



Full wwPDB NMR Structure Validation Report ⓘ

Apr 26, 2016 – 04:30 PM BST

PDB ID : 1Q5L
Title : NMR structure of the substrate binding domain of DnaK bound to the peptide
NRLLLTG
Authors : Stevens, S.Y.; Cai, S.; Pellecchia, M.; Zuiderweg, E.R.
Deposited on : 2003-08-08

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
Mogul : unknown
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
ShiftChecker : rb-20027457
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20027457

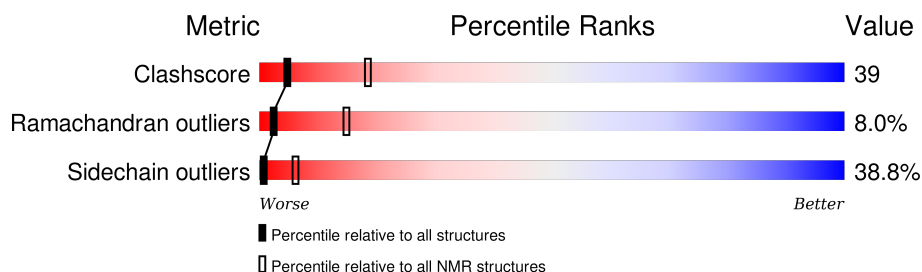
1 Overall quality at a glance

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	114402	11133
Ramachandran outliers	111179	9975
Sidechain outliers	111093	9958

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	135	
2	B	7	

2 Ensemble composition and analysis

This entry contains 15 models. Model 2 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *closest to the average*.

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:394-A:503, B:902-B:907 (116)	0.72	2

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 and 1 single-model cluster was found.

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

3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 1707 atoms, of which 795 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Chaperone protein dnaK.

Mol	Chain	Residues	Atoms						Trace
1	A	115	Total	C	H	N	O	S	0
			1595	529	738	151	174	3	

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	373	MET	-	CLONING ARTIFACT	UNP P0A6Y8
A	374	GLY	-	CLONING ARTIFACT	UNP P0A6Y8
A	375	SER	-	CLONING ARTIFACT	UNP P0A6Y8
A	376	SER	-	CLONING ARTIFACT	UNP P0A6Y8
A	377	HIS	-	CLONING ARTIFACT	UNP P0A6Y8
A	378	HIS	-	CLONING ARTIFACT	UNP P0A6Y8
A	379	HIS	-	CLONING ARTIFACT	UNP P0A6Y8
A	380	HIS	-	CLONING ARTIFACT	UNP P0A6Y8
A	381	HIS	-	CLONING ARTIFACT	UNP P0A6Y8
A	382	HIS	-	CLONING ARTIFACT	UNP P0A6Y8
A	383	GLY	-	CLONING ARTIFACT	UNP P0A6Y8
A	384	LEU	-	CLONING ARTIFACT	UNP P0A6Y8
A	385	VAL	-	CLONING ARTIFACT	UNP P0A6Y8
A	386	PRO	-	CLONING ARTIFACT	UNP P0A6Y8
A	387	ARG	-	CLONING ARTIFACT	UNP P0A6Y8
A	388	GLY	-	CLONING ARTIFACT	UNP P0A6Y8
A	389	SER	-	CLONING ARTIFACT	UNP P0A6Y8
A	390	HIS	-	CLONING ARTIFACT	UNP P0A6Y8
A	391	MET	-	CLONING ARTIFACT	UNP P0A6Y8
A	392	VAL	-	CLONING ARTIFACT	UNP P0A6Y8

- Molecule 2 is a protein called peptide NRLLLTG.

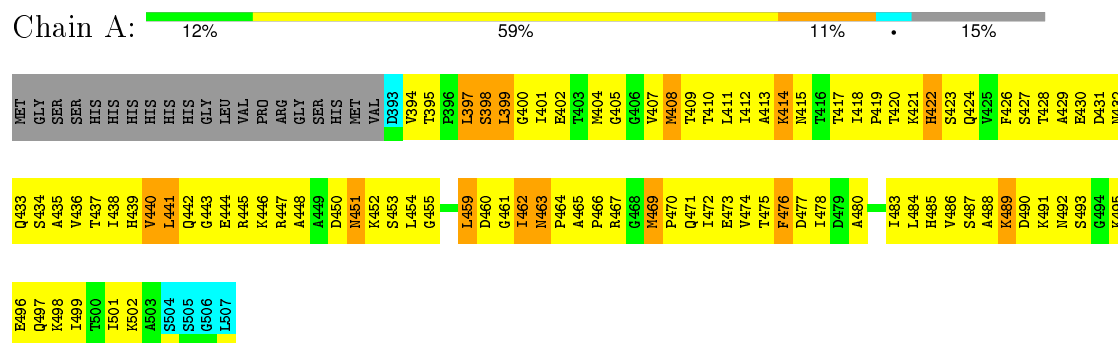
Mol	Chain	Residues	Atoms					Trace
2	B	7	Total	C	H	N	O	0
			112	34	57	11	10	

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: Chaperone protein dnaK



- Molecule 2: peptide NRLLLTG

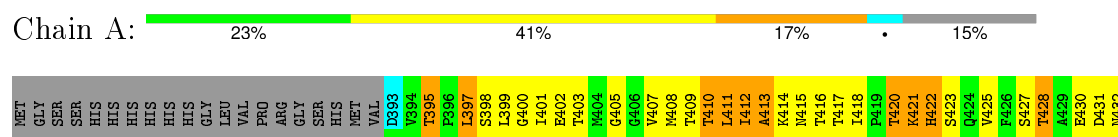


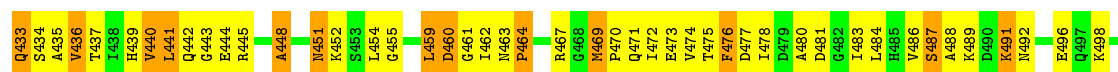
4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

- Molecule 1: Chaperone protein dnaK



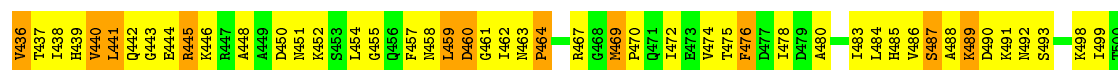
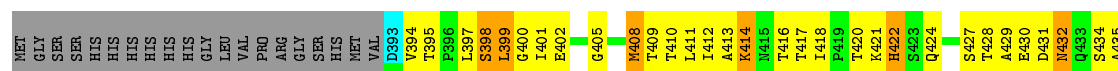
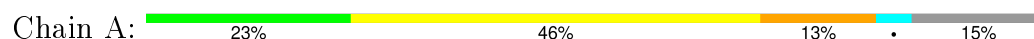


- Molecule 2: peptide NRLLLTG



4.2.2 Score per residue for model 2 (medoid)

- Molecule 1: Chaperone protein dnaK

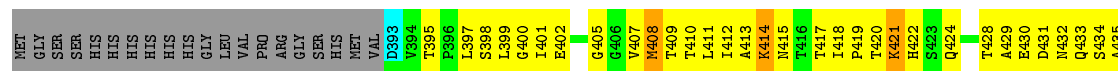
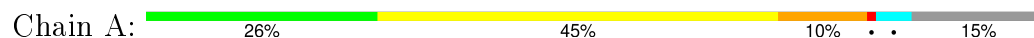


- Molecule 2: peptide NRLLLTG



4.2.3 Score per residue for model 3

- Molecule 1: Chaperone protein dnaK



6506
L507

- Molecule 2: peptide NRLLLTG

Chain B: 14% 57% 14% 14%

1901
1902
1903
1904
1905
1906
1907

4.2.4 Score per residue for model 4

- Molecule 1: Chaperone protein dnaK

Chain A: 24% 47% 9% • • 15%

MET GLY SER SER HIS HIS HIS HIS HIS HIS LEU VAL PRO ARG GLY SER HIS HIS MET VAL
D393 V394 T395 P396 I397 S398 G400 I401 I402 E403 M404 G405 G406 V407 M408 T409 T410 L411 L412 A413 K414
T418 P419 T420 K421 H422 S423 S424 Q425 V426 F427 S428 T429 A430 D431 H432 Q433 S434
A435 V436 T437 I438 H439 V440 H441 L442 Q443 G444 E445 R446 K447 A448
M451 K452 S453 L454 M455 L459 I462 I463 P464 A465 P466 R467 G468 M469 Q470 Q471 I472 E473 F476
L484 H485 V486 S487 A488 K489 D490 K491 N492 S493 G494 K495 E496 Q497 K498 I499 K502 A503 S504 S505 G506

L507

- Molecule 2: peptide NRLLLTG

Chain B: 43% 14% 29% 14%

1901
1902
1903
1904
1907

4.2.5 Score per residue for model 5

- Molecule 1: Chaperone protein dnaK

Chain A: 19% 41% 22% • 15%

MET GLY SER SER HIS HIS HIS HIS HIS HIS LEU VAL PRO ARG GLY SER HIS HIS MET VAL
D393 V394 T395 P396 I397 S398 G400 I401 I402 E403 M404 G405 G406 V407 M408 T409 T410 L411 L412 A413 K414
T418 P419 T420 K421 H422 S423 S424 Q425 V426 F427 S428 T429 A430 D431 H432 Q433 S434
A435 V436 T437 I438 H439 V440 H441 L442 Q443 G444 E445 R446 K447 A448
M451 K452 S453 L454 M455 L459 I462 I463 P464 A465 P466 R467 G468 M469 Q470 Q471 I472 E473 F476
L484 H485 V486 S487 A488 K489 D490 K491 N492 S493 G494 K495 E496 Q497 K498 I499 K502 A503 S504 S505 G506

