



Full wwPDB NMR Structure Validation Report ⓘ

Mar 6, 2026 – 04:08 AM UTC

PDB ID : 1DMZ / pdb_00001dmz
Title : A REFINED NMR STRUCTURE OF A NEW PHOPHOPEPTIDE-BINDING
G DOMAIN CONTAINING THE FHA2 OF RAD53
Authors : Byeon, I.-J.L.; Liao, H.; Tsai, M.-D.
Deposited on : 1999-12-15

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

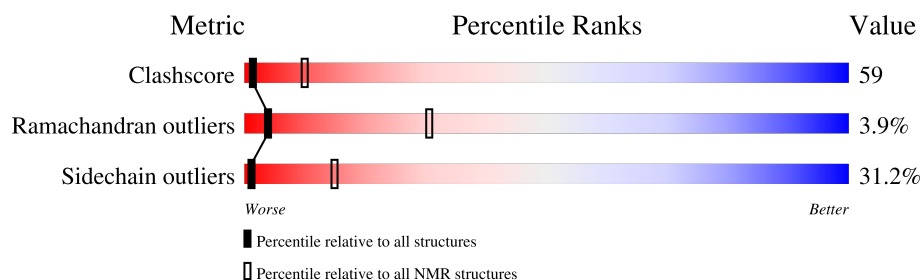
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

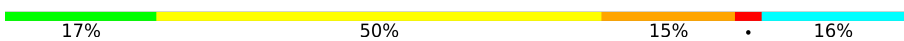
The overall completeness of chemical shifts assignment was not calculated.

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	158	

2 Ensemble composition and analysis

This entry contains 20 models. Model 4 is the overall representative, medoid model (most similar to other models). The authors have identified model 20 as representative.

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:576-A:630, A:644-A:704, A:714-A:730 (133)	0.44	4

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

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

The models can be grouped into 2 clusters and 16 single-model clusters were found.

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

3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 2548 atoms, of which 1274 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called PROTEIN (PROTEIN KINASE SPK1).

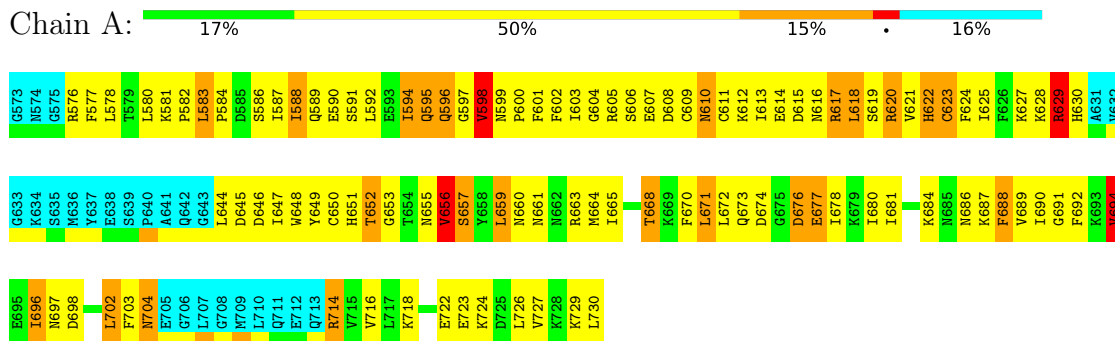
Mol	Chain	Residues	Atoms						Trace
1	A	158	Total	C	H	N	O	S	0
			2548	806	1274	222	239	7	

4 Residue-property plots

4.1 Average score per residue in the NMR ensemble

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

- Molecule 1: PROTEIN (PROTEIN KINASE SPK1)

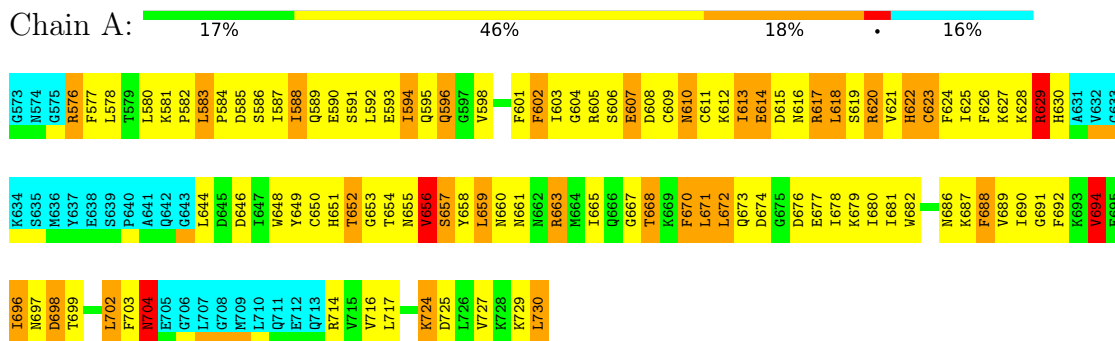


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

- Molecule 1: PROTEIN (PROTEIN KINASE SPK1)



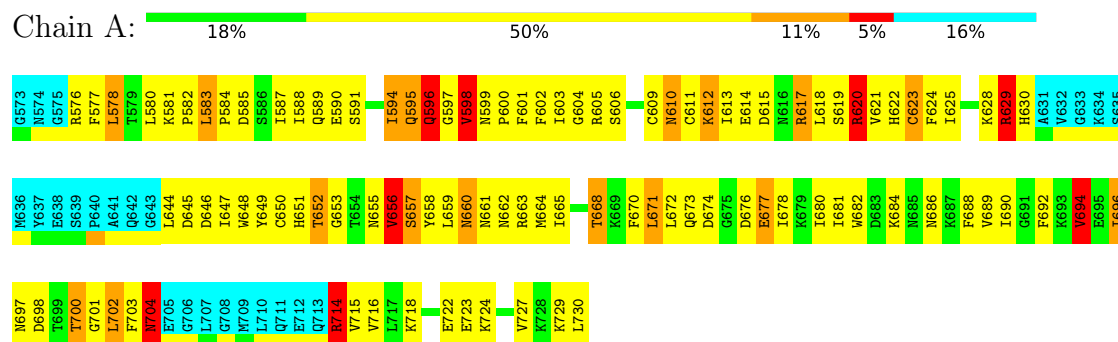
4.2.2 Score per residue for model 2

- Molecule 1: PROTEIN (PROTEIN KINASE SPK1)



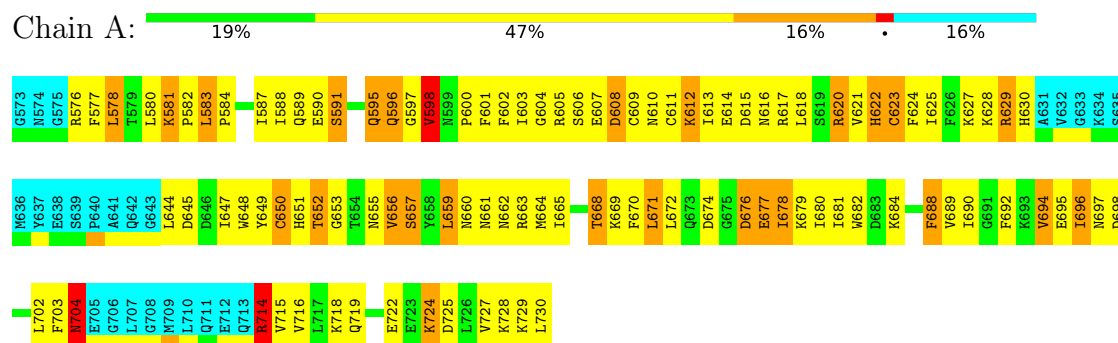
4.2.3 Score per residue for model 3

- Molecule 1: PROTEIN (PROTEIN KINASE SPK1)



4.2.4 Score per residue for model 4 (medoid)

- Molecule 1: PROTEIN (PROTEIN KINASE SPK1)



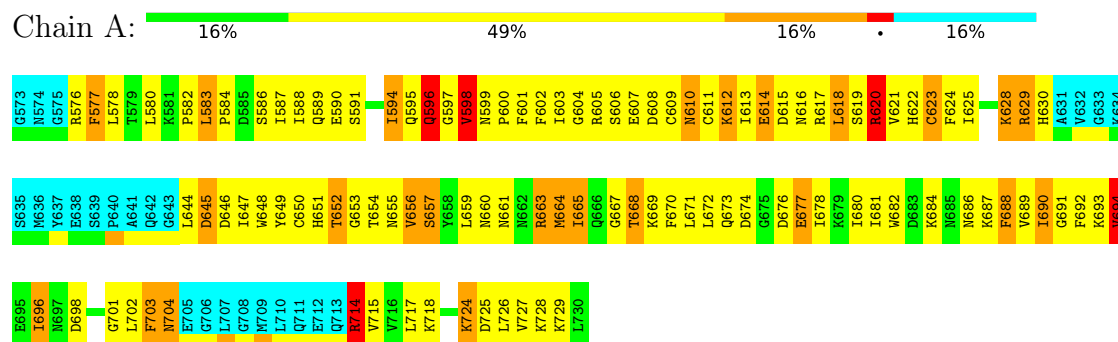
4.2.5 Score per residue for model 5

- Molecule 1: PROTEIN (PROTEIN KINASE SPK1)



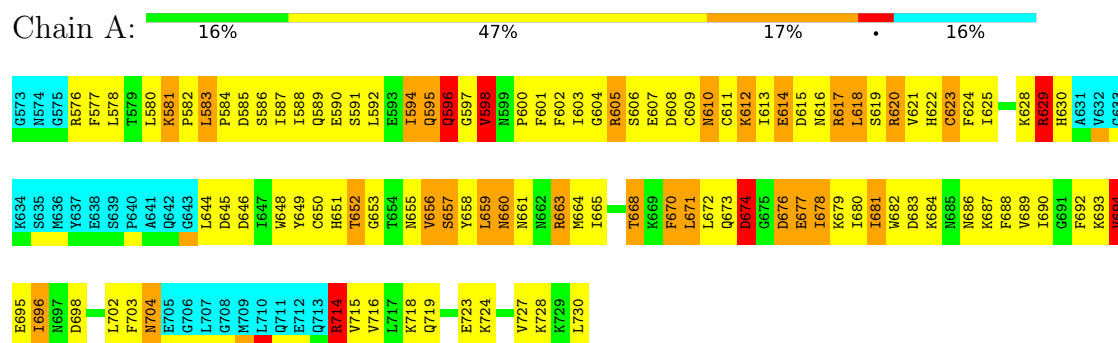
4.2.6 Score per residue for model 6

- Molecule 1: PROTEIN (PROTEIN KINASE SPK1)



