



Full wwPDB NMR Structure Validation Report ⓘ

Apr 26, 2016 – 05:29 PM BST

PDB ID : 1UTA
Title : SOLUTION STRUCTURE OF THE C-TERMINAL RNP DOMAIN FROM
THE DIVISOME PROTEIN FTSN
Authors : Yang, J.-C.; Van Den Ent, F.; Neuhaus, D.; Brevier, J.; Lowe, J.
Deposited on : 2003-12-04

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

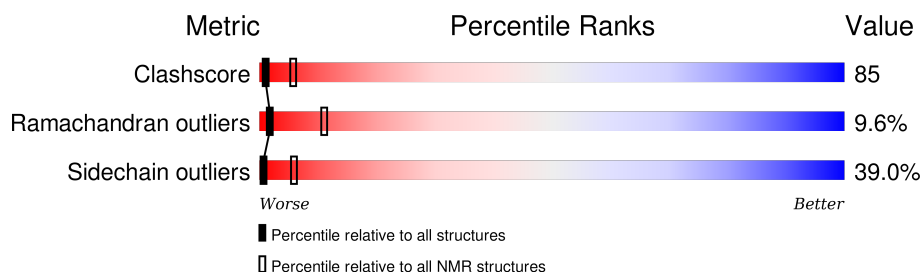
1 Overall quality at a glance

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	81	

2 Ensemble composition and analysis

This entry contains 45 models. Model 5 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 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:247-A:317 (71)	0.42	5

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 8 clusters and 7 single-model clusters were found.

Cluster number	Models
1	9, 10, 16, 19, 21, 29, 30, 36, 37
2	5, 6, 14, 15, 18, 20, 25
3	1, 2, 3, 4, 12, 13, 17
4	11, 27, 28, 32, 33, 34
5	23, 38, 40
6	44, 45
7	24, 35
8	31, 42
Single-model clusters	7; 8; 22; 26; 39; 41; 43

3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 1181 atoms, of which 588 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called CELL DIVISION PROTEIN FTSN.

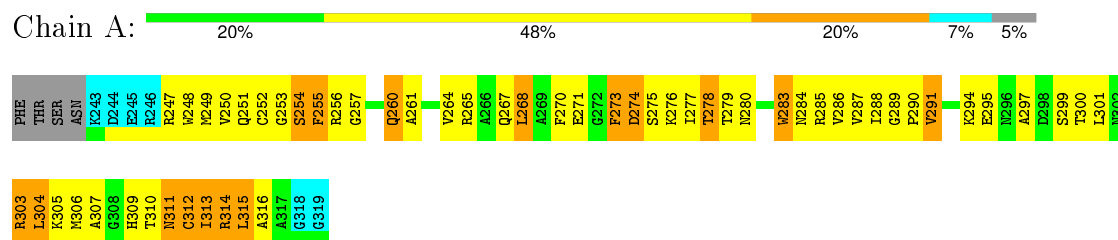
Mol	Chain	Residues	Atoms						Trace
1	A	77	Total	C	H	N	O	S	0
			1181	362	588	116	111	4	

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: CELL DIVISION PROTEIN FTSN