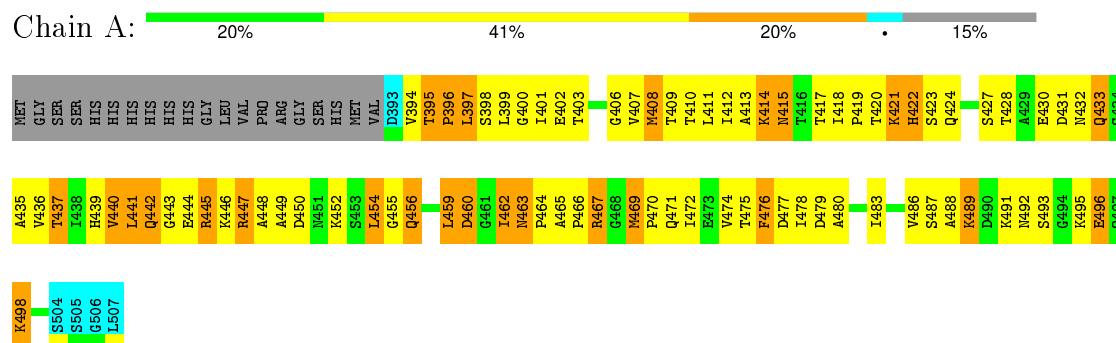
1501
1502
1503
1504
1505
1506
1507

- Molecule 2: peptide NRLLLTG



4.2.6 Score per residue for model 6

- Molecule 1: Chaperone protein dnaK

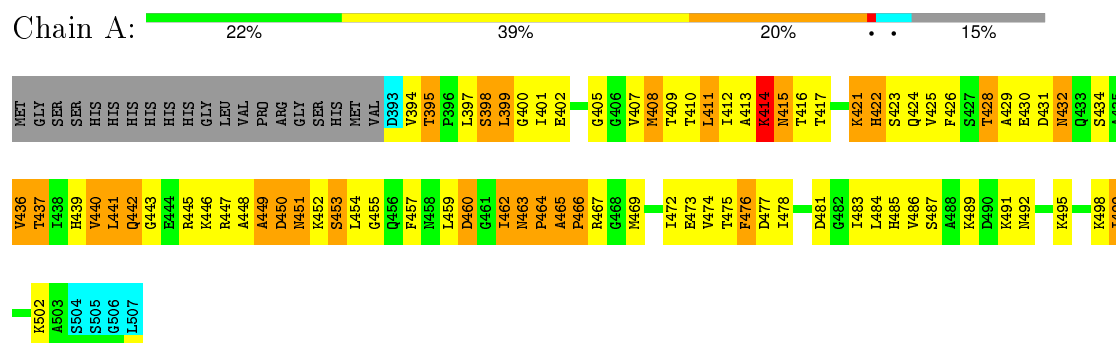


- Molecule 2: peptide NRLLLTG



4.2.7 Score per residue for model 7

- Molecule 1: Chaperone protein dnaK

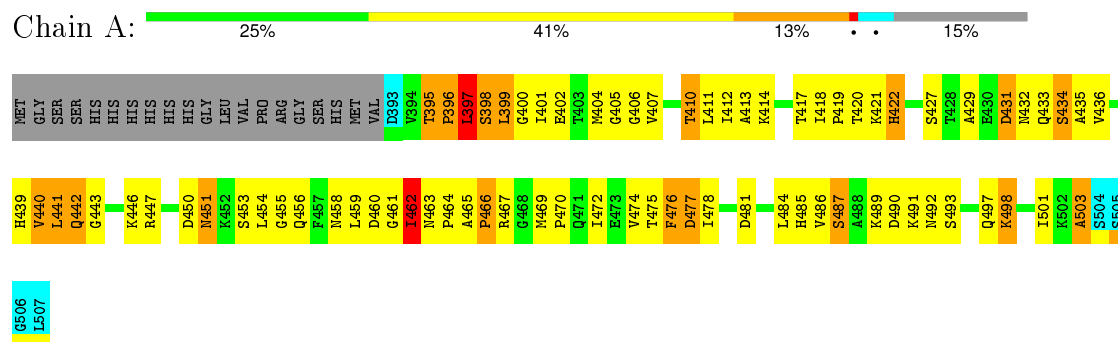


- Molecule 2: peptide NRLLLTG

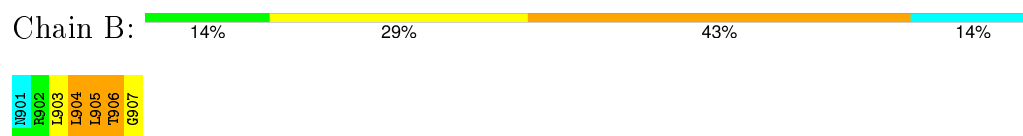


4.2.8 Score per residue for model 8

- Molecule 1: Chaperone protein dnaK

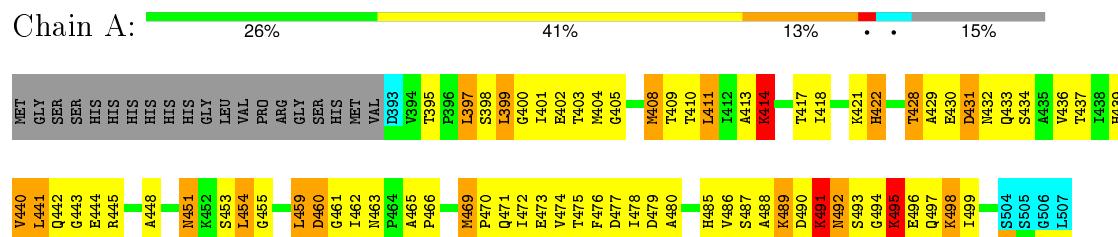


- Molecule 2: peptide NRLLLTG



4.2.9 Score per residue for model 9

- Molecule 1: Chaperone protein dnaK

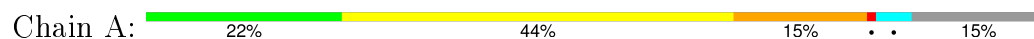


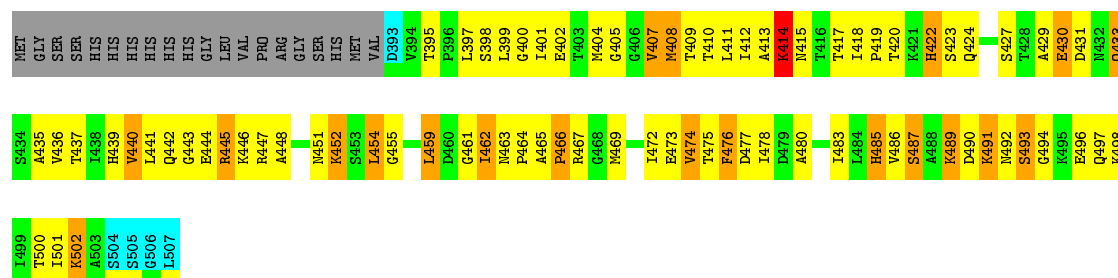
- Molecule 2: peptide NRLLLTG



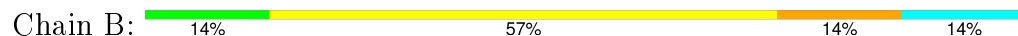
4.2.10 Score per residue for model 10

- Molecule 1: Chaperone protein dnaK



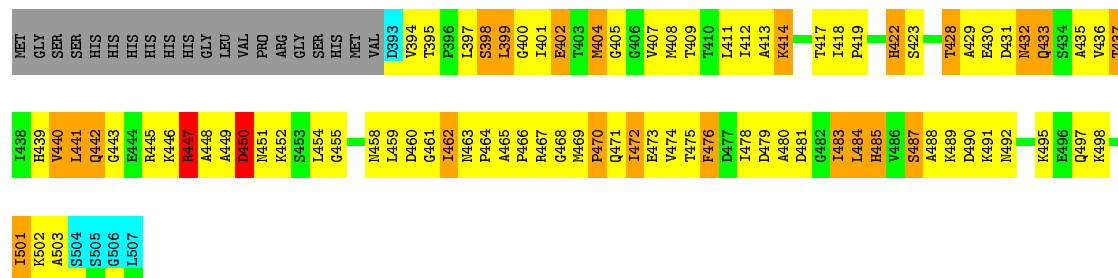
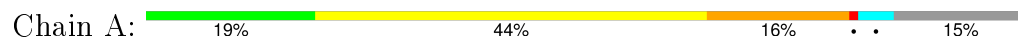


- Molecule 2: peptide NRLLLTG



4.2.11 Score per residue for model 11

- Molecule 1: Chaperone protein dnaK

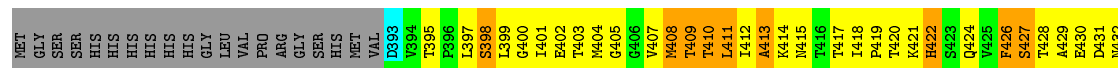
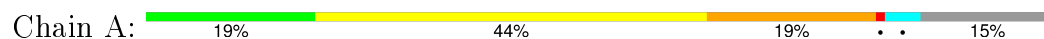


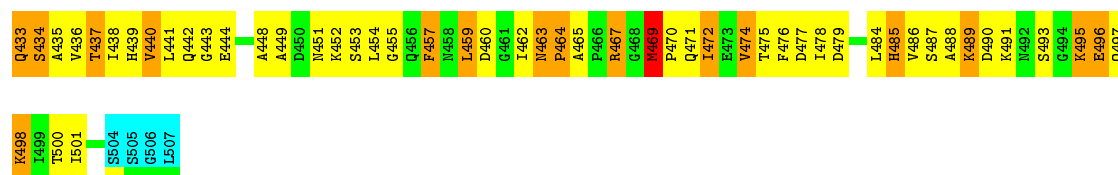
- Molecule 2: peptide NRLLLTG



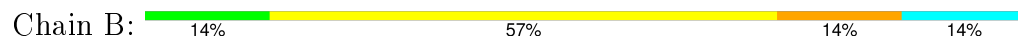
4.2.12 Score per residue for model 12

- Molecule 1: Chaperone protein dnaK



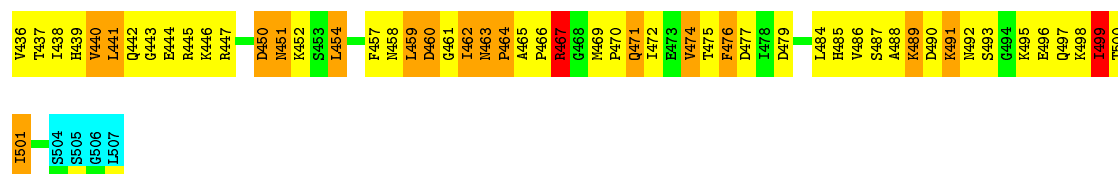
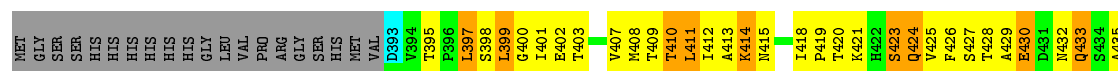
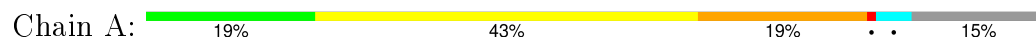