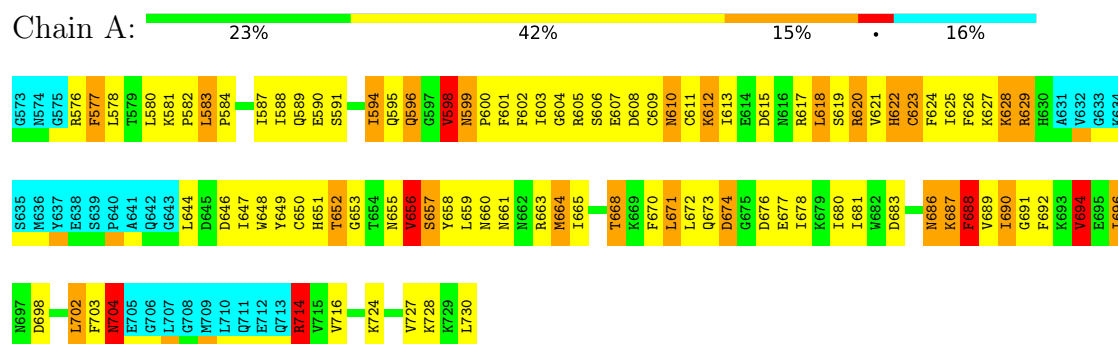
4.2.7 Score per residue for model 7

- Molecule 1: PROTEIN (PROTEIN KINASE SPK1)



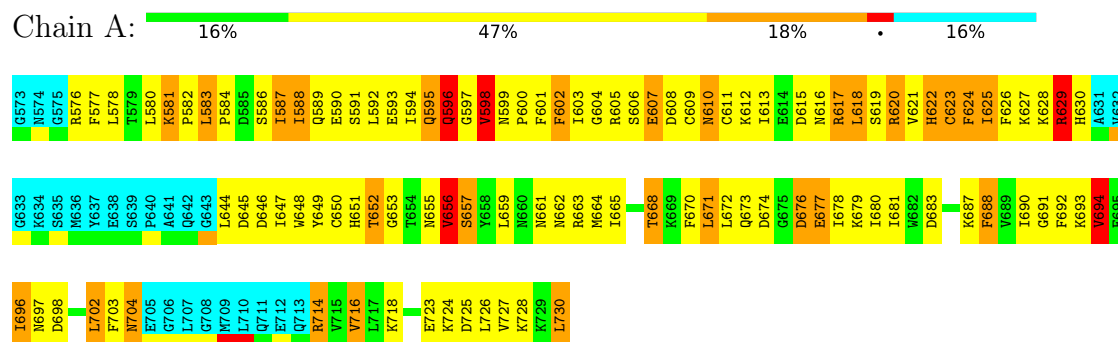
4.2.8 Score per residue for model 8

- Molecule 1: PROTEIN (PROTEIN KINASE SPK1)



4.2.9 Score per residue for model 9

- Molecule 1: PROTEIN (PROTEIN KINASE SPK1)



4.2.10 Score per residue for model 10

- Molecule 1: PROTEIN (PROTEIN KINASE SPK1)



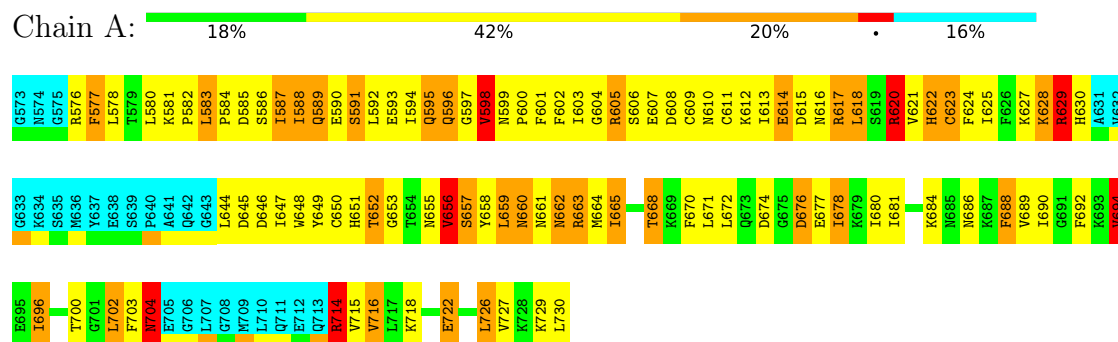
4.2.14 Score per residue for model 14

- Molecule 1: PROTEIN (PROTEIN KINASE SPK1)



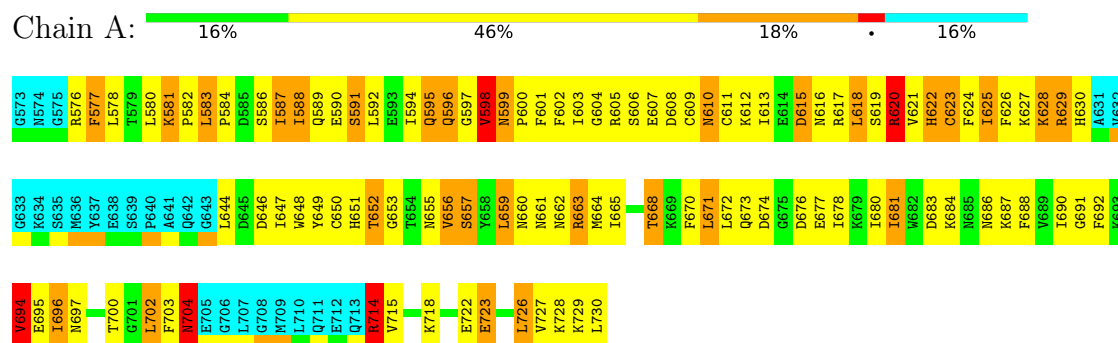
4.2.15 Score per residue for model 15

- Molecule 1: PROTEIN (PROTEIN KINASE SPK1)



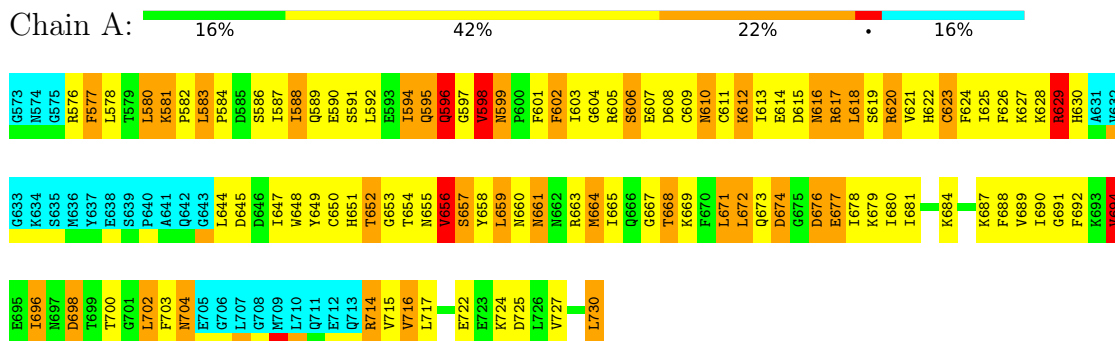
4.2.16 Score per residue for model 16

- Molecule 1: PROTEIN (PROTEIN KINASE SPK1)



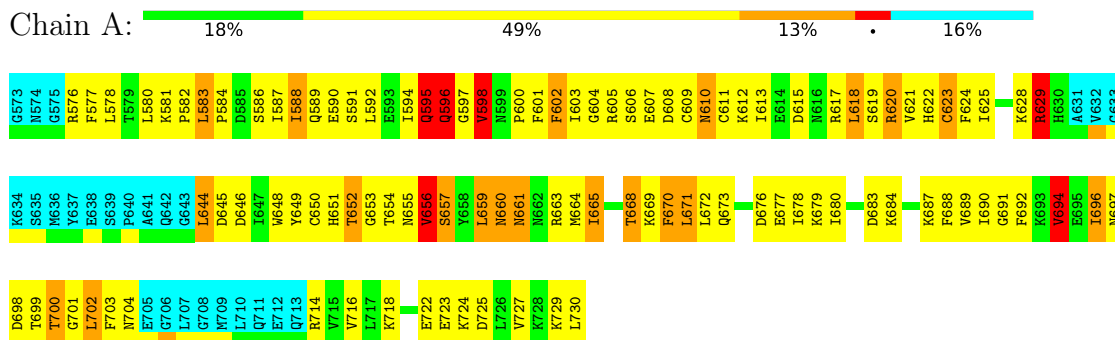
4.2.17 Score per residue for model 17

- Molecule 1: PROTEIN (PROTEIN KINASE SPK1)



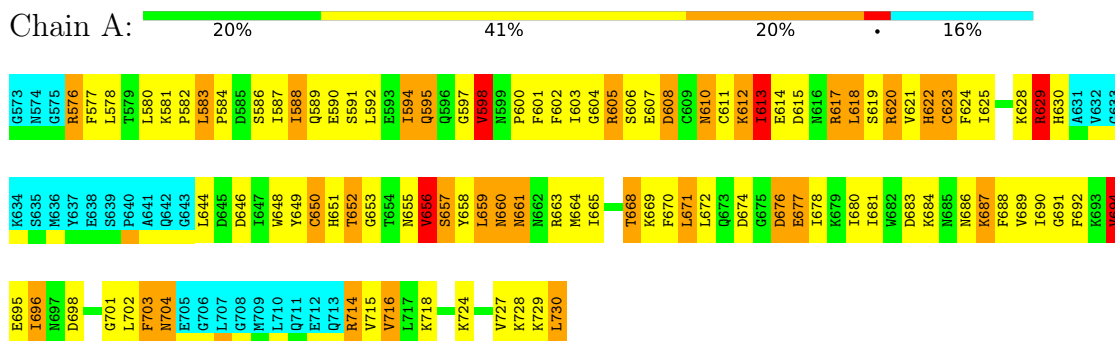
4.2.18 Score per residue for model 18

- Molecule 1: PROTEIN (PROTEIN KINASE SPK1)



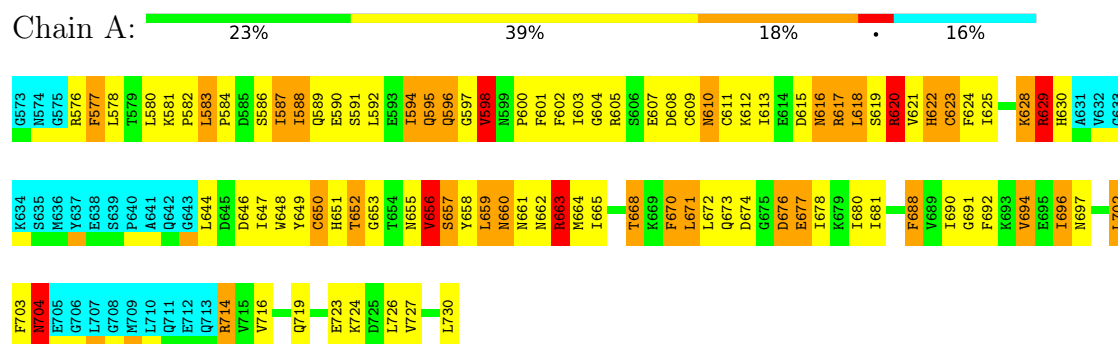
4.2.19 Score per residue for model 19

- Molecule 1: PROTEIN (PROTEIN KINASE SPK1)



4.2.20 Score per residue for model 20

• Molecule 1: PROTEIN (PROTEIN KINASE SPK1)



5 Refinement protocol and experimental data overview

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

Of the 35 calculated structures, 20 were deposited, based on the following criterion: *structures with the lowest energy*.

