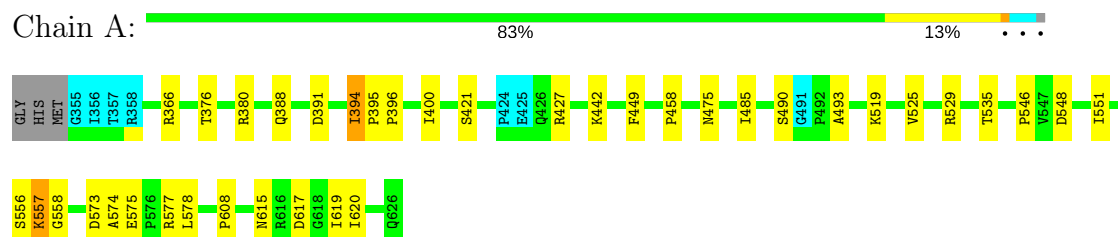
- Molecule 1: Serine/threonine-protein kinase pknB





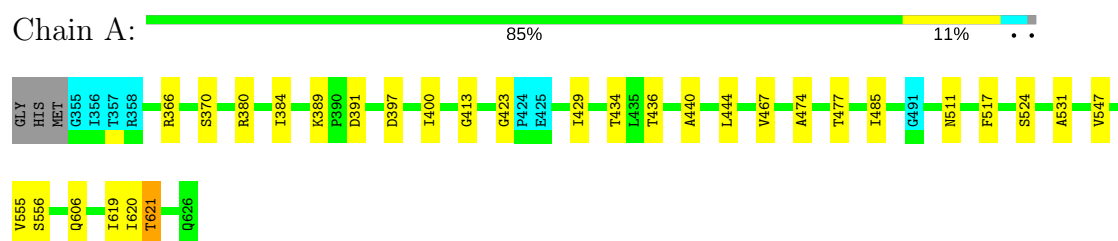
4.2.3 Score per residue for model 3

- Molecule 1: Serine/threonine-protein kinase pknB



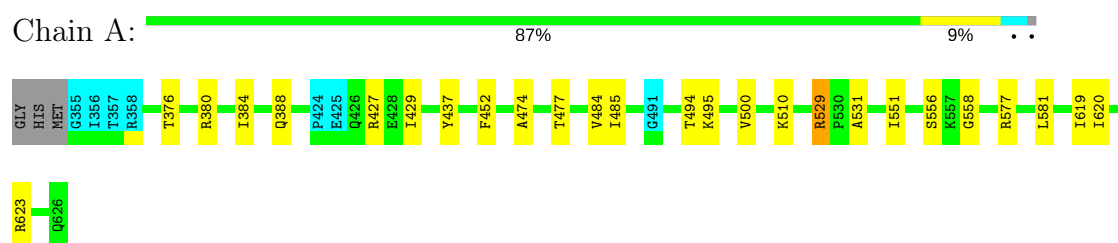
4.2.4 Score per residue for model 4

- Molecule 1: Serine/threonine-protein kinase pknB



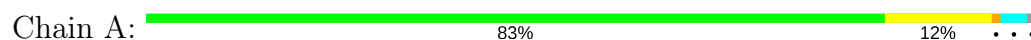
4.2.5 Score per residue for model 5

- Molecule 1: Serine/threonine-protein kinase pknB



4.2.6 Score per residue for model 6

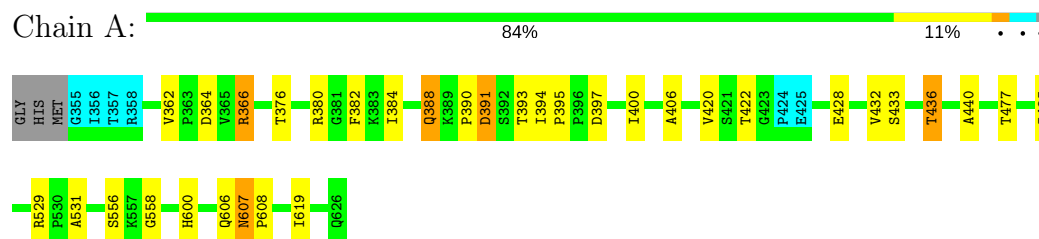
- Molecule 1: Serine/threonine-protein kinase pknB