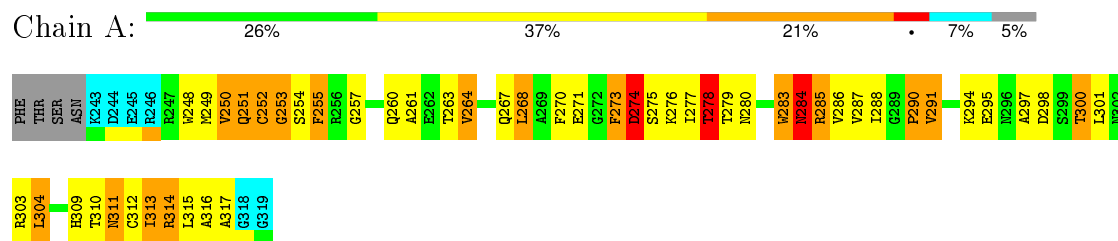


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

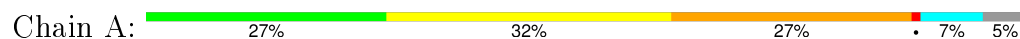
4.2.1 Score per residue for model 1

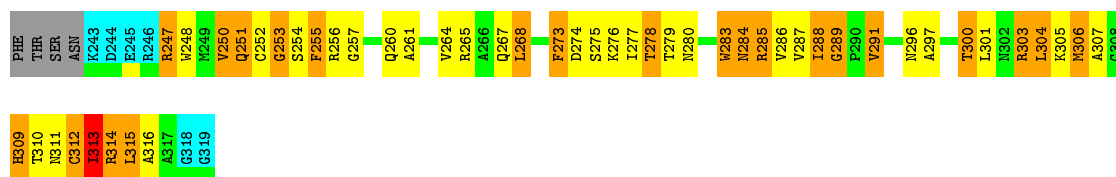
- Molecule 1: CELL DIVISION PROTEIN FTSN



4.2.2 Score per residue for model 2

- Molecule 1: CELL DIVISION PROTEIN FTSN

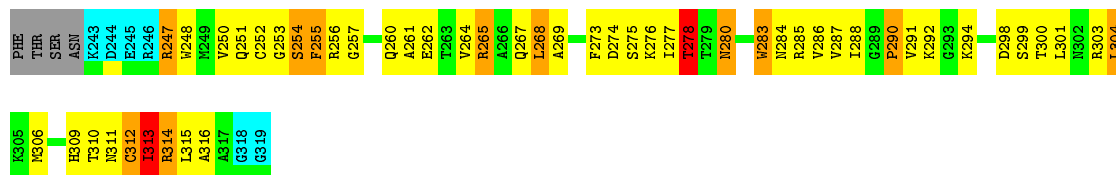




4.2.3 Score per residue for model 3

- Molecule 1: CELL DIVISION PROTEIN FTSN

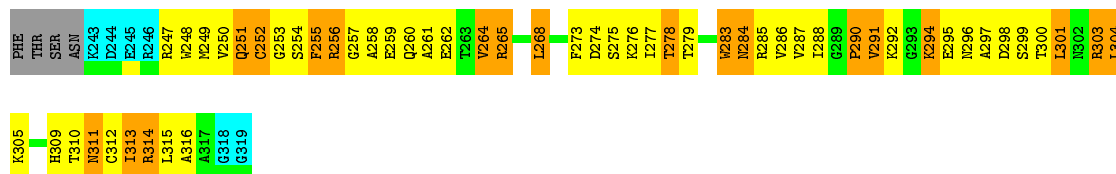
Chain A:



4.2.4 Score per residue for model 4

- Molecule 1: CELL DIVISION PROTEIN FTSN

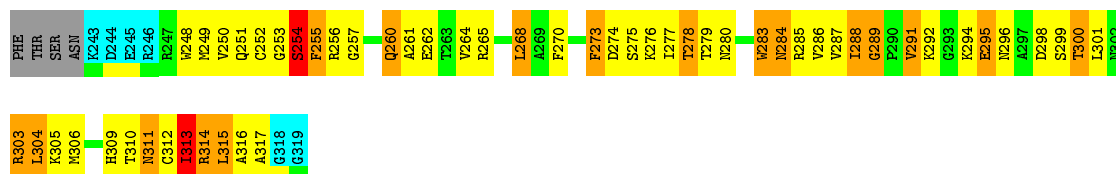
Chain A:



4.2.5 Score per residue for model 5 (medoid)

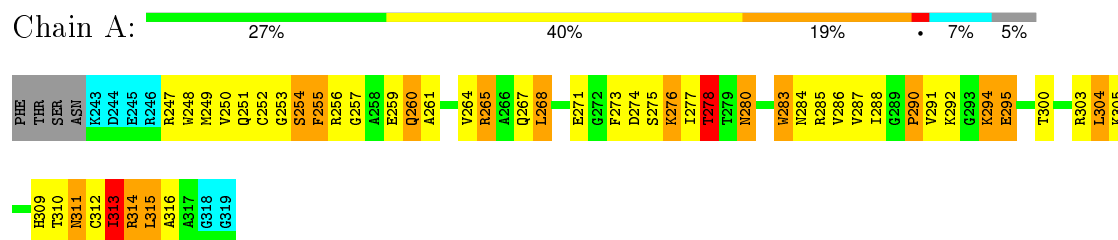
- Molecule 1: CELL DIVISION PROTEIN FTSN