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

Software name	Classification	Version
TALOS	refinement	98.040.21.02
X-PLOR X-PLOR (ONLINE)	structure solution	3.851

No chemical shift data was provided.

6 Model quality i

6.1 Standard geometry i

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the (average) root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#Z>5	RMSZ	#Z>5
1	A	1.45±0.00	0±0/1119 (0.0± 0.0%)	1.61±0.01	6±1/1504 (0.4± 0.1%)
All	All	1.45	0/22380 (0.0%)	1.61	120/30080 (0.4%)

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	7.0±0.0
All	All	0	140

There are no bond-length outliers.

All unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	696	ILE	N-CA-CB	-6.31	105.09	111.90	9	18
1	A	588	ILE	N-CA-CB	-6.29	103.86	111.21	12	13
1	A	598	VAL	N-CA-CB	-6.18	105.22	111.90	15	17
1	A	715	VAL	N-CA-CB	-6.04	105.46	112.34	7	1
1	A	594	ILE	N-CA-CB	-5.85	104.61	111.39	13	10
1	A	670	PHE	CA-CB-CG	-5.75	108.05	113.80	7	6
1	A	694	VAL	N-CA-CB	-5.56	104.94	111.39	10	18
1	A	602	PHE	CA-CB-CG	-5.54	108.25	113.80	5	7
1	A	704	ASN	N-CA-CB	-5.43	103.31	111.56	16	11
1	A	716	VAL	N-CA-CB	-5.42	104.81	110.72	14	7
1	A	689	VAL	N-CA-CB	-5.30	104.63	110.99	4	3
1	A	613	ILE	N-CA-CB	-5.21	105.57	112.34	1	2
1	A	703	PHE	CA-CB-CG	-5.14	108.66	113.80	6	2
1	A	690	ILE	N-CA-CB	-5.12	105.99	112.60	8	2
1	A	625	ILE	N-CA-CB	-5.11	105.24	111.21	16	1

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	577	PHE	N-CA-CB	-5.09	103.03	110.40	5	1
1	A	651	HIS	N-CA-CB	-5.05	103.46	110.38	2	1

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	576	ARG	Sidechain	20
1	A	605	ARG	Sidechain	20
1	A	617	ARG	Sidechain	20
1	A	620	ARG	Sidechain	20
1	A	629	ARG	Sidechain	20
1	A	663	ARG	Sidechain	20
1	A	714	ARG	Sidechain	20

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	1099	1110	1110	130±10
All	All	21980	22200	22200	2610

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 59.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:582:PRO:HD2	1:A:590:GLU:O	1.08	1.48	18	20
1:A:578:LEU:HD22	1:A:594:ILE:HD12	1.08	1.14	16	7
1:A:659:LEU:HD13	1:A:678:ILE:HG22	1.01	1.32	6	4
1:A:580:LEU:HD11	1:A:625:ILE:HD12	0.98	1.35	18	12
1:A:583:LEU:HB2	1:A:584:PRO:HD2	0.97	1.35	17	20
1:A:583:LEU:N	1:A:583:LEU:HD13	0.92	1.80	5	2
1:A:578:LEU:HD11	1:A:647:ILE:HD13	0.91	1.42	3	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:578:LEU:HD23	1:A:594:ILE:HD12	0.90	1.41	9	8
1:A:621:VAL:HG11	1:A:727:VAL:HG23	0.90	1.42	19	3
1:A:677:GLU:HA	1:A:692:PHE:O	0.86	1.70	16	20
1:A:648:TRP:CH2	1:A:671:LEU:HD22	0.86	2.05	17	5
1:A:659:LEU:HD23	1:A:670:PHE:CD2	0.85	2.06	6	5
1:A:659:LEU:CD2	1:A:678:ILE:HG22	0.85	2.01	16	3
1:A:582:PRO:CD	1:A:590:GLU:O	0.84	2.24	10	20
1:A:649:TYR:CB	1:A:672:LEU:HD11	0.83	2.02	14	2
1:A:603:ILE:HG23	1:A:611:CYS:HB3	0.82	1.51	1	20
1:A:588:ILE:CD1	1:A:690:ILE:HD12	0.82	2.02	13	1
1:A:588:ILE:HG21	1:A:692:PHE:CZ	0.81	2.09	17	11
1:A:659:LEU:HD21	1:A:714:ARG:NH1	0.81	1.89	12	5
1:A:618:LEU:HD13	1:A:681:ILE:HD11	0.80	1.53	3	6
1:A:604:GLY:HA2	1:A:618:LEU:HD21	0.79	1.53	13	16
1:A:659:LEU:HD21	1:A:678:ILE:HG22	0.79	1.53	16	2
1:A:659:LEU:CD1	1:A:678:ILE:HG22	0.78	2.07	6	5
1:A:582:PRO:HB2	1:A:588:ILE:HG23	0.78	1.53	7	6
1:A:702:LEU:HD23	1:A:704:ASN:O	0.78	1.79	13	8
1:A:615:ASP:OD2	1:A:690:ILE:HD11	0.77	1.79	8	10
1:A:622:HIS:O	1:A:652:THR:N	0.76	2.17	7	20
1:A:659:LEU:HD13	1:A:678:ILE:CG2	0.76	2.10	6	5
1:A:659:LEU:HD11	1:A:676:ASP:OD1	0.76	1.80	3	1
1:A:649:TYR:HB2	1:A:672:LEU:HD11	0.76	1.58	19	19
1:A:659:LEU:HD13	1:A:678:ILE:HG12	0.75	1.58	3	2
1:A:583:LEU:CB	1:A:584:PRO:HD2	0.75	2.12	15	20
1:A:582:PRO:C	1:A:583:LEU:HD13	0.75	2.07	5	2
1:A:644:LEU:HD22	1:A:702:LEU:O	0.74	1.83	11	14
1:A:621:VAL:HG11	1:A:727:VAL:CG2	0.74	2.12	14	3
1:A:623:CYS:SG	1:A:680:ILE:HD13	0.74	2.23	3	20
1:A:602:PHE:C	1:A:609:CYS:HB3	0.73	2.08	10	7
1:A:592:LEU:HD13	1:A:611:CYS:SG	0.73	2.24	14	11
1:A:659:LEU:HD23	1:A:670:PHE:CD1	0.73	2.19	12	2
1:A:588:ILE:HD12	1:A:613:ILE:HA	0.72	1.61	14	11
1:A:659:LEU:HD23	1:A:670:PHE:CE2	0.72	2.19	9	5
1:A:615:ASP:HB3	1:A:618:LEU:CB	0.72	2.14	1	13
1:A:604:GLY:HA3	1:A:620:ARG:O	0.71	1.84	19	20
1:A:580:LEU:HD11	1:A:625:ILE:CD1	0.70	2.16	6	19
1:A:577:PHE:CE2	1:A:702:LEU:HD11	0.70	2.22	6	1
1:A:688:PHE:CG	1:A:688:PHE:O	0.70	2.45	7	1
1:A:613:ILE:HG22	1:A:618:LEU:HD22	0.70	1.62	19	11
1:A:618:LEU:HD12	1:A:622:HIS:CE1	0.70	2.22	3	8