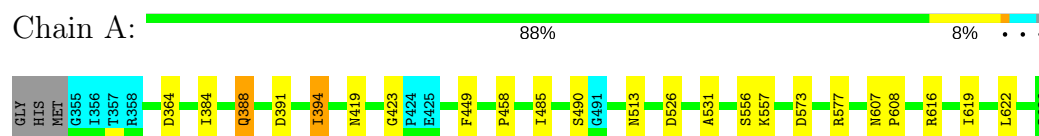
4.2.7 Score per residue for model 7

- Molecule 1: Serine/threonine-protein kinase pknB



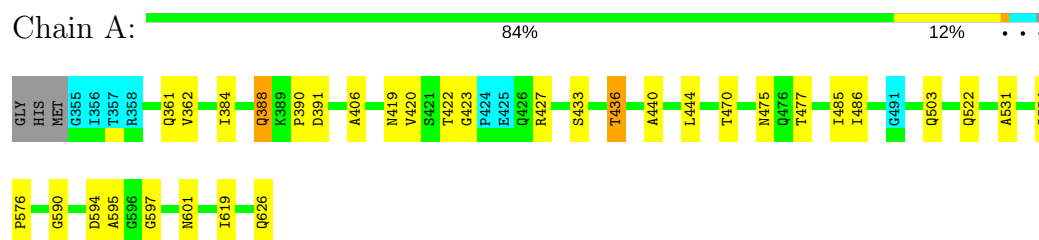
4.2.8 Score per residue for model 8

- Molecule 1: Serine/threonine-protein kinase pknB



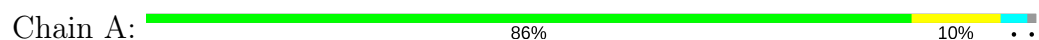
4.2.9 Score per residue for model 9

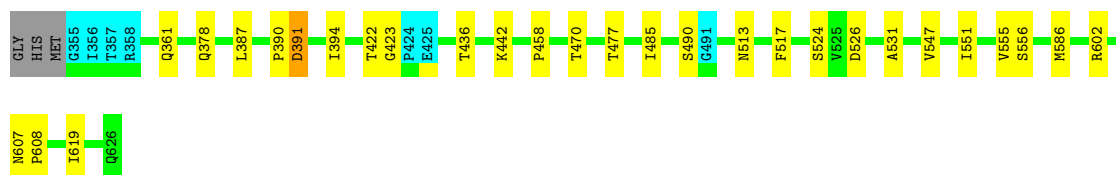
- Molecule 1: Serine/threonine-protein kinase pknB



4.2.10 Score per residue for model 10

- Molecule 1: Serine/threonine-protein kinase pknB





4.2.11 Score per residue for model 11

- Molecule 1: Serine/threonine-protein kinase pknB

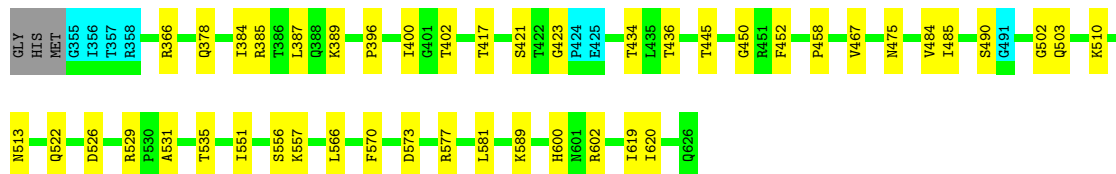
Chain A: 87% 8% . . .



4.2.12 Score per residue for model 12

- Molecule 1: Serine/threonine-protein kinase pknB

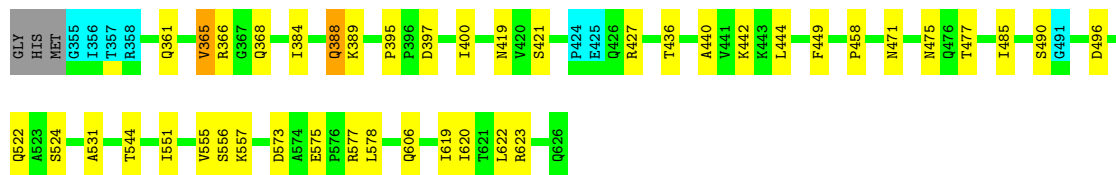
Chain A: 80% 16% . .



4.2.13 Score per residue for model 13

- Molecule 1: Serine/threonine-protein kinase pknB

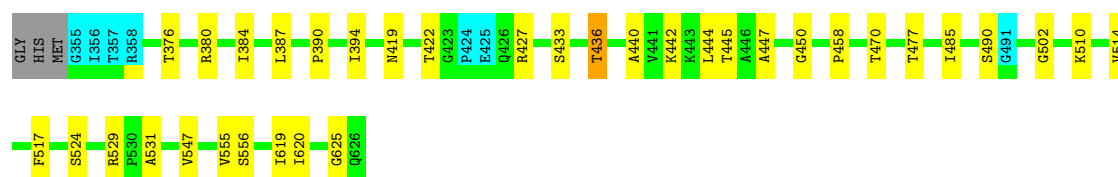
Chain A: 81% 15% . . .