- Molecule 2: peptide NRLLLTG



4.2.13 Score per residue for model 13

- Molecule 1: Chaperone protein dnaK

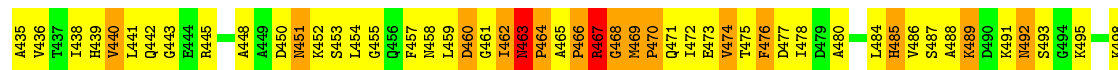
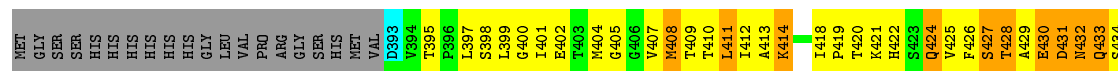
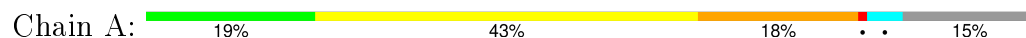


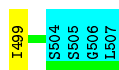
- Molecule 2: peptide NRLLLTG



4.2.14 Score per residue for model 14

- Molecule 1: Chaperone protein dnaK



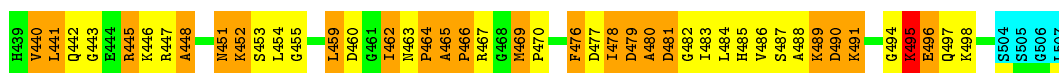
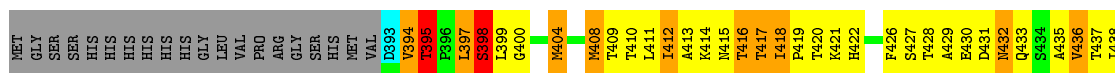
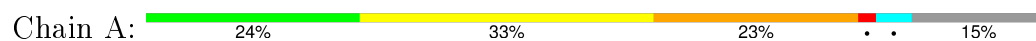


- Molecule 2: peptide NRLLLTG

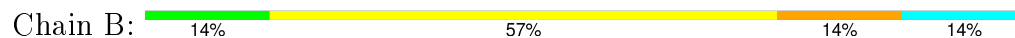


4.2.15 Score per residue for model 15

- Molecule 1: Chaperone protein dnaK



- Molecule 2: peptide NRLLLTG



5 Refinement protocol and experimental data overview

The models were refined using the following method: *torsion angle dynamics*.

Of the 60 calculated structures, 15 were deposited, based on the following criterion: *structures with acceptable covalent geometry, structures with the least restraint violations, structures with the lowest energy*.

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

Software name	Classification	Version
ARIA/(CNS)	structure solution	1.0
ARIA/(CNS)	refinement	1.0

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

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	824	714	842	68±16
2	B	47	50	56	6±3
All	All	13065	11460	13470	1026