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:613:ILE:CD1	1:A:680:ILE:HD12	0.69	2.17	19	18
1:A:646:ASP:CG	1:A:671:LEU:HD11	0.69	2.12	6	2
1:A:659:LEU:HD13	1:A:678:ILE:CG1	0.69	2.17	12	2
1:A:648:TRP:CZ3	1:A:671:LEU:HD22	0.69	2.23	12	5
1:A:664:MET:CG	1:A:716:VAL:HG21	0.69	2.16	8	1
1:A:588:ILE:HD12	1:A:690:ILE:HD12	0.69	1.63	13	1
1:A:655:ASN:C	1:A:656:VAL:HG13	0.69	2.13	1	8
1:A:659:LEU:HD21	1:A:678:ILE:CG1	0.69	2.18	8	1
1:A:613:ILE:CG2	1:A:690:ILE:HD13	0.69	2.18	5	2
1:A:656:VAL:HG22	1:A:664:MET:O	0.69	1.87	2	7
1:A:578:LEU:HD22	1:A:594:ILE:CD1	0.68	2.07	16	1
1:A:613:ILE:O	1:A:613:ILE:HG23	0.68	1.87	17	1
1:A:583:LEU:HB2	1:A:584:PRO:CD	0.68	2.16	17	8
1:A:659:LEU:HD23	1:A:670:PHE:CE1	0.68	2.24	13	2
1:A:644:LEU:HD23	1:A:701:GLY:O	0.68	1.88	3	1
1:A:596:GLN:CD	1:A:700:THR:HG21	0.68	2.13	17	1
1:A:588:ILE:CG1	1:A:613:ILE:HA	0.67	2.18	19	2
1:A:602:PHE:C	1:A:609:CYS:HB2	0.67	2.15	18	2
1:A:588:ILE:CD1	1:A:613:ILE:HA	0.67	2.19	20	12
1:A:618:LEU:CD1	1:A:681:ILE:HD11	0.67	2.18	8	6
1:A:655:ASN:CG	1:A:681:ILE:HG23	0.67	2.14	2	3
1:A:583:LEU:HD22	1:A:583:LEU:H	0.67	1.49	5	2
1:A:687:LYS:O	1:A:689:VAL:HG23	0.67	1.89	6	3
1:A:603:ILE:HG22	1:A:613:ILE:HD12	0.67	1.65	12	10
1:A:672:LEU:HD23	1:A:676:ASP:OD2	0.67	1.89	11	7
1:A:587:ILE:HG21	1:A:615:ASP:OD1	0.67	1.88	5	1
1:A:587:ILE:HG22	1:A:690:ILE:CD1	0.66	2.20	19	12
1:A:592:LEU:HD22	1:A:592:LEU:N	0.66	2.05	12	2
1:A:649:TYR:HB3	1:A:672:LEU:HD11	0.66	1.68	14	1
1:A:615:ASP:OD2	1:A:681:ILE:HD13	0.66	1.89	5	1
1:A:664:MET:SD	1:A:716:VAL:HG13	0.66	2.31	15	3
1:A:644:LEU:HD13	1:A:703:PHE:HA	0.66	1.68	16	15
1:A:646:ASP:OD2	1:A:671:LEU:HD21	0.66	1.91	7	8
1:A:587:ILE:HG21	1:A:614:GLU:O	0.66	1.91	13	4
1:A:583:LEU:HD13	1:A:585:ASP:OD2	0.65	1.91	10	1
1:A:648:TRP:CH2	1:A:671:LEU:HD13	0.65	2.26	15	2
1:A:615:ASP:HB3	1:A:618:LEU:HB2	0.65	1.69	17	16
1:A:603:ILE:HG23	1:A:611:CYS:SG	0.65	2.31	10	10
1:A:578:LEU:CD1	1:A:647:ILE:HD13	0.65	2.20	2	9
1:A:578:LEU:HD21	1:A:694:VAL:HG22	0.65	1.68	13	2
1:A:613:ILE:HG23	1:A:690:ILE:HD13	0.64	1.69	5	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:644:LEU:HD12	1:A:703:PHE:N	0.64	2.07	18	1
1:A:659:LEU:HD21	1:A:676:ASP:OD2	0.64	1.93	5	4
1:A:595:GLN:O	1:A:596:GLN:C	0.64	2.41	11	10
1:A:648:TRP:CZ3	1:A:671:LEU:HG	0.64	2.28	8	13
1:A:646:ASP:OD1	1:A:671:LEU:HD21	0.64	1.93	19	6
1:A:586:SER:HA	1:A:689:VAL:O	0.64	1.93	7	3
1:A:585:ASP:O	1:A:689:VAL:HG23	0.63	1.93	3	3
1:A:645:ASP:O	1:A:702:LEU:HD23	0.63	1.94	6	1
1:A:655:ASN:O	1:A:656:VAL:HG22	0.63	1.94	10	8
1:A:615:ASP:OD2	1:A:681:ILE:HD12	0.63	1.93	8	1
1:A:669:LYS:HE2	1:A:717:LEU:HD11	0.63	1.71	6	1
1:A:588:ILE:HG12	1:A:613:ILE:HA	0.63	1.68	13	1
1:A:686:ASN:O	1:A:687:LYS:C	0.63	2.41	19	1
1:A:670:PHE:CE2	1:A:716:VAL:HG22	0.63	2.29	12	2
1:A:587:ILE:HD13	1:A:688:PHE:HB2	0.62	1.72	7	1
1:A:659:LEU:HD22	1:A:678:ILE:CG2	0.62	2.25	11	1
1:A:723:GLU:O	1:A:727:VAL:HG12	0.62	1.94	2	4
1:A:586:SER:O	1:A:589:GLN:NE2	0.62	2.33	12	7
1:A:578:LEU:CD2	1:A:594:ILE:HD12	0.62	2.24	5	4
1:A:646:ASP:CG	1:A:671:LEU:HD21	0.62	2.20	19	6
1:A:615:ASP:CG	1:A:690:ILE:HD11	0.62	2.19	5	5
1:A:615:ASP:OD1	1:A:690:ILE:HD11	0.62	1.95	11	2
1:A:651:HIS:NE2	1:A:653:GLY:O	0.62	2.33	17	6
1:A:613:ILE:HD11	1:A:692:PHE:CE1	0.62	2.29	7	16
1:A:583:LEU:N	1:A:583:LEU:CD1	0.62	2.53	5	2
1:A:595:GLN:O	1:A:597:GLY:N	0.62	2.31	12	17
1:A:655:ASN:OD1	1:A:681:ILE:HD12	0.62	1.95	5	1
1:A:670:PHE:CD2	1:A:716:VAL:HG22	0.62	2.30	12	3
1:A:615:ASP:HB3	1:A:618:LEU:HB3	0.61	1.72	1	1
1:A:582:PRO:CB	1:A:588:ILE:HG23	0.61	2.25	7	6
1:A:624:PHE:CZ	1:A:626:PHE:CD1	0.61	2.88	12	1
1:A:681:ILE:HG22	1:A:690:ILE:CG1	0.61	2.26	13	1
1:A:664:MET:HG2	1:A:716:VAL:HG13	0.61	1.71	7	8
1:A:618:LEU:HD12	1:A:681:ILE:CD1	0.61	2.25	14	3
1:A:618:LEU:HD12	1:A:681:ILE:HD11	0.61	1.72	9	3
1:A:594:ILE:HG23	1:A:598:VAL:HG12	0.61	1.73	3	4
1:A:644:LEU:CD1	1:A:701:GLY:O	0.61	2.49	18	1
1:A:580:LEU:HD21	1:A:694:VAL:HG23	0.60	1.71	17	1
1:A:598:VAL:HG12	1:A:598:VAL:O	0.60	1.96	12	18
1:A:659:LEU:HD11	1:A:676:ASP:OD2	0.60	1.96	9	2
1:A:577:PHE:CD2	1:A:698:ASP:O	0.60	2.55	10	6

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:588:ILE:N	1:A:588:ILE:HD13	0.60	2.12	5	4
1:A:577:PHE:CZ	1:A:702:LEU:HD13	0.60	2.32	9	4
1:A:578:LEU:C	1:A:578:LEU:HD23	0.60	2.20	8	6
1:A:603:ILE:HG23	1:A:611:CYS:CB	0.59	2.27	18	14
1:A:583:LEU:CB	1:A:584:PRO:CD	0.59	2.80	15	20
1:A:615:ASP:CG	1:A:681:ILE:HD12	0.59	2.22	4	7
1:A:648:TRP:CZ2	1:A:671:LEU:HD13	0.59	2.31	15	2
1:A:659:LEU:HD21	1:A:714:ARG:CZ	0.59	2.26	6	3
1:A:659:LEU:HD13	1:A:670:PHE:CD1	0.59	2.33	18	1
1:A:598:VAL:HG13	1:A:598:VAL:O	0.58	1.97	1	2
1:A:687:LYS:O	1:A:688:PHE:C	0.58	2.45	8	6
1:A:703:PHE:CZ	1:A:704:ASN:CG	0.58	2.82	12	1
1:A:665:ILE:CG1	1:A:668:THR:HG23	0.58	2.28	16	20
1:A:664:MET:HG3	1:A:716:VAL:HG21	0.58	1.75	8	1
1:A:621:VAL:HB	1:A:727:VAL:HG23	0.58	1.73	18	8
1:A:649:TYR:CD2	1:A:664:MET:HE1	0.58	2.34	9	4
1:A:587:ILE:C	1:A:588:ILE:HD13	0.58	2.24	5	2
1:A:646:ASP:OD2	1:A:671:LEU:HD11	0.58	1.98	15	4
1:A:578:LEU:HD11	1:A:647:ILE:CD1	0.58	2.23	3	3
1:A:700:THR:HG23	1:A:700:THR:O	0.58	1.99	13	1
1:A:622:HIS:O	1:A:652:THR:OG1	0.58	2.20	19	20
1:A:588:ILE:HG12	1:A:612:LYS:O	0.58	1.98	8	6
1:A:588:ILE:HG13	1:A:613:ILE:HG23	0.58	1.75	10	1
1:A:588:ILE:HB	1:A:613:ILE:HA	0.57	1.76	17	2
1:A:651:HIS:CE1	1:A:656:VAL:C	0.57	2.82	20	20
1:A:613:ILE:CG2	1:A:618:LEU:HD22	0.57	2.28	5	14
1:A:656:VAL:HG13	1:A:664:MET:O	0.57	1.99	6	3
1:A:672:LEU:HD13	1:A:694:VAL:HG21	0.57	1.77	18	1
1:A:613:ILE:HD11	1:A:690:ILE:CG2	0.57	2.28	17	1
1:A:594:ILE:HG23	1:A:598:VAL:HB	0.57	1.76	5	10
1:A:588:ILE:HG21	1:A:692:PHE:HZ	0.57	1.60	2	6
1:A:588:ILE:HD13	1:A:613:ILE:CA	0.57	2.29	17	3
1:A:578:LEU:HD11	1:A:694:VAL:HG22	0.57	1.77	7	4
1:A:648:TRP:CH2	1:A:671:LEU:HD12	0.56	2.35	14	3
1:A:664:MET:SD	1:A:716:VAL:HG22	0.56	2.40	17	2
1:A:630:HIS:CE1	1:A:703:PHE:CD2	0.56	2.92	17	16
1:A:580:LEU:HD12	1:A:594:ILE:HG13	0.56	1.76	20	2
1:A:624:PHE:CE2	1:A:626:PHE:HB3	0.56	2.35	12	1
1:A:580:LEU:CD1	1:A:594:ILE:HD11	0.56	2.31	8	4
1:A:598:VAL:O	1:A:598:VAL:CG1	0.56	2.54	3	18
1:A:600:PRO:HG2	1:A:602:PHE:CZ	0.56	2.36	19	16