4.2.14 Score per residue for model 14

- Molecule 1: Serine/threonine-protein kinase pknB

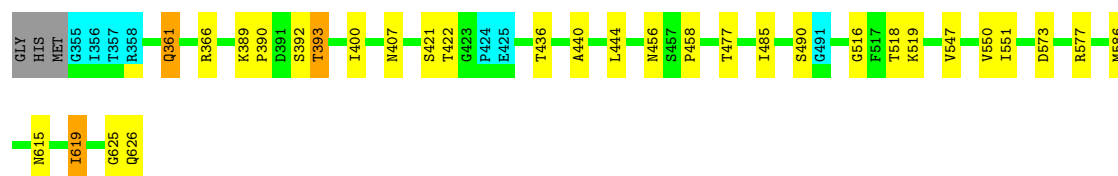
Chain A: 84% 12% . .



4.2.15 Score per residue for model 15

- Molecule 1: Serine/threonine-protein kinase pknB

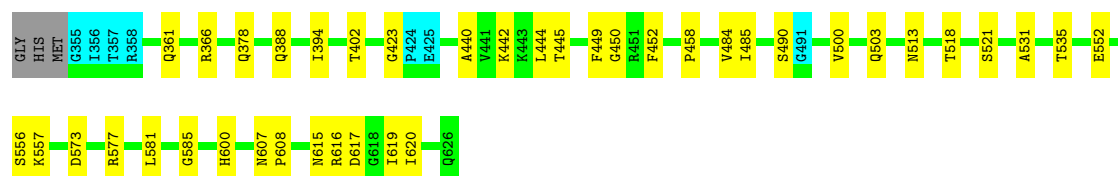
Chain A: 85% 10% ..



4.2.16 Score per residue for model 16 (medoid)

- Molecule 1: Serine/threonine-protein kinase pknB

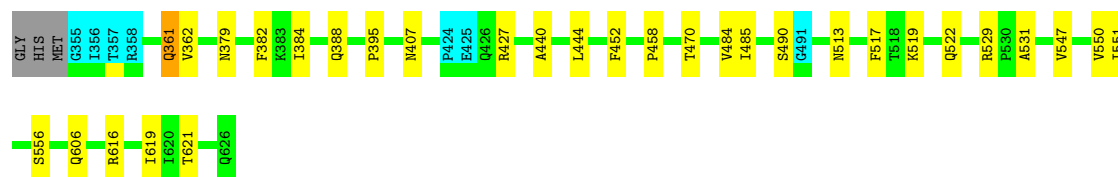
Chain A: 82% 15% ..



4.2.17 Score per residue for model 17

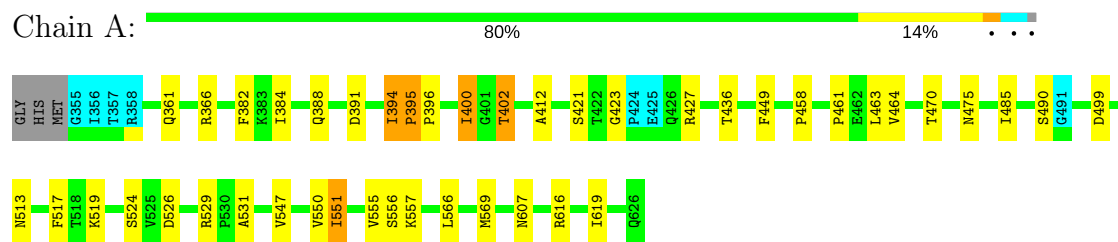
- Molecule 1: Serine/threonine-protein kinase pknB

Chain A: 85% 11% ..