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 39.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:489:LYS:HB3	1:A:496:GLU:HA	0.93	1.40	12	1
1:A:416:THR:HG21	1:A:478:ILE:HD12	0.83	1.50	15	1
1:A:440:VAL:HB	1:A:454:LEU:HB2	0.82	1.48	10	4
1:A:440:VAL:HG11	1:A:486:VAL:HG21	0.81	1.52	15	7
1:A:463:ASN:HB3	1:A:464:PRO:HD3	0.81	1.51	14	2
1:A:427:SER:HB2	2:B:904:LEU:HD12	0.80	1.52	14	1
1:A:400:GLY:HA3	1:A:410:THR:HA	0.80	1.50	15	3
1:A:489:LYS:HG2	1:A:496:GLU:HB3	0.80	1.54	15	1
1:A:402:GLU:HB3	1:A:439:HIS:HB3	0.80	1.51	4	12
1:A:398:SER:N	1:A:414:LYS:HG3	0.79	1.93	6	1
1:A:408:MET:HB3	1:A:448:ALA:HB2	0.78	1.55	4	7
1:A:397:LEU:CB	1:A:414:LYS:HB3	0.77	2.09	15	1
1:A:412:ILE:HD11	1:A:476:PHE:HB2	0.77	1.55	6	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:429:ALA:HB3	2:B:905:LEU:HA	0.77	1.56	8	2
1:A:397:LEU:HB2	1:A:414:LYS:HD3	0.77	1.56	15	1
1:A:401:ILE:HG22	1:A:440:VAL:HG13	0.77	1.57	10	1
1:A:440:VAL:HG23	1:A:455:GLY:H	0.77	1.39	11	13
1:A:417:THR:HA	1:A:482:GLY:H	0.76	1.38	15	1
1:A:435:ALA:O	2:B:906:THR:HG22	0.75	1.81	10	2
1:A:402:GLU:HB2	1:A:439:HIS:HB3	0.75	1.57	2	1
1:A:436:VAL:HG21	1:A:472:ILE:HG12	0.74	1.56	14	3
1:A:431:ASP:N	1:A:467:ARG:HB2	0.73	1.98	14	1
1:A:395:THR:HG21	1:A:412:ILE:HG22	0.73	1.61	15	1
1:A:420:THR:HG22	1:A:478:ILE:HB	0.73	1.61	15	5
1:A:417:THR:HA	1:A:482:GLY:N	0.72	2.00	15	1
1:A:397:LEU:HB3	1:A:414:LYS:HB3	0.71	1.60	15	1
1:A:395:THR:HB	1:A:414:LYS:HB3	0.71	1.59	6	1
1:A:442:GLN:HB2	1:A:454:LEU:HD22	0.71	1.61	13	1
1:A:429:ALA:HB2	2:B:903:LEU:HD23	0.71	1.61	15	3
1:A:427:SER:CB	2:B:904:LEU:HD12	0.70	2.15	14	1
1:A:395:THR:HA	1:A:414:LYS:O	0.70	1.85	15	1
1:A:440:VAL:HG23	1:A:455:GLY:N	0.70	2.02	8	12
1:A:399:LEU:HD12	1:A:442:GLN:HG3	0.70	1.64	15	3
1:A:436:VAL:HG12	1:A:459:LEU:HB3	0.70	1.62	13	12
1:A:498:LYS:O	1:A:499:ILE:HG23	0.70	1.87	13	1
1:A:397:LEU:HG	1:A:398:SER:H	0.70	1.45	6	1
1:A:394:VAL:O	1:A:395:THR:HG23	0.69	1.86	15	1
1:A:427:SER:HA	2:B:904:LEU:HD23	0.69	1.62	13	1
1:A:397:LEU:N	1:A:414:LYS:HB2	0.69	2.02	6	1
1:A:427:SER:HB2	1:A:472:ILE:HB	0.69	1.64	4	2
1:A:404:MET:H	2:B:904:LEU:HA	0.68	1.46	14	5
1:A:431:ASP:HA	1:A:466:PRO:HD2	0.68	1.64	9	2
1:A:489:LYS:HA	1:A:496:GLU:H	0.68	1.48	9	1
1:A:428:THR:HB	1:A:467:ARG:C	0.68	2.08	14	1
1:A:399:LEU:HA	1:A:442:GLN:HB2	0.68	1.64	11	1
1:A:397:LEU:HB3	1:A:414:LYS:H	0.68	1.49	15	1
1:A:491:LYS:HB3	1:A:494:GLY:H	0.68	1.49	5	2
1:A:408:MET:HG2	1:A:450:ASP:HB3	0.67	1.65	11	1
1:A:399:LEU:HD13	1:A:413:ALA:C	0.67	2.08	15	1
1:A:472:ILE:HA	1:A:489:LYS:O	0.67	1.90	5	14
1:A:412:ILE:HG21	1:A:420:THR:HG21	0.66	1.66	14	5
1:A:442:GLN:CB	1:A:454:LEU:HD22	0.66	2.19	13	1
1:A:442:GLN:HG2	1:A:454:LEU:HG	0.66	1.68	3	3
1:A:402:GLU:HB3	1:A:439:HIS:HB2	0.66	1.67	10	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:435:ALA:HA	1:A:459:LEU:O	0.66	1.91	8	4
1:A:436:VAL:HA	2:B:907:GLY:HA2	0.66	1.67	10	1
1:A:408:MET:HG3	1:A:449:ALA:HB3	0.65	1.69	11	2
1:A:404:MET:HG3	2:B:905:LEU:HD23	0.65	1.67	8	1
1:A:431:ASP:HB3	1:A:466:PRO:HA	0.65	1.69	5	1
1:A:397:LEU:HB3	1:A:414:LYS:HE2	0.65	1.67	6	1
1:A:433:GLN:HG3	2:B:906:THR:HA	0.65	1.66	8	1
1:A:473:GLU:O	1:A:488:ALA:HA	0.65	1.91	14	5
1:A:441:LEU:HB3	1:A:450:ASP:HB3	0.64	1.67	7	1
1:A:430:GLU:C	1:A:466:PRO:O	0.64	2.36	14	1
1:A:395:THR:HG22	1:A:413:ALA:O	0.64	1.93	15	1
1:A:433:GLN:O	1:A:462:ILE:HB	0.64	1.93	14	1
1:A:442:GLN:HB3	1:A:454:LEU:HD11	0.63	1.69	3	4
1:A:473:GLU:H	1:A:489:LYS:HB3	0.63	1.51	9	1
1:A:474:VAL:HA	1:A:487:SER:O	0.63	1.94	6	10
1:A:442:GLN:HB2	1:A:454:LEU:HD11	0.63	1.67	5	7
1:A:432:ASN:O	1:A:433:GLN:HB2	0.63	1.93	14	1
1:A:398:SER:O	1:A:442:GLN:HB2	0.63	1.93	4	2
1:A:432:ASN:H	1:A:467:ARG:HB3	0.63	1.53	14	1
1:A:427:SER:CB	2:B:904:LEU:HD11	0.63	2.23	4	1
1:A:397:LEU:HG	1:A:398:SER:N	0.63	2.09	6	2
1:A:445:ARG:HD2	1:A:451:ASN:HB2	0.63	1.71	2	1
1:A:398:SER:HA	1:A:414:LYS:N	0.62	2.08	11	9
1:A:394:VAL:HG23	1:A:416:THR:O	0.62	1.93	7	1
1:A:400:GLY:HA3	1:A:409:THR:O	0.62	1.93	12	13
1:A:429:ALA:N	1:A:467:ARG:N	0.62	2.47	14	1
1:A:397:LEU:H	1:A:414:LYS:HB3	0.62	1.54	8	1
1:A:430:GLU:N	1:A:466:PRO:O	0.62	2.32	14	1
1:A:404:MET:HG3	2:B:905:LEU:HD21	0.62	1.69	15	1
1:A:436:VAL:HB	1:A:462:ILE:HD11	0.62	1.70	13	3
1:A:399:LEU:HD11	1:A:484:LEU:HD22	0.62	1.71	5	2
1:A:469:MET:N	1:A:470:PRO:HD2	0.62	2.09	9	3
1:A:466:PRO:O	1:A:467:ARG:HB2	0.62	1.93	14	1
1:A:445:ARG:CZ	1:A:451:ASN:HB2	0.61	2.25	15	1
1:A:476:PHE:HB3	1:A:484:LEU:HD11	0.61	1.71	8	8
1:A:432:ASN:HA	1:A:464:PRO:HA	0.61	1.71	13	3
1:A:471:GLN:O	1:A:490:ASP:HA	0.61	1.96	12	1
1:A:401:ILE:HG12	1:A:411:LEU:HD23	0.61	1.72	8	7
1:A:464:PRO:HD2	1:A:466:PRO:HD3	0.61	1.72	10	1
1:A:435:ALA:HB1	1:A:459:LEU:O	0.61	1.96	14	5
1:A:429:ALA:HB3	2:B:905:LEU:HB2	0.61	1.71	2	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:429:ALA:O	1:A:430:GLU:HB2	0.61	1.96	14	3
1:A:418:ILE:HB	1:A:419:PRO:HD3	0.61	1.71	11	8
1:A:435:ALA:HA	1:A:460:ASP:HA	0.61	1.72	13	7
1:A:448:ALA:HA	1:A:451:ASN:ND2	0.61	2.10	3	1
1:A:479:ASP:HB2	1:A:483:ILE:HD12	0.60	1.72	11	2
1:A:429:ALA:HB3	2:B:905:LEU:HB3	0.60	1.71	13	1
1:A:412:ILE:HG12	1:A:420:THR:HG21	0.60	1.72	1	2
1:A:398:SER:HA	1:A:413:ALA:HA	0.60	1.72	1	12
1:A:436:VAL:HG12	1:A:459:LEU:CB	0.60	2.27	15	4
1:A:448:ALA:O	1:A:450:ASP:N	0.59	2.34	7	1
1:A:491:LYS:HD3	1:A:493:SER:H	0.59	1.57	5	1
1:A:488:ALA:O	1:A:496:GLU:HB3	0.59	1.98	9	1
1:A:421:LYS:HA	1:A:476:PHE:O	0.59	1.97	15	12
1:A:404:MET:N	2:B:904:LEU:HA	0.59	2.12	4	2
1:A:452:LYS:HG3	1:A:454:LEU:HB3	0.59	1.74	13	1
1:A:398:SER:HA	1:A:414:LYS:H	0.59	1.58	1	7
1:A:459:LEU:HD13	1:A:488:ALA:O	0.59	1.98	12	1
1:A:465:ALA:H	1:A:466:PRO:HD2	0.59	1.56	7	1
1:A:440:VAL:C	1:A:454:LEU:HD12	0.59	2.18	6	9
1:A:431:ASP:O	1:A:464:PRO:HB2	0.59	1.98	14	1
1:A:432:ASN:HB3	1:A:463:ASN:O	0.59	1.98	15	1
1:A:476:PHE:HA	1:A:485:HIS:O	0.59	1.97	10	11
1:A:475:THR:HB	1:A:487:SER:OG	0.58	1.98	14	3
1:A:463:ASN:HB2	1:A:464:PRO:HD3	0.58	1.75	5	2
1:A:489:LYS:HD3	1:A:495:LYS:HA	0.58	1.75	9	1
1:A:463:ASN:N	1:A:464:PRO:HD3	0.58	2.13	10	1
1:A:430:GLU:HG3	2:B:905:LEU:HG	0.58	1.75	10	1
1:A:432:ASN:ND2	1:A:464:PRO:HD3	0.58	2.13	7	2
1:A:428:THR:HG21	1:A:470:PRO:HG2	0.58	1.76	13	2
1:A:397:LEU:HA	1:A:414:LYS:HD2	0.58	1.74	11	3
1:A:395:THR:CG2	1:A:412:ILE:HG22	0.58	2.29	15	1
1:A:412:ILE:HD13	1:A:478:ILE:CG1	0.57	2.29	15	1
1:A:438:ILE:HG13	1:A:488:ALA:HB2	0.57	1.76	15	6
1:A:395:THR:HB	1:A:413:ALA:HB3	0.57	1.75	15	1
1:A:435:ALA:O	2:B:906:THR:HG21	0.57	1.99	14	1
1:A:399:LEU:HD11	1:A:503:ALA:HB1	0.57	1.76	8	1
1:A:416:THR:HG21	1:A:478:ILE:CD1	0.57	2.27	15	1
1:A:397:LEU:H	1:A:414:LYS:HB2	0.57	1.59	6	1
1:A:442:GLN:HG3	1:A:443:GLY:N	0.57	2.14	6	1
1:A:466:PRO:HA	1:A:470:PRO:HG2	0.57	1.74	3	1
1:A:436:VAL:HA	2:B:906:THR:O	0.57	1.99	10	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:402:GLU:HA	1:A:407:VAL:O	0.57	1.99	8	7
1:A:463:ASN:HB3	1:A:464:PRO:CD	0.57	2.26	14	1
1:A:394:VAL:HG21	1:A:417:THR:HG22	0.57	1.75	15	1
1:A:419:PRO:HA	1:A:478:ILE:O	0.57	2.00	15	1
1:A:399:LEU:HD13	1:A:478:ILE:HD11	0.57	1.77	5	5
1:A:440:VAL:O	1:A:454:LEU:HB2	0.57	1.99	12	10
1:A:472:ILE:HD13	1:A:489:LYS:O	0.57	2.00	13	1
1:A:476:PHE:N	1:A:476:PHE:CD1	0.57	2.73	15	2
1:A:411:LEU:HG	1:A:476:PHE:CZ	0.56	2.35	5	7
1:A:491:LYS:O	1:A:491:LYS:HG2	0.56	1.99	15	2
1:A:427:SER:O	1:A:472:ILE:HD13	0.56	2.00	14	1
1:A:469:MET:HB3	1:A:470:PRO:HD3	0.56	1.77	3	7
1:A:397:LEU:CG	1:A:398:SER:N	0.56	2.66	8	2
1:A:466:PRO:HD2	1:A:470:PRO:HD3	0.56	1.77	8	1
1:A:465:ALA:O	1:A:466:PRO:O	0.56	2.22	14	1
1:A:412:ILE:HG23	1:A:416:THR:HG21	0.56	1.76	1	1
1:A:418:ILE:HG21	1:A:480:ALA:HA	0.56	1.76	6	7
1:A:422:HIS:O	1:A:475:THR:HA	0.56	2.01	12	12
1:A:438:ILE:O	1:A:457:PHE:HB2	0.56	2.01	2	1
1:A:412:ILE:HD13	1:A:478:ILE:HG13	0.56	1.77	15	3
1:A:445:ARG:NH1	1:A:448:ALA:HA	0.56	2.14	15	1
1:A:432:ASN:C	1:A:465:ALA:O	0.56	2.43	14	1
1:A:416:THR:HG23	1:A:482:GLY:HA2	0.56	1.76	15	1
1:A:440:VAL:HB	1:A:454:LEU:CD1	0.56	2.30	11	7
1:A:442:GLN:CB	1:A:454:LEU:HD11	0.56	2.30	11	1
1:A:459:LEU:HD13	1:A:488:ALA:HB3	0.56	1.77	3	3
1:A:441:LEU:HD22	1:A:448:ALA:HB1	0.56	1.77	10	1
1:A:478:ILE:HA	1:A:483:ILE:O	0.56	2.00	15	2
1:A:399:LEU:HA	1:A:442:GLN:CB	0.56	2.31	11	1
1:A:411:LEU:HG	1:A:476:PHE:CE1	0.55	2.37	10	5
1:A:491:LYS:HB3	1:A:494:GLY:N	0.55	2.15	5	1
1:A:487:SER:HB2	1:A:498:LYS:HB3	0.55	1.77	12	1
1:A:489:LYS:CB	1:A:496:GLU:HA	0.55	2.26	12	1
1:A:486:VAL:N	1:A:499:ILE:HG22	0.55	2.16	13	1
1:A:465:ALA:HB1	1:A:466:PRO:HD2	0.55	1.78	15	1
1:A:394:VAL:HG22	1:A:395:THR:H	0.55	1.61	7	1
1:A:443:GLY:O	1:A:450:ASP:HB2	0.55	2.01	11	1
1:A:476:PHE:CE2	1:A:486:VAL:HG13	0.55	2.37	12	1
1:A:472:ILE:HD12	1:A:488:ALA:HB1	0.55	1.79	11	1
1:A:477:ASP:HB3	1:A:485:HIS:NE2	0.55	2.15	5	1
1:A:428:THR:HG22	1:A:467:ARG:H	0.55	1.61	14	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:442:GLN:HG2	1:A:442:GLN:O	0.54	2.02	11	3
1:A:440:VAL:CG1	1:A:486:VAL:HG21	0.54	2.28	15	2
1:A:465:ALA:N	1:A:466:PRO:HD3	0.54	2.17	9	3
1:A:459:LEU:HD13	1:A:460:ASP:H	0.54	1.62	1	3
1:A:440:VAL:HG23	1:A:455:GLY:O	0.54	2.03	9	1
1:A:491:LYS:HB2	1:A:495:LYS:H	0.54	1.63	5	1
1:A:442:GLN:HG2	1:A:452:LYS:N	0.54	2.17	6	1
1:A:426:PHE:CD1	2:B:904:LEU:HD11	0.54	2.38	12	2
1:A:433:GLN:HA	1:A:466:PRO:N	0.54	2.17	14	1
1:A:440:VAL:HG21	1:A:486:VAL:HG21	0.54	1.80	9	2
1:A:476:PHE:CD2	1:A:484:LEU:HD11	0.54	2.37	4	1
1:A:425:VAL:HG23	1:A:472:ILE:O	0.54	2.03	14	1
1:A:463:ASN:HB3	1:A:464:PRO:HD2	0.54	1.78	1	2
1:A:404:MET:C	2:B:905:LEU:HB2	0.54	2.22	10	2
1:A:433:GLN:OE1	1:A:466:PRO:HD2	0.53	2.02	10	1