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:723:GLU:HA	1:A:726:LEU:HD21	0.56	1.78	12	1
1:A:648:TRP:CH2	1:A:671:LEU:CD1	0.56	2.89	9	9
1:A:582:PRO:HB3	1:A:692:PHE:CZ	0.55	2.36	7	15
1:A:624:PHE:CZ	1:A:650:CYS:HB3	0.55	2.35	7	11
1:A:655:ASN:HB3	1:A:681:ILE:HG23	0.55	1.77	3	4
1:A:669:LYS:CE	1:A:717:LEU:HD11	0.55	2.31	6	1
1:A:722:GLU:O	1:A:726:LEU:HD23	0.55	2.02	15	4
1:A:655:ASN:CG	1:A:681:ILE:HD12	0.55	2.26	5	1
1:A:580:LEU:CD2	1:A:694:VAL:HG23	0.55	2.32	17	1
1:A:603:ILE:HG12	1:A:611:CYS:CB	0.55	2.31	3	19
1:A:624:PHE:CE2	1:A:650:CYS:CB	0.55	2.89	9	5
1:A:659:LEU:HD23	1:A:678:ILE:HG22	0.55	1.77	18	1
1:A:651:HIS:CD2	1:A:652:THR:N	0.55	2.74	8	20
1:A:622:HIS:HA	1:A:653:GLY:N	0.55	2.17	12	8
1:A:577:PHE:CZ	1:A:578:LEU:HB2	0.55	2.37	6	5
1:A:627:LYS:CE	1:A:647:ILE:HG23	0.54	2.33	9	1
1:A:651:HIS:CB	1:A:657:SER:OG	0.54	2.55	15	11
1:A:621:VAL:CG1	1:A:727:VAL:HG22	0.54	2.33	15	3
1:A:603:ILE:HD11	1:A:625:ILE:HG13	0.54	1.78	20	8
1:A:659:LEU:O	1:A:661:ASN:N	0.54	2.41	11	20
1:A:665:ILE:HG13	1:A:668:THR:HG23	0.54	1.80	4	13
1:A:659:LEU:CG	1:A:678:ILE:HG22	0.54	2.32	17	2
1:A:587:ILE:HD12	1:A:614:GLU:O	0.54	2.02	1	1
1:A:580:LEU:HD12	1:A:594:ILE:HD11	0.54	1.79	6	1
1:A:577:PHE:CE1	1:A:702:LEU:HD21	0.54	2.38	12	1
1:A:588:ILE:HG13	1:A:613:ILE:HA	0.54	1.79	19	1
1:A:659:LEU:HD21	1:A:678:ILE:HG13	0.54	1.78	8	1
1:A:703:PHE:CE2	1:A:704:ASN:HB3	0.54	2.38	20	19
1:A:581:LYS:O	1:A:583:LEU:CD1	0.53	2.55	5	2
1:A:681:ILE:HG22	1:A:690:ILE:HB	0.53	1.79	5	1
1:A:659:LEU:HD21	1:A:678:ILE:HG12	0.53	1.79	8	1
1:A:621:VAL:O	1:A:622:HIS:C	0.53	2.52	14	20
1:A:609:CYS:SG	1:A:730:LEU:HD21	0.53	2.43	10	1
1:A:578:LEU:HD21	1:A:580:LEU:HG	0.53	1.80	16	1
1:A:650:CYS:HA	1:A:668:THR:O	0.53	2.04	20	18
1:A:613:ILE:O	1:A:613:ILE:CG2	0.53	2.56	17	1
1:A:624:PHE:CZ	1:A:650:CYS:CB	0.53	2.91	16	18
1:A:583:LEU:N	1:A:583:LEU:HD23	0.53	2.19	9	2
1:A:592:LEU:HD22	1:A:611:CYS:HA	0.53	1.81	14	7
1:A:602:PHE:CG	1:A:730:LEU:HD23	0.53	2.38	15	3
1:A:627:LYS:HE2	1:A:647:ILE:HG23	0.53	1.79	9	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:588:ILE:HG13	1:A:612:LYS:O	0.53	2.03	19	1
1:A:624:PHE:CD1	1:A:624:PHE:C	0.53	2.87	19	12
1:A:651:HIS:CG	1:A:657:SER:OG	0.53	2.61	2	18
1:A:602:PHE:HB3	1:A:730:LEU:HD23	0.53	1.80	2	2
1:A:659:LEU:HG	1:A:678:ILE:HG23	0.53	1.81	8	1
1:A:580:LEU:HD11	1:A:625:ILE:HD13	0.53	1.80	16	1
1:A:583:LEU:O	1:A:588:ILE:O	0.52	2.27	18	8
1:A:613:ILE:CD1	1:A:692:PHE:CE1	0.52	2.92	7	15
1:A:577:PHE:CD1	1:A:698:ASP:O	0.52	2.62	3	5
1:A:588:ILE:HG23	1:A:588:ILE:O	0.52	2.05	6	6
1:A:629:ARG:CD	1:A:629:ARG:C	0.52	2.83	14	2
1:A:600:PRO:HB3	1:A:726:LEU:HD23	0.52	1.81	6	2
1:A:580:LEU:HD11	1:A:625:ILE:HD11	0.52	1.81	14	1
1:A:609:CYS:SG	1:A:611:CYS:O	0.52	2.64	17	2
1:A:655:ASN:C	1:A:656:VAL:HG23	0.52	2.28	13	5
1:A:621:VAL:CG1	1:A:730:LEU:HD11	0.52	2.33	17	1
1:A:622:HIS:O	1:A:652:THR:CB	0.52	2.57	8	16
1:A:659:LEU:HD22	1:A:670:PHE:CD2	0.52	2.38	20	2
1:A:577:PHE:CE2	1:A:578:LEU:HB2	0.52	2.39	20	5
1:A:577:PHE:CB	1:A:596:GLN:HA	0.52	2.35	13	10
1:A:613:ILE:HD13	1:A:680:ILE:HD12	0.52	1.80	13	8
1:A:694:VAL:O	1:A:694:VAL:HG12	0.52	2.04	3	19
1:A:582:PRO:CG	1:A:588:ILE:HG22	0.52	2.35	19	2
1:A:644:LEU:CD2	1:A:644:LEU:N	0.52	2.72	14	1
1:A:655:ASN:C	1:A:656:VAL:CG1	0.52	2.83	5	8
1:A:578:LEU:CD2	1:A:694:VAL:HG22	0.52	2.35	4	1
1:A:613:ILE:HG23	1:A:690:ILE:HD12	0.52	1.81	7	1
1:A:723:GLU:OE1	1:A:726:LEU:HD12	0.52	2.04	20	1
1:A:588:ILE:CG1	1:A:613:ILE:HG23	0.51	2.35	10	1
1:A:601:PHE:HB3	1:A:625:ILE:CG2	0.51	2.34	12	1
1:A:724:LYS:O	1:A:727:VAL:HG12	0.51	2.05	13	15
1:A:673:GLN:O	1:A:674:ASP:C	0.51	2.52	14	6
1:A:688:PHE:O	1:A:688:PHE:CD1	0.51	2.64	7	1
1:A:648:TRP:CH2	1:A:671:LEU:HG	0.51	2.41	14	12
1:A:615:ASP:CB	1:A:618:LEU:HB2	0.51	2.35	17	4
1:A:659:LEU:HD12	1:A:670:PHE:CD2	0.51	2.41	16	1
1:A:659:LEU:HD11	1:A:678:ILE:HG21	0.51	1.80	1	4
1:A:659:LEU:HG	1:A:678:ILE:HG22	0.51	1.83	17	8
1:A:618:LEU:HB2	1:A:681:ILE:HD11	0.51	1.82	4	2
1:A:659:LEU:CD2	1:A:670:PHE:CD1	0.51	2.94	12	2
1:A:681:ILE:HG22	1:A:690:ILE:HG13	0.51	1.83	13	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:615:ASP:OD2	1:A:681:ILE:HG21	0.51	2.06	5	1
1:A:651:HIS:CE1	1:A:656:VAL:O	0.50	2.64	18	7
1:A:577:PHE:HB3	1:A:596:GLN:HA	0.50	1.83	13	2
1:A:659:LEU:HD22	1:A:670:PHE:CE2	0.50	2.41	20	1
1:A:577:PHE:CE1	1:A:702:LEU:HD13	0.50	2.41	9	2
1:A:624:PHE:CE2	1:A:726:LEU:CD1	0.50	2.93	12	1
1:A:587:ILE:CG1	1:A:690:ILE:HG12	0.50	2.36	1	1
1:A:601:PHE:CE1	1:A:610:ASN:HB3	0.50	2.40	12	12
1:A:594:ILE:HG23	1:A:598:VAL:CG1	0.50	2.36	3	2
1:A:599:ASN:ND2	1:A:627:LYS:O	0.50	2.45	12	3
1:A:580:LEU:CD1	1:A:625:ILE:HD12	0.50	2.34	5	4
1:A:657:SER:HG	1:A:664:MET:HE2	0.50	1.66	10	1
1:A:621:VAL:CB	1:A:727:VAL:HG23	0.50	2.37	8	1
1:A:655:ASN:O	1:A:656:VAL:HG12	0.50	2.06	12	7
1:A:649:TYR:CE2	1:A:664:MET:HE1	0.50	2.42	9	2
1:A:592:LEU:HD13	1:A:611:CYS:HA	0.50	1.83	9	1
1:A:629:ARG:HA	1:A:644:LEU:O	0.50	2.06	16	16
1:A:644:LEU:HD22	1:A:701:GLY:C	0.50	2.32	6	2
1:A:582:PRO:CG	1:A:590:GLU:O	0.49	2.60	12	20
1:A:581:LYS:O	1:A:583:LEU:HD23	0.49	2.07	9	2
1:A:649:TYR:CZ	1:A:678:ILE:HD12	0.49	2.42	1	1
1:A:648:TRP:CH2	1:A:671:LEU:CD2	0.49	2.95	4	4
1:A:686:ASN:O	1:A:688:PHE:N	0.49	2.45	13	5
1:A:622:HIS:O	1:A:653:GLY:N	0.49	2.45	9	2
1:A:577:PHE:CZ	1:A:702:LEU:CD2	0.49	2.95	10	1
1:A:603:ILE:HG22	1:A:613:ILE:CD1	0.49	2.36	12	2
1:A:588:ILE:HD11	1:A:690:ILE:HD12	0.49	1.83	13	1
1:A:644:LEU:HD12	1:A:701:GLY:C	0.49	2.32	14	1
1:A:613:ILE:CG1	1:A:692:PHE:CZ	0.49	2.95	18	15
1:A:628:LYS:O	1:A:646:ASP:N	0.49	2.44	8	9
1:A:588:ILE:HG13	1:A:613:ILE:HG12	0.49	1.85	15	4
1:A:644:LEU:HD12	1:A:644:LEU:N	0.49	2.23	9	10
1:A:586:SER:HB2	1:A:690:ILE:HA	0.49	1.82	2	4
1:A:601:PHE:CD1	1:A:610:ASN:HB3	0.49	2.43	8	16
1:A:624:PHE:CE1	1:A:650:CYS:CB	0.49	2.95	3	3
1:A:580:LEU:HD11	1:A:594:ILE:HD11	0.49	1.83	1	3
1:A:583:LEU:N	1:A:583:LEU:HD22	0.49	2.21	5	2
1:A:624:PHE:CZ	1:A:650:CYS:HB2	0.49	2.42	5	7
1:A:605:ARG:HA	1:A:613:ILE:O	0.49	2.07	5	3
1:A:644:LEU:CD1	1:A:703:PHE:HA	0.49	2.37	19	3
1:A:664:MET:HG2	1:A:716:VAL:HG21	0.49	1.81	8	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:622:HIS:ND1	1:A:653:GLY:HA3	0.49	2.23	15	18
1:A:588:ILE:HD13	1:A:612:LYS:C	0.49	2.32	17	3
1:A:578:LEU:HD12	1:A:696:ILE:CG1	0.49	2.38	9	1
1:A:607:GLU:O	1:A:608:ASP:C	0.48	2.56	18	16
1:A:655:ASN:OD1	1:A:681:ILE:HG23	0.48	2.08	2	1
1:A:592:LEU:N	1:A:592:LEU:CD2	0.48	2.76	16	2
1:A:577:PHE:CD1	1:A:596:GLN:HA	0.48	2.43	17	3
1:A:646:ASP:O	1:A:648:TRP:CD1	0.48	2.66	12	1
1:A:577:PHE:CD1	1:A:577:PHE:C	0.48	2.91	10	8
1:A:656:VAL:CG2	1:A:658:TYR:CE2	0.48	2.95	5	8
1:A:587:ILE:CG2	1:A:690:ILE:HD11	0.48	2.38	13	2
1:A:655:ASN:O	1:A:656:VAL:CB	0.48	2.61	9	12
1:A:621:VAL:HG13	1:A:730:LEU:HD11	0.48	1.84	17	1
1:A:582:PRO:HB3	1:A:692:PHE:CE2	0.48	2.44	13	5
1:A:670:PHE:CE1	1:A:715:VAL:O	0.48	2.67	4	7
1:A:582:PRO:CB	1:A:588:ILE:CG2	0.48	2.92	13	7
1:A:703:PHE:CZ	1:A:704:ASN:ND2	0.48	2.81	12	1
1:A:615:ASP:CB	1:A:618:LEU:CB	0.48	2.92	15	15
1:A:582:PRO:CB	1:A:588:ILE:HG22	0.48	2.39	19	2
1:A:587:ILE:HG22	1:A:690:ILE:HD11	0.48	1.85	19	2
1:A:629:ARG:O	1:A:629:ARG:HG3	0.48	2.09	19	3
1:A:578:LEU:HD13	1:A:696:ILE:CG1	0.48	2.38	18	1
1:A:644:LEU:HD12	1:A:702:LEU:C	0.48	2.34	18	1
1:A:649:TYR:CE2	1:A:678:ILE:HD12	0.48	2.43	15	2
1:A:592:LEU:HD12	1:A:611:CYS:SG	0.48	2.49	9	1
1:A:596:GLN:HG3	1:A:700:THR:HG21	0.48	1.85	13	1
1:A:586:SER:CB	1:A:691:GLY:N	0.48	2.77	9	9
1:A:586:SER:OG	1:A:690:ILE:HA	0.48	2.09	5	2
1:A:659:LEU:HD22	1:A:714:ARG:NH2	0.48	2.24	8	1
1:A:659:LEU:CD2	1:A:678:ILE:HG21	0.48	2.38	11	1
1:A:577:PHE:CZ	1:A:702:LEU:HD21	0.48	2.44	12	2
1:A:587:ILE:HD11	1:A:615:ASP:CG	0.48	2.34	15	1
1:A:644:LEU:CB	1:A:703:PHE:N	0.47	2.77	13	8
1:A:662:ASN:OD1	1:A:716:VAL:HG23	0.47	2.09	15	1
1:A:578:LEU:O	1:A:594:ILE:N	0.47	2.47	14	9
1:A:649:TYR:N	1:A:672:LEU:CD1	0.47	2.77	19	2
1:A:602:PHE:HB3	1:A:609:CYS:SG	0.47	2.49	5	4
1:A:651:HIS:CG	1:A:652:THR:N	0.47	2.82	2	2
1:A:630:HIS:ND1	1:A:703:PHE:CD2	0.47	2.82	6	3
1:A:644:LEU:HB2	1:A:703:PHE:CA	0.47	2.39	17	7
1:A:703:PHE:CD1	1:A:704:ASN:N	0.47	2.82	4	12