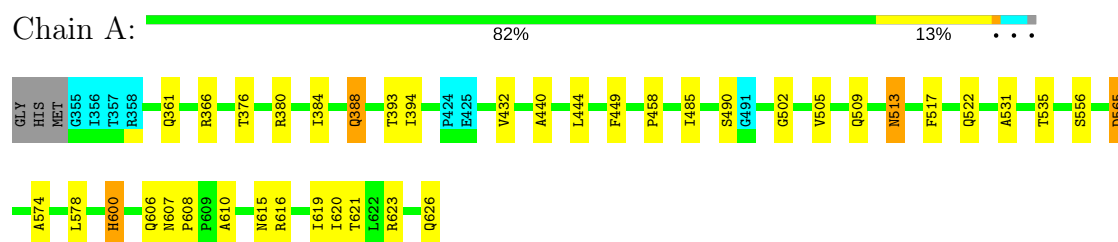
4.2.18 Score per residue for model 18

- Molecule 1: Serine/threonine-protein kinase pknB



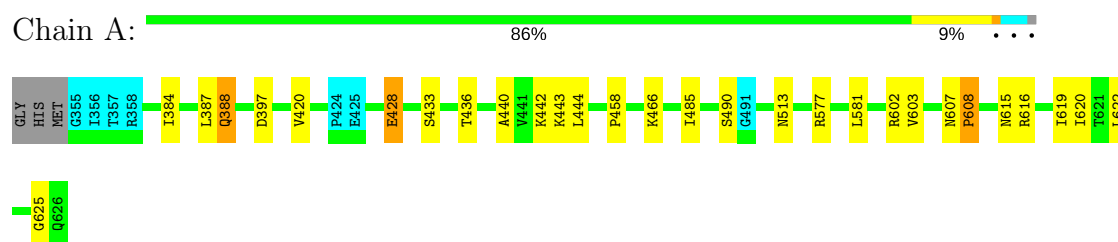
4.2.19 Score per residue for model 19

- Molecule 1: Serine/threonine-protein kinase pknB



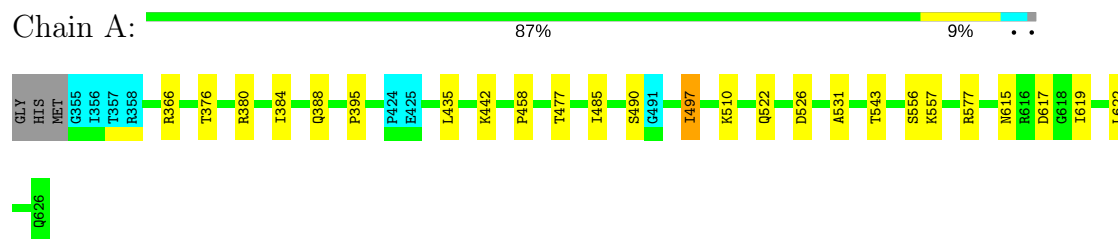
4.2.20 Score per residue for model 20

- Molecule 1: Serine/threonine-protein kinase pknB



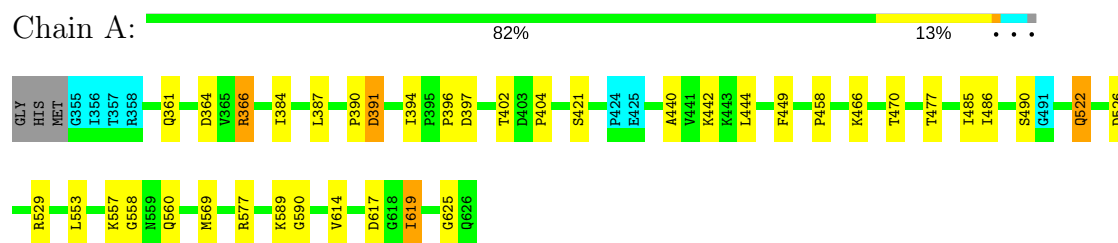
4.2.21 Score per residue for model 21

- Molecule 1: Serine/threonine-protein kinase pknB



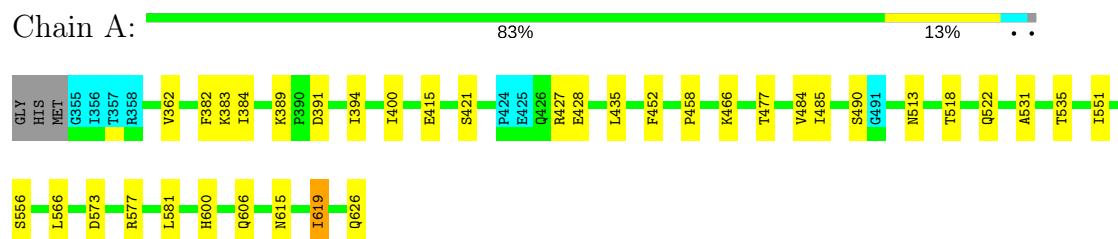
4.2.22 Score per residue for model 22

- Molecule 1: Serine/threonine-protein kinase pknB



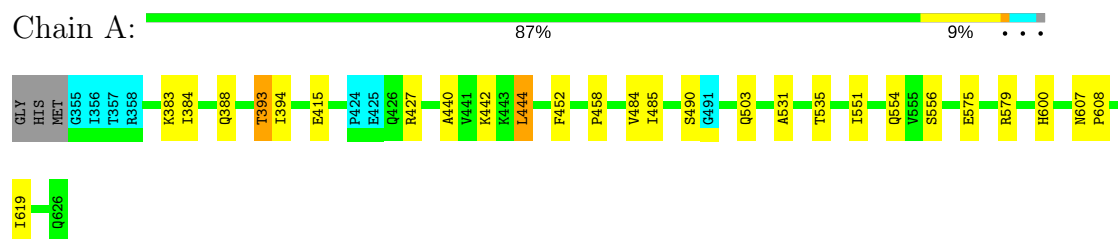
4.2.23 Score per residue for model 23

- Molecule 1: Serine/threonine-protein kinase pknB



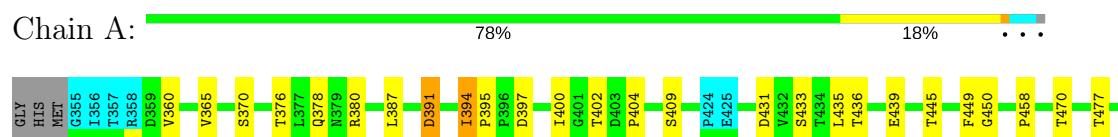
4.2.24 Score per residue for model 24

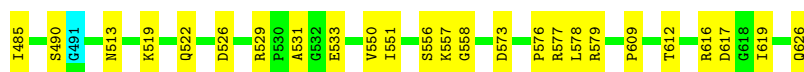
- Molecule 1: Serine/threonine-protein kinase pknB



4.2.25 Score per residue for model 25

- Molecule 1: Serine/threonine-protein kinase pknB

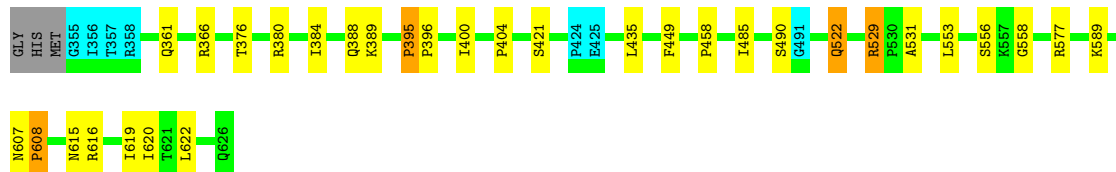




4.2.26 Score per residue for model 26

- Molecule 1: Serine/threonine-protein kinase pknB

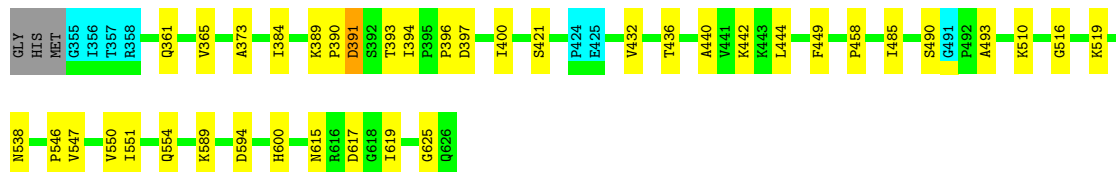
Chain A: 85% 10% ...