1:A:397:LEU:HD23	1:A:442:GLN:HG2	0.53	1.80	10	1
1:A:423:SER:HA	1:A:474:VAL:O	0.53	2.03	6	4
1:A:436:VAL:HG21	1:A:472:ILE:HG13	0.53	1.78	4	2
1:A:447:ARG:O	1:A:449:ALA:N	0.53	2.41	6	1
1:A:469:MET:H	1:A:470:PRO:HD2	0.53	1.62	14	2
1:A:445:ARG:O	1:A:449:ALA:HA	0.53	2.04	7	1
1:A:432:ASN:HA	1:A:463:ASN:O	0.53	2.04	4	3
1:A:441:LEU:CB	1:A:450:ASP:HB3	0.53	2.34	7	1
1:A:434:SER:HB2	1:A:463:ASN:O	0.53	2.04	14	1
1:A:463:ASN:CB	1:A:464:PRO:HD3	0.53	2.31	14	1
1:A:466:PRO:HG2	2:B:906:THR:H	0.53	1.64	14	1
1:A:408:MET:HG2	1:A:451:ASN:HD21	0.53	1.64	5	1
1:A:441:LEU:HB3	1:A:450:ASP:CB	0.53	2.33	7	1
1:A:398:SER:O	1:A:442:GLN:HG3	0.53	2.04	1	2
1:A:448:ALA:HA	1:A:451:ASN:HD21	0.53	1.64	5	2
1:A:445:ARG:HG2	1:A:451:ASN:HD22	0.53	1.63	9	1
1:A:462:ILE:HD12	2:B:907:GLY:HA2	0.53	1.81	8	1
1:A:472:ILE:HD13	1:A:472:ILE:N	0.53	2.18	5	1
1:A:399:LEU:HD21	1:A:484:LEU:HD22	0.52	1.80	4	1
1:A:491:LYS:HE3	1:A:492:ASN:N	0.52	2.19	13	1
1:A:430:GLU:HG3	2:B:905:LEU:HD21	0.52	1.81	12	1
1:A:433:GLN:HG3	2:B:906:THR:HG23	0.52	1.80	13	1
1:A:427:SER:HB3	1:A:436:VAL:HG21	0.52	1.81	13	1
1:A:403:THR:HB	2:B:903:LEU:O	0.52	2.05	1	4
1:A:431:ASP:C	1:A:465:ALA:O	0.52	2.47	14	1
1:A:426:PHE:HA	1:A:471:GLN:HG2	0.52	1.81	4	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:401:ILE:O	1:A:409:THR:N	0.52	2.43	10	3
1:A:397:LEU:HD23	1:A:398:SER:N	0.52	2.19	15	2
1:A:463:ASN:H	1:A:463:ASN:ND2	0.52	2.02	5	1
1:A:408:MET:CG	1:A:449:ALA:HB3	0.52	2.34	7	1
1:A:431:ASP:O	1:A:432:ASN:HB2	0.52	2.04	4	6
1:A:443:GLY:HA3	1:A:451:ASN:ND2	0.52	2.20	2	1
1:A:408:MET:HG2	1:A:451:ASN:ND2	0.52	2.20	5	1
1:A:489:LYS:HE2	1:A:495:LYS:HB3	0.52	1.81	9	1
1:A:496:GLU:HG3	1:A:497:GLN:N	0.52	2.20	9	1
1:A:400:GLY:O	1:A:441:LEU:O	0.52	2.28	7	7
1:A:427:SER:HB3	2:B:904:LEU:HD11	0.52	1.81	4	1
1:A:489:LYS:HG3	1:A:490:ASP:N	0.52	2.20	13	2
1:A:444:GLU:C	1:A:445:ARG:HG2	0.51	2.25	10	2
1:A:441:LEU:HD22	1:A:451:ASN:HD21	0.51	1.64	4	1
1:A:407:VAL:O	1:A:441:LEU:HD23	0.51	2.05	6	1
1:A:429:ALA:HB3	2:B:905:LEU:CA	0.51	2.36	3	1
1:A:451:ASN:CG	1:A:452:LYS:H	0.51	2.09	11	1
1:A:397:LEU:O	1:A:414:LYS:HD2	0.51	2.05	8	1
1:A:462:ILE:HG22	1:A:465:ALA:HB2	0.51	1.81	8	1
1:A:408:MET:HB3	1:A:448:ALA:N	0.51	2.20	2	1
1:A:491:LYS:HB2	1:A:495:LYS:N	0.51	2.20	5	1
1:A:395:THR:HB	1:A:414:LYS:CB	0.51	2.33	6	1
1:A:397:LEU:HD21	1:A:442:GLN:NE2	0.51	2.19	6	1
1:A:498:LYS:C	1:A:499:ILE:HD13	0.51	2.25	13	1
1:A:429:ALA:HA	1:A:467:ARG:HA	0.51	1.81	14	1
1:A:476:PHE:CD1	1:A:476:PHE:N	0.51	2.79	10	7
1:A:496:GLU:HG2	1:A:497:GLN:N	0.51	2.21	5	1
1:A:499:ILE:HG13	1:A:500:THR:N	0.51	2.18	5	1
1:A:489:LYS:HD3	1:A:495:LYS:O	0.51	2.04	12	1
1:A:466:PRO:HG3	2:B:906:THR:HG23	0.51	1.81	14	1
1:A:472:ILE:HD12	1:A:490:ASP:OD1	0.51	2.06	5	1
1:A:477:ASP:N	1:A:485:HIS:HB2	0.51	2.20	13	1
1:A:420:THR:O	1:A:477:ASP:HA	0.51	2.05	5	5
1:A:408:MET:CG	1:A:450:ASP:HB3	0.51	2.35	11	1
1:A:399:LEU:HD22	1:A:478:ILE:HD11	0.51	1.81	11	1
1:A:479:ASP:HB2	1:A:483:ILE:HB	0.51	1.82	15	1
1:A:442:GLN:O	1:A:452:LYS:HB3	0.50	2.05	11	3
1:A:459:LEU:HD13	1:A:460:ASP:N	0.50	2.21	2	2
1:A:440:VAL:HB	1:A:454:LEU:HD13	0.50	1.82	3	8
1:A:491:LYS:C	1:A:491:LYS:HE3	0.50	2.27	10	2
1:A:462:ILE:O	1:A:464:PRO:HD2	0.50	2.06	14	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:410:THR:C	1:A:411:LEU:HD22	0.50	2.27	15	1
1:A:479:ASP:C	1:A:481:ASP:H	0.50	2.10	15	1
1:A:486:VAL:O	1:A:498:LYS:O	0.50	2.30	13	1
1:A:459:LEU:HD11	1:A:496:GLU:HG2	0.50	1.82	9	1
1:A:442:GLN:HB2	1:A:454:LEU:HD21	0.50	1.82	10	1
1:A:500:THR:O	1:A:501:ILE:HD13	0.50	2.07	13	1
1:A:433:GLN:HG3	1:A:466:PRO:CA	0.50	2.36	14	1
1:A:398:SER:O	1:A:443:GLY:N	0.50	2.45	10	8
1:A:437:THR:OG1	2:B:906:THR:HA	0.50	2.07	15	4
1:A:489:LYS:HD3	1:A:490:ASP:N	0.50	2.22	15	1
1:A:473:GLU:HB3	1:A:489:LYS:HB3	0.50	1.83	10	1
1:A:396:PRO:O	1:A:397:LEU:HB2	0.50	2.05	6	1
1:A:478:ILE:HD13	1:A:484:LEU:HB2	0.50	1.83	8	4
1:A:462:ILE:HB	2:B:907:GLY:O	0.50	2.07	8	1
1:A:433:GLN:HA	1:A:465:ALA:C	0.50	2.27	14	1
1:A:441:LEU:HD22	1:A:451:ASN:HB2	0.50	1.82	12	1
1:A:440:VAL:O	1:A:454:LEU:HD12	0.50	2.07	6	1
1:A:394:VAL:CG2	1:A:417:THR:HG22	0.50	2.37	15	1
1:A:394:VAL:O	1:A:416:THR:HA	0.50	2.07	15	1
1:A:412:ILE:HD11	1:A:476:PHE:CB	0.49	2.33	6	1
1:A:432:ASN:O	1:A:433:GLN:C	0.49	2.50	8	1
1:A:473:GLU:HB2	1:A:489:LYS:HG2	0.49	1.83	7	1
1:A:397:LEU:HD23	1:A:442:GLN:CD	0.49	2.28	11	1
1:A:418:ILE:HG23	1:A:478:ILE:HG22	0.49	1.85	11	1
1:A:395:THR:CG2	1:A:416:THR:HB	0.49	2.36	15	1
1:A:481:ASP:HB3	1:A:483:ILE:HD11	0.49	1.85	11	1
1:A:471:GLN:HB3	1:A:491:LYS:HB2	0.49	1.83	1	1
1:A:489:LYS:HA	1:A:496:GLU:N	0.49	2.20	9	1
1:A:434:SER:HA	1:A:462:ILE:H	0.49	1.67	2	1
1:A:490:ASP:HB2	1:A:494:GLY:O	0.49	2.07	15	1
1:A:440:VAL:HB	1:A:454:LEU:CD2	0.49	2.38	10	1
1:A:417:THR:O	1:A:480:ALA:HA	0.49	2.07	15	1
1:A:440:VAL:CB	1:A:454:LEU:HB2	0.49	2.30	10	1
1:A:399:LEU:CD1	1:A:442:GLN:HG3	0.49	2.35	11	1
2:B:903:LEU:O	2:B:904:LEU:HD22	0.49	2.08	13	2
1:A:400:GLY:O	1:A:441:LEU:N	0.49	2.46	10	8
1:A:448:ALA:O	1:A:449:ALA:C	0.49	2.51	7	1
1:A:431:ASP:HA	1:A:466:PRO:HB2	0.49	1.83	7	1
1:A:472:ILE:HG21	1:A:488:ALA:HB1	0.49	1.85	4	1
1:A:404:MET:HA	2:B:905:LEU:H	0.49	1.68	11	2
1:A:461:GLY:C	1:A:462:ILE:HG13	0.49	2.28	14	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:429:ALA:O	1:A:430:GLU:CB	0.49	2.61	14	1
1:A:434:SER:HB2	1:A:463:ASN:H	0.49	1.68	12	1
1:A:438:ILE:HD13	2:B:904:LEU:HD21	0.48	1.85	3	1
1:A:489:LYS:HD2	1:A:494:GLY:HA2	0.48	1.85	10	1
1:A:443:GLY:HA3	1:A:451:ASN:CG	0.48	2.29	2	2
1:A:465:ALA:N	1:A:466:PRO:CD	0.48	2.76	7	1
1:A:447:ARG:O	1:A:448:ALA:HB3	0.48	2.09	11	1
1:A:401:ILE:CG2	1:A:440:VAL:HG13	0.48	2.37	10	1
1:A:429:ALA:HB3	2:B:905:LEU:HG	0.48	1.85	7	1
1:A:397:LEU:HB3	1:A:414:LYS:HG3	0.48	1.84	6	1
1:A:443:GLY:N	1:A:450:ASP:HA	0.48	2.22	7	1
1:A:401:ILE:HG23	1:A:411:LEU:HD22	0.48	1.84	6	1
1:A:466:PRO:HG2	1:A:469:MET:HB2	0.48	1.85	8	1
1:A:442:GLN:HG3	1:A:442:GLN:O	0.48	2.09	3	1
1:A:465:ALA:N	1:A:466:PRO:HD2	0.48	2.23	7	1
1:A:433:GLN:OE1	1:A:462:ILE:HB	0.48	2.09	11	2
1:A:440:VAL:HG22	1:A:454:LEU:HG	0.48	1.86	13	1
1:A:476:PHE:CB	1:A:484:LEU:HD11	0.48	2.37	8	2
1:A:471:GLN:C	1:A:472:ILE:HD13	0.48	2.29	5	1
1:A:434:SER:O	1:A:462:ILE:HG13	0.48	2.09	4	1
1:A:443:GLY:HA3	1:A:450:ASP:O	0.48	2.07	7	1
1:A:431:ASP:N	1:A:466:PRO:O	0.48	2.47	14	1
1:A:429:ALA:H	1:A:466:PRO:HB3	0.48	1.68	14	1
1:A:416:THR:OG1	1:A:478:ILE:HG21	0.48	2.08	15	1
1:A:433:GLN:O	1:A:435:ALA:N	0.47	2.47	8	2
1:A:481:ASP:HB2	1:A:483:ILE:HD11	0.47	1.85	1	1
1:A:431:ASP:HA	1:A:465:ALA:O	0.47	2.09	6	4
1:A:425:VAL:HG21	1:A:471:GLN:HG2	0.47	1.86	14	1
1:A:445:ARG:O	1:A:446:LYS:HB2	0.47	2.09	6	1
1:A:464:PRO:O	1:A:466:PRO:HD3	0.47	2.09	13	2
1:A:395:THR:HG21	1:A:412:ILE:CG2	0.47	2.35	15	1
1:A:428:THR:HB	1:A:468:GLY:N	0.47	2.23	14	1
1:A:457:PHE:HZ	1:A:501:ILE:HD11	0.47	1.68	5	1
1:A:436:VAL:HG22	2:B:904:LEU:HD13	0.47	1.84	4	1
1:A:395:THR:O	1:A:414:LYS:HA	0.47	2.08	8	1
1:A:483:ILE:HG22	1:A:484:LEU:N	0.47	2.25	15	1
1:A:408:MET:HG3	1:A:408:MET:O	0.47	2.09	14	1
1:A:442:GLN:CG	1:A:443:GLY:N	0.47	2.78	6	1
1:A:476:PHE:HB3	1:A:485:HIS:O	0.47	2.09	13	1
1:A:436:VAL:HG23	2:B:907:GLY:HA2	0.47	1.86	10	1
1:A:467:ARG:O	1:A:469:MET:N	0.47	2.47	14	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:430:GLU:O	1:A:433:GLN:HG2	0.47	2.09	15	2
1:A:401:ILE:O	1:A:409:THR:HB	0.47	2.09	12	2
1:A:463:ASN:CB	1:A:464:PRO:HD2	0.47	2.40	13	1
1:A:471:GLN:O	1:A:489:LYS:O	0.47	2.32	5	1
1:A:398:SER:HB3	1:A:443:GLY:O	0.47	2.10	15	1
1:A:432:ASN:H	1:A:467:ARG:CB	0.47	2.23	14	1
1:A:408:MET:HB2	1:A:448:ALA:HB2	0.47	1.86	2	1
1:A:424:GLN:O	1:A:474:VAL:HG23	0.46	2.10	14	2
1:A:457:PHE:CE1	1:A:486:VAL:HB	0.46	2.44	14	1
1:A:399:LEU:CD1	1:A:478:ILE:HD11	0.46	2.40	12	1
1:A:439:HIS:CD2	1:A:441:LEU:HD13	0.46	2.45	11	1
1:A:491:LYS:HB2	1:A:496:GLU:HB3	0.46	1.87	12	1
1:A:440:VAL:O	1:A:454:LEU:N	0.46	2.48	7	2
1:A:394:VAL:HG21	1:A:415:ASN:N	0.46	2.25	7	1
1:A:408:MET:SD	1:A:447:ARG:HA	0.46	2.51	6	1
1:A:399:LEU:HD23	1:A:400:GLY:N	0.46	2.25	12	3
1:A:429:ALA:H	1:A:466:PRO:CB	0.46	2.22	14	1
1:A:470:PRO:HA	1:A:491:LYS:HD2	0.46	1.88	13	1
1:A:434:SER:HA	1:A:462:ILE:C	0.46	2.31	4	2
1:A:429:ALA:HB2	2:B:903:LEU:HB3	0.46	1.85	4	2
1:A:441:LEU:HB3	1:A:450:ASP:OD1	0.46	2.11	11	1
1:A:430:GLU:HB2	2:B:905:LEU:HG	0.46	1.85	11	1
1:A:440:VAL:CG2	1:A:454:LEU:HG	0.46	2.40	13	1
1:A:428:THR:HG22	1:A:470:PRO:HG2	0.46	1.87	1	1
1:A:420:THR:CG2	1:A:478:ILE:HG13	0.46	2.40	15	1
1:A:426:PHE:CE1	2:B:904:LEU:HD11	0.46	2.46	12	1
1:A:476:PHE:CD1	1:A:486:VAL:HA	0.46	2.46	9	1
1:A:412:ILE:CG2	1:A:420:THR:HG21	0.46	2.41	10	2
1:A:474:VAL:HG12	1:A:476:PHE:CE2	0.46	2.46	14	1
1:A:443:GLY:O	1:A:450:ASP:HA	0.46	2.10	7	1
1:A:394:VAL:HG11	1:A:414:LYS:HG3	0.46	1.88	7	1
1:A:433:GLN:HG3	1:A:466:PRO:HA	0.46	1.87	14	1
1:A:489:LYS:HD3	1:A:494:GLY:HA2	0.46	1.87	5	1
1:A:484:LEU:O	1:A:501:ILE:HD12	0.46	2.10	5	1
1:A:434:SER:O	1:A:460:ASP:HA	0.46	2.10	9	1
1:A:434:SER:HB2	1:A:464:PRO:O	0.46	2.10	14	1
1:A:440:VAL:O	1:A:454:LEU:HD22	0.46	2.10	10	1
1:A:442:GLN:O	1:A:442:GLN:HG3	0.46	2.11	4	1
1:A:440:VAL:HG23	1:A:454:LEU:HD21	0.46	1.87	13	1
1:A:463:ASN:O	1:A:465:ALA:N	0.46	2.49	13	3
1:A:430:GLU:H	1:A:433:GLN:HE22	0.46	1.53	10	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:469:MET:N	1:A:470:PRO:CD	0.46	2.79	9	2
1:A:416:THR:HG23	1:A:417:THR:N	0.45	2.26	7	1
1:A:491:LYS:HD3	1:A:496:GLU:OE1	0.45	2.11	12	1
1:A:438:ILE:HB	1:A:457:PHE:CE2	0.45	2.45	12	1
1:A:397:LEU:C	1:A:414:LYS:HB2	0.45	2.32	6	1
1:A:471:GLN:H	1:A:491:LYS:HD3	0.45	1.71	13	1