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:586:SER:HB2	1:A:691:GLY:N	0.47	2.25	20	5
1:A:580:LEU:N	1:A:592:LEU:O	0.47	2.48	20	2
1:A:577:PHE:HB3	1:A:596:GLN:CA	0.47	2.39	16	5
1:A:703:PHE:CE1	1:A:704:ASN:CG	0.47	2.93	12	1
1:A:649:TYR:N	1:A:672:LEU:HD11	0.47	2.24	19	1
1:A:630:HIS:N	1:A:644:LEU:O	0.47	2.47	3	8
1:A:664:MET:HE3	1:A:670:PHE:HB2	0.47	1.87	8	2
1:A:702:LEU:HD12	1:A:704:ASN:O	0.47	2.10	16	1
1:A:644:LEU:HB2	1:A:703:PHE:N	0.47	2.24	8	9
1:A:578:LEU:CD1	1:A:647:ILE:CD1	0.47	2.93	15	8
1:A:664:MET:CG	1:A:716:VAL:HG13	0.47	2.40	7	1
1:A:622:HIS:CD2	1:A:680:ILE:CG2	0.47	2.97	9	2
1:A:622:HIS:O	1:A:652:THR:CA	0.47	2.63	8	15
1:A:649:TYR:N	1:A:670:PHE:O	0.47	2.46	6	3
1:A:615:ASP:HA	1:A:688:PHE:CE2	0.47	2.45	1	2
1:A:618:LEU:HD12	1:A:681:ILE:HG13	0.47	1.86	12	2
1:A:659:LEU:CD2	1:A:670:PHE:CD2	0.47	2.96	14	5
1:A:670:PHE:CD1	1:A:671:LEU:N	0.47	2.83	8	2
1:A:587:ILE:HG23	1:A:588:ILE:HD13	0.47	1.87	14	4
1:A:618:LEU:HB2	1:A:681:ILE:HD12	0.46	1.86	6	4
1:A:603:ILE:HG12	1:A:611:CYS:HB3	0.46	1.87	3	4
1:A:656:VAL:CG2	1:A:658:TYR:CZ	0.46	2.98	3	2
1:A:613:ILE:HG12	1:A:692:PHE:CZ	0.46	2.45	14	15
1:A:602:PHE:O	1:A:611:CYS:N	0.46	2.47	6	7
1:A:588:ILE:CG2	1:A:612:LYS:O	0.46	2.64	5	1
1:A:651:HIS:CD2	1:A:665:ILE:O	0.46	2.69	1	15
1:A:703:PHE:CZ	1:A:704:ASN:HB3	0.46	2.46	14	6
1:A:587:ILE:N	1:A:689:VAL:O	0.46	2.47	5	1
1:A:657:SER:OG	1:A:664:MET:HB2	0.46	2.11	15	3
1:A:577:PHE:CG	1:A:578:LEU:N	0.46	2.82	17	4
1:A:586:SER:HB3	1:A:691:GLY:N	0.46	2.25	18	2
1:A:582:PRO:HB2	1:A:588:ILE:HG22	0.46	1.87	19	1
1:A:603:ILE:CG2	1:A:611:CYS:HB3	0.46	2.34	1	5
1:A:644:LEU:HD22	1:A:702:LEU:C	0.46	2.35	16	7
1:A:601:PHE:HB3	1:A:625:ILE:HG23	0.46	1.88	12	1
1:A:596:GLN:CG	1:A:700:THR:HG21	0.46	2.40	17	1
1:A:582:PRO:HG2	1:A:590:GLU:O	0.46	2.10	15	16
1:A:578:LEU:HD23	1:A:594:ILE:CD1	0.46	2.40	5	3
1:A:603:ILE:N	1:A:623:CYS:O	0.46	2.48	15	20
1:A:604:GLY:HA2	1:A:618:LEU:CD2	0.46	2.41	18	13
1:A:621:VAL:CG1	1:A:727:VAL:CG2	0.46	2.94	15	4