4.2.27 Score per residue for model 27

- Molecule 1: Serine/threonine-protein kinase pknB

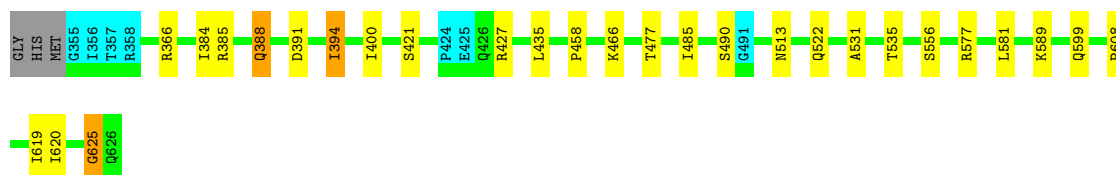
Chain A: 82% 14% ...



4.2.28 Score per residue for model 28

- Molecule 1: Serine/threonine-protein kinase pknB

Chain A: 86% 9% ...



5 Refinement protocol and experimental data overview

The models were refined using the following method: *restrained molecular dynamics in a hydrated environment*.

Of the 30 calculated structures, 28 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
CNS	refinement	1.2

No chemical shift data was provided. No validations of the models with respect to experimental NMR restraints is performed at this time.

6 Model quality [i](#)

6.1 Standard geometry [i](#)

There are no covalent bond-length or bond-angle outliers.

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	Chirality	Planarity
1	A	0.0±0.0	0.3±0.5
All	All	0	8

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

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

Mol	Chain	Res	Type	Group	Models (Total)
1	A	616	ARG	Sidechain	2
1	A	366	ARG	Sidechain	2
1	A	602	ARG	Sidechain	1
1	A	623	ARG	Sidechain	1
1	A	577	ARG	Sidechain	1
1	A	427	ARG	Sidechain	1

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	1952	1938	1938	11±3
All	All	54656	54264	54264	307