1:A:439:HIS:CE1	1:A:441:LEU:HD13	0.45	2.46	7	1
1:A:398:SER:CA	1:A:413:ALA:HA	0.45	2.42	12	7
1:A:427:SER:OG	2:B:904:LEU:HG	0.45	2.11	13	1
1:A:484:LEU:O	1:A:501:ILE:HG12	0.45	2.11	13	1
1:A:435:ALA:CB	1:A:459:LEU:O	0.45	2.65	14	1
1:A:428:THR:O	2:B:903:LEU:HB3	0.45	2.12	4	1
1:A:417:THR:OG1	1:A:419:PRO:HD2	0.45	2.12	11	1
2:B:906:THR:OG1	2:B:907:GLY:N	0.45	2.49	3	1
1:A:407:VAL:HG12	1:A:447:ARG:HA	0.45	1.87	10	1
1:A:433:GLN:HG3	1:A:466:PRO:CD	0.45	2.41	14	1
1:A:433:GLN:OE1	2:B:906:THR:HG23	0.45	2.11	15	1
1:A:399:LEU:HD23	1:A:484:LEU:HD22	0.45	1.87	3	1
1:A:500:THR:C	1:A:501:ILE:HG13	0.45	2.32	10	1
1:A:472:ILE:HG23	1:A:489:LYS:O	0.45	2.11	4	1
1:A:399:LEU:CD2	1:A:478:ILE:HD11	0.45	2.42	11	1
1:A:397:LEU:N	1:A:414:LYS:HD2	0.45	2.26	8	1
1:A:433:GLN:HB3	2:B:907:GLY:N	0.45	2.27	8	1
1:A:399:LEU:HG	1:A:442:GLN:HB2	0.44	1.88	11	1
1:A:429:ALA:O	1:A:466:PRO:HB2	0.44	2.12	14	1
1:A:430:GLU:CA	1:A:466:PRO:O	0.44	2.65	14	1
1:A:409:THR:CG2	1:A:410:THR:N	0.44	2.80	12	1
1:A:465:ALA:H	1:A:466:PRO:CD	0.44	2.25	7	1
1:A:402:GLU:HG2	1:A:406:GLY:H	0.44	1.72	8	1
1:A:433:GLN:HB3	1:A:462:ILE:CD1	0.44	2.42	14	1
1:A:397:LEU:CA	1:A:414:LYS:HD2	0.44	2.43	8	1
1:A:433:GLN:CG	1:A:466:PRO:HA	0.44	2.43	14	1
1:A:408:MET:N	1:A:448:ALA:HB2	0.44	2.28	12	2
1:A:425:VAL:HA	1:A:472:ILE:O	0.44	2.12	13	1
1:A:459:LEU:HD21	1:A:496:GLU:CD	0.44	2.33	9	1
1:A:441:LEU:HG	1:A:450:ASP:HB3	0.44	1.89	7	1
1:A:429:ALA:CB	2:B:905:LEU:HB3	0.44	2.41	13	1
1:A:433:GLN:O	1:A:434:SER:C	0.44	2.55	8	2
1:A:417:THR:H	1:A:418:ILE:HG23	0.44	1.72	15	1
1:A:408:MET:SD	1:A:441:LEU:HD12	0.44	2.53	2	1
1:A:433:GLN:C	1:A:435:ALA:H	0.44	2.16	5	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:428:THR:HG22	1:A:466:PRO:HA	0.44	1.89	15	1
1:A:418:ILE:N	1:A:419:PRO:HD2	0.44	2.27	12	2
1:A:462:ILE:O	1:A:463:ASN:O	0.44	2.36	3	1
1:A:496:GLU:CG	1:A:497:GLN:N	0.44	2.81	9	1
1:A:397:LEU:CG	1:A:398:SER:H	0.44	2.13	6	1
1:A:433:GLN:C	1:A:435:ALA:N	0.44	2.70	12	5
1:A:397:LEU:HB2	1:A:414:LYS:CD	0.44	2.37	15	1
1:A:399:LEU:N	1:A:413:ALA:HA	0.44	2.28	15	1
1:A:462:ILE:C	1:A:464:PRO:HD3	0.44	2.33	10	1
1:A:399:LEU:HB2	1:A:412:ILE:O	0.44	2.13	11	2
1:A:439:HIS:ND1	1:A:456:GLN:HB2	0.44	2.27	6	1
1:A:486:VAL:O	1:A:498:LYS:HA	0.44	2.12	6	3
1:A:395:THR:HG21	1:A:412:ILE:HG21	0.44	1.89	1	1
1:A:408:MET:HG3	1:A:448:ALA:CA	0.44	2.43	10	1
1:A:441:LEU:HD22	1:A:451:ASN:ND2	0.44	2.27	4	1
1:A:432:ASN:HB2	1:A:464:PRO:HB2	0.44	1.89	14	1
1:A:430:GLU:O	1:A:433:GLN:HG3	0.44	2.13	5	1
1:A:442:GLN:CG	1:A:442:GLN:O	0.43	2.65	11	1
1:A:450:ASP:O	1:A:451:ASN:HB3	0.43	2.13	11	1
1:A:397:LEU:CB	1:A:414:LYS:HE2	0.43	2.39	6	1
1:A:500:THR:C	1:A:501:ILE:HD13	0.43	2.32	13	1
1:A:408:MET:CE	1:A:441:LEU:HD12	0.43	2.43	13	1
1:A:451:ASN:CG	1:A:452:LYS:N	0.43	2.71	11	2
1:A:487:SER:CA	1:A:498:LYS:O	0.43	2.66	13	1
1:A:396:PRO:HA	1:A:414:LYS:HB2	0.43	1.89	8	1
1:A:448:ALA:O	1:A:449:ALA:HB3	0.43	2.13	11	1
1:A:435:ALA:CA	1:A:459:LEU:O	0.43	2.64	8	1
1:A:411:LEU:HG	1:A:476:PHE:CE2	0.43	2.49	9	1
1:A:454:LEU:O	1:A:501:ILE:HG21	0.43	2.14	10	1
1:A:428:THR:HG21	1:A:466:PRO:HB3	0.43	1.91	7	1
1:A:394:VAL:HG12	1:A:417:THR:HA	0.43	1.91	11	1
1:A:398:SER:HB3	1:A:414:LYS:HD3	0.43	1.89	13	1
1:A:402:GLU:HG2	1:A:439:HIS:ND1	0.43	2.27	10	1
1:A:394:VAL:HG13	1:A:395:THR:N	0.43	2.28	7	1
1:A:442:GLN:HB3	1:A:452:LYS:O	0.43	2.14	6	1
1:A:394:VAL:HG12	1:A:416:THR:O	0.43	2.13	2	1
1:A:467:ARG:HD3	2:B:903:LEU:HD21	0.43	1.91	13	1
2:B:905:LEU:HG	2:B:906:THR:N	0.43	2.29	14	1
1:A:408:MET:HB2	1:A:441:LEU:HG	0.43	1.90	1	1
1:A:462:ILE:HG21	1:A:470:PRO:HB3	0.43	1.91	1	1
1:A:459:LEU:HG	1:A:488:ALA:HB3	0.43	1.89	15	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:489:LYS:CE	1:A:495:LYS:HA	0.43	2.43	15	1
1:A:434:SER:HA	1:A:462:ILE:HB	0.43	1.91	12	1
1:A:485:HIS:HA	1:A:499:ILE:O	0.43	2.13	9	1
1:A:430:GLU:N	1:A:433:GLN:NE2	0.42	2.67	10	1
1:A:428:THR:CG2	1:A:466:PRO:HB3	0.42	2.44	7	1
1:A:437:THR:OG1	2:B:906:THR:HG23	0.42	2.14	7	1
1:A:441:LEU:HD21	1:A:448:ALA:HB1	0.42	1.90	11	1
1:A:474:VAL:HB	1:A:476:PHE:HE1	0.42	1.74	6	1
1:A:457:PHE:HD2	1:A:498:LYS:HB3	0.42	1.74	13	1
1:A:402:GLU:HG3	1:A:407:VAL:O	0.42	2.14	8	1
1:A:434:SER:HA	1:A:463:ASN:N	0.42	2.28	3	1
1:A:436:VAL:CA	2:B:907:GLY:HA2	0.42	2.43	10	1
1:A:402:GLU:N	1:A:439:HIS:O	0.42	2.51	14	2
1:A:444:GLU:HG3	1:A:450:ASP:HB3	0.42	1.89	6	1
1:A:457:PHE:CD2	1:A:498:LYS:HB3	0.42	2.49	13	1
1:A:472:ILE:HG13	1:A:489:LYS:O	0.42	2.14	9	1
1:A:451:ASN:OD1	1:A:451:ASN:N	0.42	2.51	4	1
1:A:487:SER:HA	1:A:498:LYS:O	0.42	2.13	13	1
1:A:428:THR:HG22	1:A:467:ARG:N	0.42	2.29	14	1
1:A:401:ILE:HG12	1:A:411:LEU:CD2	0.42	2.44	5	2
1:A:467:ARG:H	1:A:469:MET:HE2	0.42	1.75	5	1
1:A:436:VAL:HG12	1:A:459:LEU:HB2	0.42	1.92	9	1
1:A:428:THR:HG23	1:A:465:ALA:HB1	0.42	1.91	13	1
1:A:428:THR:CG2	1:A:429:ALA:N	0.42	2.81	15	1
1:A:398:SER:N	1:A:414:LYS:CG	0.42	2.77	6	1
1:A:431:ASP:O	1:A:432:ASN:CB	0.42	2.68	5	1
1:A:483:ILE:HG22	1:A:484:LEU:H	0.42	1.73	15	1
1:A:426:PHE:HE1	2:B:902:ARG:HB2	0.42	1.74	15	1
1:A:428:THR:HG23	1:A:429:ALA:N	0.42	2.29	11	1
1:A:401:ILE:CG2	1:A:411:LEU:HD22	0.42	2.44	6	1
1:A:432:ASN:CB	1:A:464:PRO:HD2	0.42	2.44	14	1
1:A:462:ILE:HG12	1:A:490:ASP:OD2	0.42	2.14	15	1
1:A:411:LEU:HD22	1:A:476:PHE:CD1	0.42	2.50	12	1
1:A:476:PHE:CE1	1:A:486:VAL:HG13	0.42	2.50	9	1
1:A:437:THR:O	2:B:904:LEU:HD22	0.42	2.15	4	1
1:A:433:GLN:HB3	1:A:462:ILE:HD12	0.42	1.91	14	1
1:A:442:GLN:HB3	1:A:452:LYS:H	0.42	1.75	6	1
1:A:397:LEU:C	1:A:414:LYS:HB3	0.42	2.34	13	1
1:A:427:SER:O	2:B:903:LEU:HA	0.42	2.14	2	2
1:A:408:MET:CB	1:A:448:ALA:HB2	0.42	2.45	3	2
1:A:414:LYS:CG	1:A:415:ASN:N	0.42	2.82	15	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:463:ASN:HB2	1:A:464:PRO:HD2	0.42	1.92	3	1
2:B:904:LEU:C	2:B:906:THR:H	0.42	2.18	3	1
1:A:426:PHE:O	1:A:426:PHE:CG	0.42	2.73	4	1
1:A:475:THR:O	1:A:486:VAL:HA	0.42	2.15	5	1
1:A:412:ILE:HG22	1:A:416:THR:HG21	0.41	1.92	7	1
1:A:397:LEU:N	1:A:414:LYS:HG3	0.41	2.30	11	1
1:A:484:LEU:HB2	1:A:501:ILE:O	0.41	2.15	11	1
1:A:499:ILE:N	1:A:499:ILE:HD13	0.41	2.29	3	1
1:A:432:ASN:HB3	1:A:462:ILE:O	0.41	2.15	14	1
1:A:400:GLY:CA	1:A:410:THR:HA	0.41	2.32	15	1
1:A:420:THR:HG22	1:A:478:ILE:CB	0.41	2.40	15	1
1:A:404:MET:HA	2:B:905:LEU:N	0.41	2.30	10	1
1:A:440:VAL:HB	1:A:454:LEU:HD12	0.41	1.91	11	1
1:A:470:PRO:HG2	1:A:490:ASP:OD1	0.41	2.16	11	1
1:A:471:GLN:HG3	1:A:489:LYS:HE3	0.41	1.91	5	1
1:A:472:ILE:HG23	1:A:490:ASP:OD1	0.41	2.14	5	1
1:A:397:LEU:HB2	1:A:414:LYS:HB3	0.41	1.90	15	1
1:A:443:GLY:HA3	1:A:445:ARG:HE	0.41	1.75	15	1
1:A:412:ILE:HD13	1:A:478:ILE:HG12	0.41	1.92	11	1
1:A:485:HIS:HB3	1:A:499:ILE:CG2	0.41	2.45	13	1
1:A:418:ILE:O	1:A:478:ILE:HB	0.41	2.16	2	2
1:A:445:ARG:HG3	1:A:447:ARG:O	0.41	2.16	15	1
1:A:472:ILE:HG22	1:A:474:VAL:HG22	0.41	1.92	12	1
1:A:427:SER:O	2:B:904:LEU:HD12	0.41	2.16	12	1
1:A:489:LYS:HB2	1:A:495:LYS:CB	0.41	2.44	9	1
1:A:491:LYS:O	1:A:492:ASN:HB2	0.41	2.15	9	1
1:A:442:GLN:HB3	1:A:452:LYS:N	0.41	2.30	6	1
1:A:402:GLU:HG3	1:A:406:GLY:H	0.41	1.74	6	1
1:A:403:THR:HA	2:B:904:LEU:CD1	0.41	2.45	13	1
1:A:429:ALA:O	2:B:905:LEU:HA	0.41	2.16	10	1
1:A:414:LYS:HG3	1:A:414:LYS:H	0.41	1.52	4	1
1:A:427:SER:HB3	1:A:436:VAL:CG2	0.41	2.45	13	1
1:A:489:LYS:HB2	1:A:496:GLU:HB2	0.41	1.92	13	2
1:A:399:LEU:CD1	1:A:484:LEU:HD22	0.41	2.46	13	1
2:B:905:LEU:HG	2:B:907:GLY:H	0.41	1.74	2	1
1:A:451:ASN:HD22	1:A:452:LYS:H	0.41	1.59	1	1
1:A:502:LYS:H	1:A:502:LYS:HG3	0.41	1.55	5	1
1:A:483:ILE:HA	1:A:502:LYS:HA	0.41	1.92	10	1
1:A:463:ASN:O	1:A:464:PRO:C	0.41	2.58	13	2
1:A:457:PHE:CE1	1:A:499:ILE:HD12	0.41	2.51	7	1
1:A:440:VAL:CG2	1:A:455:GLY:O	0.41	2.69	11	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:397:LEU:CA	1:A:414:LYS:HB2	0.41	2.46	6	1
1:A:428:THR:N	2:B:904:LEU:HB2	0.41	2.31	13	1
1:A:397:LEU:HG	1:A:398:SER:OG	0.41	2.16	8	1
1:A:431:ASP:O	1:A:465:ALA:O	0.41	2.39	14	1
1:A:408:MET:O	1:A:408:MET:HG2	0.41	2.13	4	1
1:A:397:LEU:HD23	1:A:442:GLN:NE2	0.41	2.31	11	1
1:A:489:LYS:HB2	1:A:496:GLU:HG3	0.41	1.92	6	1
1:A:474:VAL:HB	1:A:476:PHE:CZ	0.41	2.51	8	1
1:A:439:HIS:CE1	1:A:453:SER:HB3	0.41	2.51	8	1
1:A:433:GLN:C	1:A:462:ILE:HB	0.41	2.36	14	1
2:B:903:LEU:HB3	2:B:904:LEU:H	0.41	1.61	14	1
1:A:418:ILE:HD11	1:A:420:THR:HB	0.41	1.92	15	1
1:A:484:LEU:HG	1:A:485:HIS:N	0.40	2.31	13	1
1:A:410:THR:O	1:A:411:LEU:HD22	0.40	2.16	8	1
1:A:463:ASN:N	1:A:464:PRO:CD	0.40	2.84	15	1
1:A:500:THR:O	1:A:501:ILE:HG13	0.40	2.15	12	1
1:A:432:ASN:H	1:A:466:PRO:HD3	0.40	1.75	9	1
1:A:408:MET:HG3	1:A:449:ALA:CB	0.40	2.46	7	1
1:A:466:PRO:HG2	2:B:906:THR:N	0.40	2.29	14	1
1:A:395:THR:OG1	1:A:416:THR:HG22	0.40	2.16	1	1
1:A:436:VAL:HA	2:B:906:THR:HG22	0.40	1.92	3	1
1:A:428:THR:CG2	1:A:466:PRO:HB2	0.40	2.46	9	1
2:B:902:ARG:HB3	2:B:903:LEU:H	0.40	1.53	9	1
1:A:453:SER:O	1:A:454:LEU:C	0.40	2.59	7	1
1:A:427:SER:HB2	1:A:472:ILE:CB	0.40	2.41	13	1
1:A:427:SER:OG	1:A:427:SER:O	0.40	2.32	14	1
1:A:427:SER:HA	2:B:904:LEU:CD2	0.40	2.41	13	1
1:A:427:SER:OG	2:B:904:LEU:HD12	0.40	2.16	14	1
1:A:477:ASP:O	1:A:484:LEU:HA	0.40	2.17	5	1
1:A:408:MET:HG3	1:A:449:ALA:CA	0.40	2.46	7	1
1:A:430:GLU:HB3	1:A:433:GLN:HG2	0.40	1.92	4	1
1:A:395:THR:CB	1:A:413:ALA:HB3	0.40	2.44	15	1
1:A:418:ILE:O	1:A:478:ILE:O	0.40	2.40	15	1
1:A:491:LYS:C	1:A:493:SER:H	0.40	2.20	12	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	110/135 (81%)	81±4 (74±4%)	20±4 (18±3%)	9±2 (8±2%)	2	14
2	B	5/7 (71%)	3±1 (67±21%)	1±1 (28±18%)	0±1 (5±11%)	4	25
All	All	1725/2130 (81%)	1272 (74%)	315 (18%)	138 (8%)	2	15