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:588:ILE:O	1:A:588:ILE:CG2	0.46	2.64	6	4
1:A:602:PHE:O	1:A:609:CYS:HB3	0.46	2.11	1	5
1:A:698:ASP:OD1	1:A:698:ASP:N	0.46	2.49	5	13
1:A:583:LEU:N	1:A:583:LEU:CD2	0.46	2.79	9	2
1:A:588:ILE:HD13	1:A:613:ILE:HA	0.46	1.86	17	1
1:A:658:TYR:CE1	1:A:663:ARG:CG	0.46	2.99	7	4
1:A:673:GLN:O	1:A:694:VAL:HG11	0.46	2.11	12	3
1:A:624:PHE:CZ	1:A:726:LEU:HD11	0.46	2.45	12	1
1:A:659:LEU:HA	1:A:678:ILE:HG22	0.46	1.88	14	1
1:A:587:ILE:CD1	1:A:690:ILE:HD11	0.46	2.41	15	1
1:A:615:ASP:HA	1:A:688:PHE:CZ	0.46	2.46	19	1
1:A:659:LEU:CD1	1:A:670:PHE:CD1	0.46	2.99	18	1
1:A:621:VAL:HG11	1:A:727:VAL:HG22	0.45	1.88	2	2
1:A:659:LEU:HD21	1:A:676:ASP:OD1	0.45	2.10	10	1
1:A:587:ILE:CG2	1:A:690:ILE:CD1	0.45	2.92	7	5
1:A:659:LEU:CD2	1:A:678:ILE:CG1	0.45	2.94	8	1
1:A:577:PHE:CE2	1:A:702:LEU:CD2	0.45	2.99	10	1
1:A:577:PHE:CE1	1:A:702:LEU:CD2	0.45	2.99	12	1
1:A:659:LEU:CD1	1:A:678:ILE:CG2	0.45	2.94	14	1
1:A:613:ILE:HD13	1:A:618:LEU:CD1	0.45	2.41	17	1
1:A:615:ASP:O	1:A:616:ASN:C	0.45	2.58	6	11
1:A:577:PHE:CD2	1:A:578:LEU:HB2	0.45	2.47	9	2
1:A:648:TRP:CH2	1:A:671:LEU:CG	0.45	3.00	14	2
1:A:651:HIS:HB2	1:A:657:SER:HB3	0.45	1.88	6	3
1:A:609:CYS:O	1:A:610:ASN:C	0.45	2.59	15	9
1:A:615:ASP:HB2	1:A:618:LEU:HB3	0.45	1.88	13	4
1:A:615:ASP:HB2	1:A:618:LEU:CB	0.45	2.42	11	5
1:A:655:ASN:O	1:A:656:VAL:HB	0.45	2.10	6	4
1:A:615:ASP:OD1	1:A:688:PHE:CE2	0.45	2.68	15	4
1:A:700:THR:CG2	1:A:702:LEU:HD12	0.45	2.42	18	1
1:A:681:ILE:O	1:A:689:VAL:HA	0.45	2.12	1	1
1:A:615:ASP:OD2	1:A:690:ILE:CD1	0.45	2.65	4	3
1:A:583:LEU:HD22	1:A:586:SER:HB3	0.45	1.89	5	1
1:A:601:PHE:HB3	1:A:625:ILE:HB	0.45	1.88	20	1
1:A:624:PHE:CE1	1:A:650:CYS:HB3	0.45	2.46	12	4
1:A:682:TRP:C	1:A:682:TRP:CD1	0.45	2.95	6	3
1:A:586:SER:OG	1:A:691:GLY:N	0.45	2.49	12	2
1:A:618:LEU:HD11	1:A:680:ILE:HG21	0.45	1.88	16	5
1:A:604:GLY:HA3	1:A:620:ARG:C	0.45	2.36	20	7
1:A:615:ASP:CB	1:A:618:LEU:HB3	0.45	2.42	19	3
1:A:581:LYS:HG2	1:A:591:SER:HB3	0.45	1.89	16	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:622:HIS:CG	1:A:653:GLY:HA3	0.44	2.47	3	12
1:A:583:LEU:HD13	1:A:585:ASP:CG	0.44	2.37	10	1
1:A:590:GLU:CG	1:A:591:SER:N	0.44	2.81	11	2
1:A:621:VAL:O	1:A:623:CYS:N	0.44	2.50	1	5
1:A:629:ARG:HD2	1:A:644:LEU:O	0.44	2.13	8	1
1:A:659:LEU:CD2	1:A:678:ILE:CG2	0.44	2.96	11	2
1:A:644:LEU:N	1:A:644:LEU:CD2	0.44	2.80	18	1
1:A:583:LEU:HD12	1:A:586:SER:OG	0.44	2.12	1	1
1:A:584:PRO:HA	1:A:589:GLN:CD	0.44	2.38	14	3
1:A:651:HIS:ND1	1:A:657:SER:HB3	0.44	2.28	2	2
1:A:588:ILE:CG1	1:A:612:LYS:O	0.44	2.66	6	5
1:A:583:LEU:HD11	1:A:677:GLU:OE2	0.44	2.12	4	1
1:A:577:PHE:CE2	1:A:702:LEU:HD21	0.44	2.48	8	1
1:A:578:LEU:HD13	1:A:696:ILE:HG12	0.44	1.89	18	1
1:A:624:PHE:CE2	1:A:650:CYS:HB2	0.44	2.48	2	4
1:A:644:LEU:HG	1:A:703:PHE:HA	0.44	1.89	14	1
1:A:606:SER:O	1:A:609:CYS:SG	0.44	2.76	17	1
1:A:621:VAL:HG12	1:A:730:LEU:HD21	0.44	1.90	3	1
1:A:624:PHE:CE1	1:A:626:PHE:HB2	0.44	2.48	9	1
1:A:681:ILE:CG2	1:A:690:ILE:CG1	0.44	2.96	13	1
1:A:655:ASN:O	1:A:656:VAL:HG13	0.44	2.12	1	1
1:A:703:PHE:CE1	1:A:704:ASN:OD1	0.44	2.71	12	1
1:A:601:PHE:CE1	1:A:610:ASN:OD1	0.44	2.71	15	5
1:A:622:HIS:NE2	1:A:680:ILE:CG2	0.44	2.81	17	3
1:A:648:TRP:CZ3	1:A:671:LEU:CG	0.44	3.01	14	8
1:A:657:SER:OG	1:A:664:MET:CB	0.44	2.65	15	13
1:A:580:LEU:N	1:A:580:LEU:CD2	0.44	2.81	14	2
1:A:598:VAL:CG1	1:A:601:PHE:CD1	0.44	3.00	5	2
1:A:626:PHE:CE1	1:A:627:LYS:O	0.43	2.71	16	6
1:A:578:LEU:HD12	1:A:696:ILE:HG12	0.43	1.90	13	2
1:A:670:PHE:CD1	1:A:716:VAL:HG22	0.43	2.48	5	4
1:A:678:ILE:O	1:A:691:GLY:HA2	0.43	2.12	5	1
1:A:615:ASP:OD1	1:A:688:PHE:CD2	0.43	2.71	7	2
1:A:657:SER:HG	1:A:664:MET:HE3	0.43	1.73	15	1
1:A:651:HIS:CG	1:A:657:SER:CB	0.43	3.01	2	1
1:A:644:LEU:CB	1:A:703:PHE:HB3	0.43	2.44	18	1
1:A:649:TYR:HB2	1:A:672:LEU:CD1	0.43	2.43	6	6
1:A:587:ILE:H	1:A:690:ILE:HD13	0.43	1.73	13	2
1:A:694:VAL:O	1:A:694:VAL:CG1	0.43	2.66	8	1
1:A:648:TRP:CD2	1:A:669:LYS:CE	0.43	3.02	12	1
1:A:671:LEU:HD12	1:A:673:GLN:NE2	0.43	2.28	12	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:588:ILE:HD11	1:A:613:ILE:HA	0.43	1.89	19	1
1:A:602:PHE:HB2	1:A:609:CYS:HA	0.43	1.91	12	4
1:A:630:HIS:ND1	1:A:703:PHE:CG	0.43	2.87	13	3
1:A:622:HIS:CE1	1:A:681:ILE:HD11	0.43	2.48	14	1
1:A:722:GLU:O	1:A:726:LEU:CD2	0.43	2.66	16	2
1:A:670:PHE:CE1	1:A:716:VAL:HG22	0.43	2.48	5	2
1:A:655:ASN:CB	1:A:681:ILE:HG23	0.43	2.44	3	3
1:A:653:GLY:O	1:A:655:ASN:N	0.43	2.52	17	2
1:A:599:ASN:O	1:A:599:ASN:OD1	0.43	2.36	17	5
1:A:577:PHE:CD1	1:A:578:LEU:HB2	0.43	2.49	10	1
1:A:670:PHE:CE2	1:A:716:VAL:CG2	0.43	3.00	12	1
1:A:659:LEU:HD21	1:A:714:ARG:HH11	0.43	1.71	2	1
1:A:659:LEU:HD11	1:A:672:LEU:HD21	0.43	1.91	10	1
1:A:624:PHE:CD1	1:A:650:CYS:HB3	0.43	2.48	12	1
1:A:601:PHE:O	1:A:624:PHE:HA	0.43	2.14	20	1
1:A:599:ASN:OD1	1:A:599:ASN:C	0.43	2.61	3	6
1:A:681:ILE:HD12	1:A:690:ILE:HG13	0.43	1.90	10	1
1:A:577:PHE:HE1	1:A:702:LEU:HD22	0.43	1.73	13	1
1:A:582:PRO:HB2	1:A:588:ILE:CG2	0.43	2.43	19	2
1:A:659:LEU:CD1	1:A:670:PHE:CD2	0.43	3.01	16	1
1:A:613:ILE:HG12	1:A:692:PHE:CE1	0.43	2.49	1	2
1:A:603:ILE:O	1:A:623:CYS:O	0.43	2.37	12	1
1:A:613:ILE:CD1	1:A:680:ILE:CD1	0.43	2.96	1	3
1:A:659:LEU:HD11	1:A:678:ILE:CG2	0.43	2.44	1	1
1:A:580:LEU:HD12	1:A:594:ILE:CD1	0.43	2.43	6	1
1:A:587:ILE:CG2	1:A:614:GLU:O	0.43	2.66	17	2
1:A:615:ASP:HB3	1:A:618:LEU:HD13	0.43	1.91	17	1
1:A:630:HIS:CE1	1:A:646:ASP:OD2	0.42	2.72	1	2
1:A:724:LYS:O	1:A:727:VAL:CG1	0.42	2.67	9	8
1:A:583:LEU:HB3	1:A:584:PRO:HD2	0.42	1.91	11	1
1:A:605:ARG:N	1:A:618:LEU:HD23	0.42	2.29	12	2
1:A:613:ILE:HD11	1:A:690:ILE:HG21	0.42	1.90	17	1
1:A:644:LEU:HD12	1:A:701:GLY:O	0.42	2.13	18	1
1:A:601:PHE:CE1	1:A:610:ASN:CG	0.42	2.97	9	5
1:A:682:TRP:CD1	1:A:682:TRP:C	0.42	2.96	7	4
1:A:624:PHE:CE2	1:A:650:CYS:HB3	0.42	2.49	2	4
1:A:670:PHE:CE1	1:A:714:ARG:HD2	0.42	2.49	7	1
1:A:664:MET:C	1:A:665:ILE:HG23	0.42	2.40	8	1
1:A:681:ILE:CG2	1:A:690:ILE:HG12	0.42	2.45	13	2
1:A:614:GLU:CG	1:A:614:GLU:O	0.42	2.66	15	1
1:A:613:ILE:HD12	1:A:680:ILE:HD12	0.42	1.90	17	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:672:LEU:HD23	1:A:694:VAL:HG21	0.42	1.91	19	1
1:A:629:ARG:HD2	1:A:630:HIS:O	0.42	2.14	7	1
1:A:588:ILE:N	1:A:588:ILE:CD1	0.42	2.76	5	1
1:A:594:ILE:HG23	1:A:598:VAL:CB	0.42	2.43	6	4
1:A:602:PHE:CE2	1:A:730:LEU:HA	0.42	2.49	12	1
1:A:651:HIS:ND1	1:A:657:SER:CB	0.42	2.83	11	5
1:A:624:PHE:CD1	1:A:624:PHE:O	0.42	2.72	12	1
1:A:651:HIS:CG	1:A:657:SER:HB3	0.42	2.50	2	1
1:A:618:LEU:HG	1:A:622:HIS:CG	0.42	2.49	9	1
1:A:665:ILE:CG1	1:A:668:THR:CG2	0.42	2.98	20	7
1:A:578:LEU:C	1:A:578:LEU:CD2	0.42	2.92	8	1
1:A:675:GLY:N	1:A:694:VAL:O	0.42	2.52	13	1
1:A:686:ASN:O	1:A:687:LYS:HB2	0.42	2.15	13	1
1:A:644:LEU:HB2	1:A:703:PHE:HB3	0.42	1.90	14	1
1:A:600:PRO:HG2	1:A:602:PHE:CE1	0.42	2.49	15	1
1:A:580:LEU:CD1	1:A:625:ILE:CD1	0.42	2.97	17	3
1:A:588:ILE:HD13	1:A:613:ILE:N	0.42	2.30	17	1
1:A:577:PHE:CE1	1:A:578:LEU:HB2	0.42	2.50	8	2
1:A:615:ASP:CG	1:A:690:ILE:CD1	0.42	2.93	5	1
1:A:615:ASP:OD2	1:A:690:ILE:CG1	0.42	2.68	7	1
1:A:655:ASN:CB	1:A:681:ILE:HG12	0.42	2.45	7	1
1:A:592:LEU:CD1	1:A:611:CYS:SG	0.42	3.08	10	1
1:A:581:LYS:CD	1:A:591:SER:HB3	0.42	2.45	4	1
1:A:659:LEU:HD13	1:A:714:ARG:NH1	0.42	2.30	16	1
1:A:646:ASP:OD2	1:A:648:TRP:CZ2	0.42	2.73	19	1
1:A:602:PHE:CD2	1:A:730:LEU:OXT	0.41	2.73	1	2
1:A:602:PHE:CE2	1:A:730:LEU:O	0.41	2.73	8	3
1:A:630:HIS:ND1	1:A:646:ASP:OD2	0.41	2.53	9	1
1:A:588:ILE:CG2	1:A:692:PHE:CZ	0.41	2.95	17	1
1:A:587:ILE:HG12	1:A:614:GLU:O	0.41	2.15	6	3
1:A:577:PHE:HE2	1:A:702:LEU:HD11	0.41	1.69	6	1
1:A:602:PHE:CD2	1:A:730:LEU:O	0.41	2.73	9	4
1:A:690:ILE:CG2	1:A:691:GLY:N	0.41	2.83	5	1
1:A:649:TYR:CE1	1:A:678:ILE:HD11	0.41	2.49	7	1
1:A:604:GLY:CA	1:A:619:SER:O	0.41	2.68	18	1
1:A:681:ILE:HG23	1:A:688:PHE:O	0.41	2.14	19	1
1:A:603:ILE:HD11	1:A:625:ILE:HG22	0.41	1.90	12	1
1:A:578:LEU:HD13	1:A:647:ILE:HD13	0.41	1.91	20	1
1:A:613:ILE:CG2	1:A:690:ILE:CD1	0.41	2.96	5	2
1:A:580:LEU:HD21	1:A:625:ILE:CD1	0.41	2.46	2	1
1:A:619:SER:N	1:A:622:HIS:HB2	0.41	2.31	10	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:616:ASN:OD1	1:A:688:PHE:CZ	0.41	2.73	4	1
1:A:603:ILE:HB	1:A:623:CYS:O	0.41	2.15	13	3
1:A:615:ASP:CG	1:A:688:PHE:CE2	0.41	2.99	5	1
1:A:644:LEU:HD22	1:A:702:LEU:N	0.41	2.31	6	1
1:A:659:LEU:CD2	1:A:714:ARG:CZ	0.41	2.98	6	1
1:A:657:SER:OG	1:A:664:MET:HB3	0.41	2.15	8	1
1:A:672:LEU:CD2	1:A:694:VAL:HG21	0.41	2.45	14	1
1:A:686:ASN:HB3	1:A:688:PHE:CD1	0.41	2.50	7	1
1:A:690:ILE:HG22	1:A:691:GLY:N	0.41	2.31	8	1
1:A:659:LEU:CD1	1:A:678:ILE:CG1	0.41	2.96	12	1
1:A:703:PHE:CD2	1:A:704:ASN:HB3	0.41	2.51	18	1
1:A:629:ARG:CD	1:A:644:LEU:O	0.41	2.68	3	1
1:A:605:ARG:CG	1:A:615:ASP:O	0.41	2.69	7	1
1:A:670:PHE:CD1	1:A:670:PHE:C	0.41	2.98	8	1
1:A:659:LEU:HG	1:A:670:PHE:CD1	0.41	2.50	11	1
1:A:601:PHE:CD2	1:A:611:CYS:HB2	0.41	2.51	16	3
1:A:588:ILE:CB	1:A:613:ILE:HA	0.41	2.46	17	1
1:A:658:TYR:CE1	1:A:663:ARG:HG2	0.41	2.51	1	1
1:A:699:THR:O	1:A:699:THR:OG1	0.41	2.38	1	1
1:A:601:PHE:CZ	1:A:610:ASN:O	0.41	2.74	7	1
1:A:679:LYS:O	1:A:679:LYS:CG	0.41	2.68	7	1
1:A:583:LEU:HD12	1:A:583:LEU:H	0.41	1.75	19	3
1:A:607:GLU:C	1:A:609:CYS:N	0.41	2.79	12	1
1:A:622:HIS:C	1:A:652:THR:OG1	0.41	2.64	12	1
1:A:588:ILE:HG12	1:A:613:ILE:HG12	0.41	1.91	13	1
1:A:664:MET:HG2	1:A:716:VAL:CG2	0.41	2.46	14	1
1:A:703:PHE:CG	1:A:704:ASN:N	0.41	2.89	14	1
1:A:606:SER:HB2	1:A:620:ARG:CG	0.41	2.46	17	1
1:A:613:ILE:HD13	1:A:618:LEU:HD11	0.41	1.93	17	1
1:A:629:ARG:O	1:A:629:ARG:CG	0.41	2.69	18	1
1:A:699:THR:O	1:A:700:THR:O	0.41	2.38	18	1
1:A:664:MET:HG2	1:A:716:VAL:CG1	0.41	2.46	19	1
1:A:577:PHE:HB3	1:A:596:GLN:N	0.41	2.31	1	1
1:A:609:CYS:SG	1:A:620:ARG:O	0.41	2.77	3	1
1:A:583:LEU:H	1:A:583:LEU:CD2	0.41	2.25	5	1
1:A:602:PHE:CE2	1:A:730:LEU:C	0.41	2.99	9	2
1:A:587:ILE:HG13	1:A:588:ILE:HD13	0.41	1.92	15	1
1:A:659:LEU:CG	1:A:678:ILE:CG2	0.41	2.99	17	1
1:A:616:ASN:OD1	1:A:616:ASN:N	0.40	2.54	4	1
1:A:587:ILE:CG2	1:A:588:ILE:CD1	0.40	2.99	20	2
1:A:577:PHE:O	1:A:696:ILE:HA	0.40	2.15	15	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:651:HIS:CD2	1:A:651:HIS:C	0.40	2.99	1	1
1:A:659:LEU:HD11	1:A:672:LEU:CD2	0.40	2.46	8	1
1:A:655:ASN:O	1:A:656:VAL:CG1	0.40	2.69	12	1
1:A:587:ILE:HG23	1:A:588:ILE:CD1	0.40	2.46	14	1
1:A:582:PRO:HG2	1:A:590:GLU:H	0.40	1.76	16	1
1:A:593:GLU:OE1	1:A:593:GLU:N	0.40	2.54	9	1
1:A:703:PHE:N	1:A:703:PHE:CD1	0.40	2.90	14	1
1:A:616:ASN:OD1	1:A:688:PHE:CE2	0.40	2.74	15	1
1:A:665:ILE:HG12	1:A:668:THR:HG23	0.40	1.91	17	1
1:A:587:ILE:CG1	1:A:690:ILE:CG1	0.40	2.99	1	1
1:A:624:PHE:CE1	1:A:650:CYS:HB2	0.40	2.52	3	1
1:A:649:TYR:CE2	1:A:678:ILE:HG21	0.40	2.51	8	2
1:A:609:CYS:C	1:A:611:CYS:N	0.40	2.78	9	1
1:A:603:ILE:CG2	1:A:613:ILE:HD12	0.40	2.46	10	1
1:A:588:ILE:HD12	1:A:690:ILE:CD1	0.40	2.41	13	1
1:A:673:GLN:N	1:A:676:ASP:OD2	0.40	2.53	17	1
1:A:645:ASP:O	1:A:702:LEU:CD2	0.40	2.69	18	1
1:A:670:PHE:CD1	1:A:715:VAL:O	0.40	2.74	4	1
1:A:577:PHE:CE2	1:A:702:LEU:HD23	0.40	2.51	10	1
1:A:588:ILE:HD13	1:A:588:ILE:N	0.40	2.30	12	1
1:A:582:PRO:HA	1:A:691:GLY:O	0.40	2.16	14	1
1:A:619:SER:O	1:A:622:HIS:HB2	0.40	2.16	14	1