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 3.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:390:PRO:HA	1:A:422:THR:O	0.64	1.92	15	5
1:A:429:ILE:HB	1:A:474:ALA:O	0.64	1.93	4	2
1:A:458:PRO:HA	1:A:490:SER:O	0.62	1.94	18	23
1:A:389:LYS:HZ2	1:A:389:LYS:HB2	0.61	1.56	4	1
1:A:388:GLN:HA	1:A:420:VAL:O	0.60	1.97	9	2
1:A:365:VAL:HB	1:A:368:GLN:NE2	0.59	2.12	13	2
1:A:389:LYS:O	1:A:421:SER:HA	0.57	1.98	13	7
1:A:531:ALA:HA	1:A:556:SER:O	0.57	2.00	16	21
1:A:535:THR:HB	1:A:556:SER:OG	0.57	2.00	16	8
1:A:362:VAL:HG22	1:A:382:PHE:CZ	0.57	2.35	7	4
1:A:517:PHE:HA	1:A:547:VAL:O	0.57	2.00	17	4
1:A:427:ARG:NE	1:A:427:ARG:HA	0.56	2.15	9	6
1:A:376:THR:O	1:A:380:ARG:HG2	0.55	2.01	19	8
1:A:383:LYS:O	1:A:415:GLU:HA	0.55	2.01	23	2
1:A:470:THR:HG22	1:A:486:ILE:HG12	0.54	1.80	22	4
1:A:574:ALA:O	1:A:578:LEU:HG	0.53	2.03	3	2
1:A:573:ASP:O	1:A:577:ARG:HG2	0.53	2.03	8	7
1:A:606:GLN:HA	1:A:621:THR:O	0.53	2.04	17	3
1:A:445:THR:HA	1:A:450:GLY:CA	0.52	2.35	14	5
1:A:440:ALA:O	1:A:444:LEU:HG	0.52	2.05	20	10
1:A:440:ALA:O	1:A:444:LEU:HD22	0.51	2.06	1	2
1:A:370:SER:HB3	1:A:397:ASP:O	0.51	2.06	4	1
1:A:452:PHE:HA	1:A:484:VAL:O	0.51	2.06	24	7
1:A:382:PHE:CZ	1:A:412:ALA:HA	0.51	2.41	18	2
1:A:505:VAL:O	1:A:509:GLN:HG3	0.51	2.06	19	1
1:A:427:ARG:HA	1:A:427:ARG:NE	0.51	2.21	13	3
1:A:433:SER:HB2	1:A:436:THR:OG1	0.50	2.06	7	5
1:A:615:ASN:ND2	1:A:617:ASP:HB3	0.50	2.22	3	2
1:A:599:GLN:O	1:A:625:GLY:HA3	0.49	2.07	28	1
1:A:594:ASP:HA	1:A:626:GLN:OE1	0.49	2.07	9	1
1:A:364:ASP:OD2	1:A:366:ARG:HD2	0.49	2.08	7	1
1:A:396:PRO:HA	1:A:421:SER:OG	0.49	2.07	3	5
1:A:394:ILE:HG12	1:A:421:SER:OG	0.49	2.08	28	1
1:A:397:ASP:HA	1:A:420:VAL:HG13	0.49	1.83	20	3
1:A:607:ASN:HB3	1:A:608:PRO:HD3	0.49	1.83	7	10
1:A:388:GLN:N	1:A:388:GLN:HE21	0.49	2.06	9	4
1:A:622:LEU:O	1:A:623:ARG:HD2	0.49	2.08	13	1
1:A:517:PHE:CD1	1:A:547:VAL:HA	0.48	2.43	1	3
1:A:390:PRO:O	1:A:391:ASP:HB2	0.48	2.06	10	4
1:A:392:SER:O	1:A:393:THR:HB	0.48	2.08	15	1
1:A:529:ARG:O	1:A:558:GLY:HA2	0.48	2.08	26	6