All 47 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	405	GLY	11
1	A	492	ASN	10
1	A	461	GLY	9
1	A	467	ARG	8
1	A	450	ASP	7
1	A	464	PRO	7
1	A	430	GLU	6
1	A	466	PRO	6
1	A	414	LYS	5
1	A	463	ASN	5
1	A	462	ILE	5
1	A	470	PRO	3
1	A	503	ALA	3
1	A	451	ASN	3
1	A	469	MET	3
1	A	413	ALA	3
1	A	448	ALA	3
1	A	397	LEU	2
1	A	495	LYS	2
1	A	434	SER	2
1	A	447	ARG	2
1	A	449	ALA	2
1	A	465	ALA	2
1	A	396	PRO	2
1	A	452	LYS	2
2	B	903	LEU	2
1	A	468	GLY	2
1	A	432	ASN	2
1	A	398	SER	1
1	A	412	ILE	1
1	A	454	LEU	1
1	A	415	ASN	1

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Mol	Chain	Res	Type	Models (Total)
1	A	453	SER	1
1	A	394	VAL	1
1	A	491	LYS	1
1	A	417	THR	1
1	A	493	SER	1
1	A	499	ILE	1
1	A	416	THR	1
1	A	431	ASP	1
1	A	494	GLY	1
1	A	480	ALA	1
1	A	433	GLN	1
2	B	906	THR	1
2	B	904	LEU	1
1	A	404	MET	1
1	A	395	THR	1