6.3 Torsion angles [i](#)

6.3.1 Protein backbone [i](#)

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	132/158 (84%)	111±2 (84±2%)	16±2 (12±1%)	5±1 (4±1%)	4	30
All	All	2640/3160 (84%)	2228 (84%)	310 (12%)	102 (4%)	4	30

All 14 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	656	VAL	20
1	A	596	GLN	18
1	A	660	ASN	18
1	A	622	HIS	14
1	A	714	ARG	10
1	A	654	THR	5
1	A	595	GLN	5
1	A	667	GLY	3
1	A	700	THR	3
1	A	674	ASP	2
1	A	665	ILE	1
1	A	688	PHE	1
1	A	644	LEU	1
1	A	687	LYS	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	125/142 (88%)	86±3 (69±3%)	39±3 (31±3%)	1	15
All	All	2500/2840 (88%)	1720 (69%)	780 (31%)	1	15

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	583	LEU	20
1	A	591	SER	20
1	A	612	LYS	20
1	A	628	LYS	20
1	A	652	THR	20
1	A	657	SER	20
1	A	668	THR	20
1	A	694	VAL	20
1	A	581	LYS	18
1	A	606	SER	18
1	A	618	LEU	18
1	A	671	LEU	18

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Mol	Chain	Res	Type	Models (Total)
1	A	598	VAL	18
1	A	623	CYS	17
1	A	676	ASP	17
1	A	610	ASN	16
1	A	688	PHE	16
1	A	704	ASN	16
1	A	619	SER	15
1	A	656	VAL	15
1	A	718	LYS	15
1	A	589	GLN	14
1	A	595	GLN	14
1	A	677	GLU	14
1	A	684	LYS	14
1	A	629	ARG	13
1	A	729	LYS	13
1	A	659	LEU	12
1	A	687	LYS	12
1	A	702	LEU	12
1	A	697	ASN	11
1	A	587	ILE	11
1	A	617	ARG	10
1	A	730	LEU	10
1	A	662	ASN	9
1	A	683	ASP	9
1	A	728	LYS	9
1	A	596	GLN	9
1	A	645	ASP	9
1	A	660	ASN	8
1	A	620	ARG	8
1	A	695	GLU	8
1	A	577	PHE	8
1	A	614	GLU	7
1	A	725	ASP	7
1	A	669	LYS	7
1	A	714	ARG	7
1	A	722	GLU	7
1	A	607	GLU	6
1	A	679	LYS	6
1	A	723	GLU	6
1	A	650	CYS	6
1	A	719	GLN	6
1	A	693	LYS	6

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Mol	Chain	Res	Type	Models (Total)
1	A	576	ARG	5
1	A	686	ASN	5
1	A	726	LEU	5
1	A	608	ASP	5
1	A	663	ARG	5
1	A	599	ASN	5
1	A	724	LYS	4
1	A	594	ILE	4
1	A	678	ILE	4
1	A	665	ILE	4
1	A	681	ILE	4
1	A	616	ASN	4
1	A	672	LEU	3
1	A	578	LEU	3
1	A	685	ASN	3
1	A	615	ASP	3
1	A	664	MET	3
1	A	674	ASP	3
1	A	661	ASN	3
1	A	593	GLU	2
1	A	698	ASP	2
1	A	717	LEU	2
1	A	700	THR	2
1	A	588	ILE	2
1	A	624	PHE	2
1	A	625	ILE	2
1	A	585	ASP	1
1	A	627	LYS	1
1	A	590	GLU	1
1	A	580	LEU	1
1	A	592	LEU	1
1	A	613	ILE	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 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