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:496:ASP:OD1	1:A:544:THR:HB	0.48	2.08	13	1
1:A:434:THR:HB	1:A:467:VAL:O	0.48	2.09	4	2
1:A:432:VAL:HG11	1:A:440:ALA:HB2	0.48	1.86	27	3
1:A:524:SER:HA	1:A:555:VAL:O	0.47	2.09	10	6
1:A:565:ASP:HA	1:A:610:ALA:HB1	0.47	1.84	19	1
1:A:573:ASP:O	1:A:577:ARG:HD3	0.47	2.09	3	1
1:A:566:LEU:O	1:A:569:MET:HG3	0.47	2.09	18	1
1:A:563:MET:SD	1:A:620:ILE:HD12	0.47	2.50	6	1
1:A:362:VAL:HG22	1:A:382:PHE:CE1	0.47	2.45	7	1
1:A:575:GLU:O	1:A:579:ARG:HG2	0.47	2.10	11	1
1:A:364:ASP:OD1	1:A:366:ARG:HG2	0.47	2.10	22	1
1:A:428:GLU:CD	1:A:428:GLU:H	0.46	2.13	20	1
1:A:597:GLY:O	1:A:601:ASN:HB2	0.46	2.10	9	1
1:A:525:VAL:O	1:A:557:LYS:HB3	0.46	2.10	3	1
1:A:577:ARG:O	1:A:581:LEU:HG	0.46	2.11	23	7
1:A:391:ASP:OD2	1:A:393:THR:HG22	0.46	2.11	27	1
1:A:361:GLN:NE2	1:A:407:ASN:HA	0.46	2.24	15	4
1:A:497:ILE:HD13	1:A:543:THR:O	0.46	2.11	21	1
1:A:617:ASP:OD2	1:A:619:ILE:HB	0.46	2.11	22	1
1:A:575:GLU:OE2	1:A:579:ARG:HD3	0.45	2.11	24	1
1:A:461:PRO:O	1:A:464:VAL:HG22	0.45	2.11	18	1
1:A:391:ASP:HB3	1:A:394:ILE:CD1	0.45	2.41	25	1
1:A:364:ASP:OD2	1:A:366:ARG:HB3	0.45	2.12	2	1
1:A:519:LYS:O	1:A:550:VAL:HA	0.45	2.11	18	5
1:A:594:ASP:HA	1:A:600:HIS:NE2	0.45	2.27	27	1
1:A:463:LEU:O	1:A:463:LEU:HD13	0.44	2.11	18	1
1:A:394:ILE:HD13	1:A:394:ILE:H	0.44	1.72	3	3
1:A:526:ASP:HA	1:A:557:LYS:HG2	0.44	1.89	8	5
1:A:615:ASN:HD21	1:A:619:ILE:HG22	0.44	1.73	23	2
1:A:493:ALA:O	1:A:546:PRO:HA	0.44	2.13	3	2
1:A:362:VAL:HB	1:A:406:ALA:HA	0.44	1.88	7	2
1:A:391:ASP:OD1	1:A:393:THR:HG22	0.44	2.13	7	1
1:A:575:GLU:O	1:A:578:LEU:HG	0.43	2.12	13	1
1:A:600:HIS:HB2	1:A:626:GLN:H	0.43	1.74	19	1
1:A:513:ASN:HA	1:A:517:PHE:O	0.43	2.13	19	1
1:A:521:SER:O	1:A:552:GLU:HA	0.43	2.14	16	1
1:A:569:MET:SD	1:A:577:ARG:HD3	0.43	2.53	22	1
1:A:366:ARG:HD2	1:A:366:ARG:O	0.43	2.14	19	1
1:A:427:ARG:HG3	1:A:447:ALA:O	0.43	2.14	14	1
1:A:570:PHE:CD2	1:A:602:ARG:HB3	0.43	2.49	12	1
1:A:578:LEU:O	1:A:581:LEU:HG	0.43	2.14	2	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:575:GLU:HB2	1:A:576:PRO:HD3	0.43	1.91	9	1
1:A:516:GLY:O	1:A:547:VAL:HB	0.42	2.14	27	2
1:A:440:ALA:O	1:A:444:LEU:HD13	0.42	2.15	14	4
1:A:522:GLN:HA	1:A:553:LEU:O	0.42	2.14	26	3
1:A:602:ARG:HD2	1:A:603:VAL:O	0.42	2.12	20	1
1:A:519:LYS:O	1:A:551:ILE:HD13	0.42	2.14	18	1
1:A:393:THR:HG22	1:A:393:THR:O	0.42	2.14	24	1
1:A:391:ASP:HB3	1:A:394:ILE:HG12	0.42	1.91	6	1
1:A:366:ARG:HB3	1:A:402:THR:OG1	0.42	2.14	18	1
1:A:519:LYS:HD2	1:A:548:ASP:O	0.42	2.15	3	1
1:A:436:THR:HG22	1:A:439:GLU:HB3	0.42	1.91	6	2
1:A:529:ARG:HB2	1:A:556:SER:HB3	0.42	1.92	3	1
1:A:585:GLY:HA3	1:A:617:ASP:O	0.41	2.15	16	1
1:A:615:ASN:ND2	1:A:617:ASP:HB2	0.41	2.29	27	1
1:A:380:ARG:HA	1:A:380:ARG:NE	0.41	2.30	4	1
1:A:366:ARG:HD3	1:A:402:THR:OG1	0.41	2.16	16	1
1:A:385:ARG:O	1:A:417:THR:HA	0.41	2.15	12	1
1:A:578:LEU:HD12	1:A:579:ARG:N	0.41	2.31	25	1
1:A:526:ASP:HA	1:A:557:LYS:HB3	0.41	1.91	12	1
1:A:384:ILE:HA	1:A:416:ILE:O	0.41	2.15	6	1
1:A:616:ARG:HG3	1:A:617:ASP:N	0.41	2.31	6	1
1:A:510:LYS:O	1:A:514:VAL:HG23	0.41	2.15	14	1
1:A:600:HIS:HA	1:A:626:GLN:O	0.41	2.16	1	1
1:A:388:GLN:HE21	1:A:388:GLN:N	0.41	2.13	13	2
1:A:609:PRO:HB2	1:A:612:THR:OG1	0.41	2.16	25	1
1:A:389:LYS:HB2	1:A:389:LYS:NZ	0.41	2.27	4	1
1:A:449:PHE:HB3	1:A:480:ILE:HA	0.41	1.92	2	1
1:A:456:ASN:HB2	1:A:490:SER:OG	0.41	2.16	15	1
1:A:529:ARG:HD3	1:A:533:GLU:OE2	0.41	2.15	25	1
1:A:538:ASN:CA	1:A:554:GLN:HE22	0.41	2.28	27	1
1:A:360:VAL:O	1:A:409:SER:HA	0.40	2.16	25	1
1:A:426:GLN:OE1	1:A:477:THR:HB	0.40	2.15	2	1
1:A:365:VAL:CG2	1:A:373:ALA:HA	0.40	2.45	1	2
1:A:396:PRO:HA	1:A:421:SER:O	0.40	2.16	27	1
1:A:560:GLN:HA	1:A:614:VAL:O	0.40	2.17	22	1
1:A:400:ILE:HD13	1:A:400:ILE:H	0.40	1.76	18	1
1:A:573:ASP:O	1:A:576:PRO:HD2	0.40	2.16	25	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	264/275 (96%)	247±2 (94±1%)	15±2 (6±1%)	3±1 (1±0%)	25	72
All	All	7392/7700 (96%)	6913 (94%)	409 (6%)	70 (1%)	25	72