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	92/113 (81%)	56±3 (61±4%)	36±3 (39±4%)	1	6
2	B	5/6 (83%)	3±1 (59±26%)	2±1 (41±26%)	0	4
All	All	1455/1785 (82%)	891 (61%)	564 (39%)	1	6

All 86 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	395	THR	15
1	A	440	VAL	15
1	A	491	LYS	14
1	A	498	LYS	14
1	A	410	THR	13
1	A	476	PHE	12
1	A	460	ASP	12
1	A	441	LEU	12
1	A	397	LEU	12

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Mol	Chain	Res	Type	Models (Total)
1	A	422	HIS	12
1	A	459	LEU	11
1	A	487	SER	11
1	A	414	LYS	11
1	A	446	LYS	10
1	A	424	GLN	10
1	A	469	MET	10
1	A	399	LEU	10
1	A	437	THR	10
1	A	408	MET	10
1	A	462	ILE	10
1	A	467	ARG	10
2	B	902	ARG	10
1	A	428	THR	10
1	A	495	LYS	9
1	A	493	SER	9
1	A	477	ASP	9
1	A	451	ASN	9
1	A	431	ASP	9
1	A	489	LYS	9
1	A	445	ARG	9
1	A	496	GLU	8
1	A	427	SER	8
1	A	417	THR	8
1	A	490	ASP	7
1	A	497	GLN	7
1	A	415	ASN	7
1	A	433	GLN	7
2	B	905	LEU	7
1	A	499	ILE	7
1	A	411	LEU	7
1	A	398	SER	7
1	A	426	PHE	6
1	A	444	GLU	6
1	A	502	LYS	6
1	A	474	VAL	6
1	A	421	LYS	6
1	A	453	SER	6
1	A	436	VAL	5
1	A	485	HIS	5
2	B	904	LEU	5
2	B	903	LEU	5

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Mol	Chain	Res	Type	Models (Total)
1	A	471	GLN	5
1	A	458	ASN	5
1	A	463	ASN	5
1	A	423	SER	5
1	A	481	ASP	4
1	A	442	GLN	4
1	A	447	ARG	4
1	A	407	VAL	4
1	A	450	ASP	4
1	A	479	ASP	4
1	A	432	ASN	4
1	A	434	SER	4
1	A	501	ILE	4
1	A	452	LYS	4
1	A	430	GLU	4
2	B	906	THR	4
1	A	456	GLN	3
1	A	492	ASN	3
1	A	454	LEU	3
1	A	425	VAL	3
1	A	472	ILE	3
1	A	420	THR	2
1	A	394	VAL	2
1	A	483	ILE	2
1	A	404	MET	2
1	A	484	LEU	1
1	A	412	ILE	1
1	A	409	THR	1
1	A	418	ILE	1
1	A	478	ILE	1
1	A	403	THR	1
1	A	457	PHE	1
1	A	402	GLU	1
1	A	486	VAL	1
1	A	473	GLU	1

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 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