All 18 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	391	ASP	13
1	A	395	PRO	10
1	A	423	GLY	7
1	A	600	HIS	6
1	A	625	GLY	6
1	A	502	GLY	4
1	A	393	THR	3
1	A	404	PRO	3
1	A	365	VAL	3
1	A	608	PRO	3
1	A	500	VAL	3
1	A	590	GLY	2
1	A	607	ASN	2
1	A	601	ASN	1
1	A	615	ASN	1
1	A	595	ALA	1
1	A	397	ASP	1
1	A	413	GLY	1

6.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all NMR entries. The Analysed column shows the number of residues for which the sidechain conformation was analysed and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	215/222 (97%)	201±3 (94±1%)	14±3 (6±1%)	25 71
All	All	6020/6216 (97%)	5633 (94%)	387 (6%)	25 71

All 67 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	619	ILE	28
1	A	485	ILE	28
1	A	384	ILE	22
1	A	394	ILE	16
1	A	388	GLN	15
1	A	477	THR	14
1	A	522	GLN	14
1	A	361	GLN	14
1	A	551	ILE	13
1	A	513	ASN	13
1	A	400	ILE	13
1	A	366	ARG	11
1	A	620	ILE	11
1	A	449	PHE	11
1	A	436	THR	10
1	A	442	LYS	10
1	A	616	ARG	9
1	A	529	ARG	7
1	A	387	LEU	7
1	A	435	LEU	7
1	A	419	ASN	6
1	A	466	LYS	5
1	A	470	THR	5
1	A	378	GLN	5
1	A	589	LYS	5
1	A	402	THR	5
1	A	475	ASN	5
1	A	557	LYS	5
1	A	428	GLU	4
1	A	615	ASN	4
1	A	503	GLN	4
1	A	510	LYS	4
1	A	622	LEU	4
1	A	518	THR	4
1	A	626	GLN	3
1	A	600	HIS	3

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Mol	Chain	Res	Type	Models (Total)
1	A	606	GLN	3
1	A	397	ASP	3
1	A	395	PRO	2
1	A	526	ASP	2
1	A	554	GLN	2
1	A	577	ARG	2
1	A	495	LYS	2
1	A	566	LEU	2
1	A	586	MET	2
1	A	370	SER	2
1	A	575	GLU	1
1	A	617	ASP	1
1	A	444	LEU	1
1	A	553	LEU	1
1	A	560	GLN	1
1	A	494	THR	1
1	A	499	ASP	1
1	A	385	ARG	1
1	A	437	TYR	1
1	A	497	ILE	1
1	A	511	ASN	1
1	A	471	ASN	1
1	A	559	ASN	1
1	A	379	ASN	1
1	A	608	PRO	1
1	A	443	LYS	1
1	A	623	ARG	1
1	A	621	THR	1
1	A	565	ASP	1
1	A	431	ASP	1
1	A	364	ASP	1

6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

6.5 Carbohydrates [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 [i](#)

There are no chain breaks in this entry.

7 Chemical shift validation

No chemical shift data were provided