Chain A:



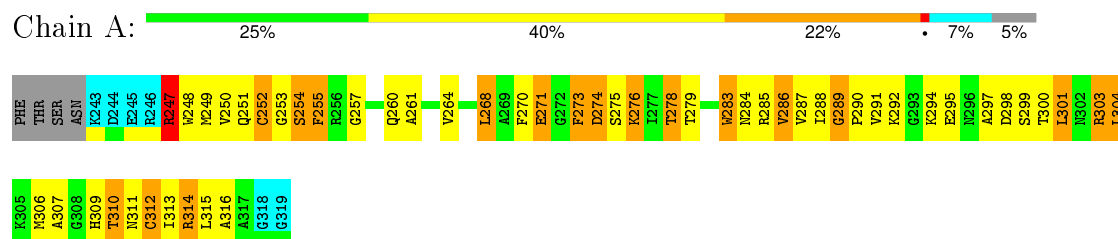
4.2.6 Score per residue for model 6

- Molecule 1: CELL DIVISION PROTEIN FTSN



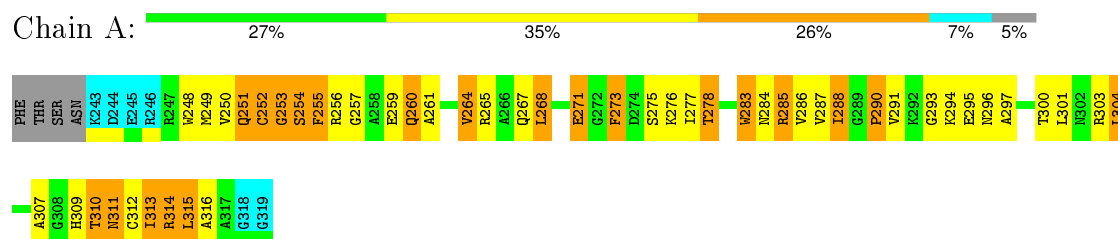
4.2.7 Score per residue for model 7

- Molecule 1: CELL DIVISION PROTEIN FTSN



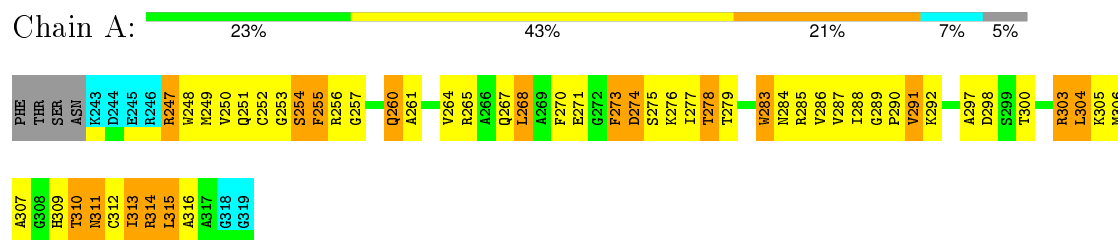
4.2.8 Score per residue for model 8

- Molecule 1: CELL DIVISION PROTEIN FTSN



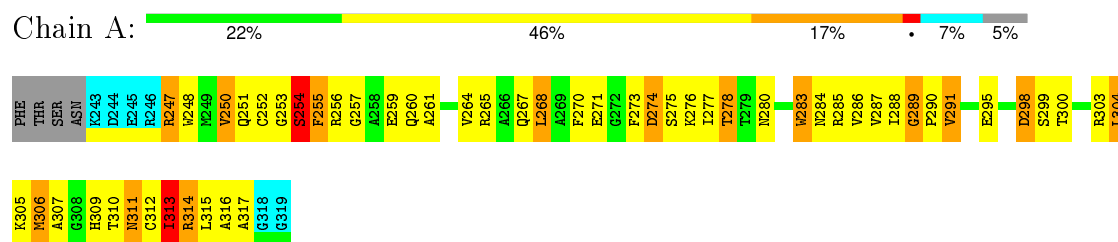
4.2.9 Score per residue for model 9

- Molecule 1: CELL DIVISION PROTEIN FTSN



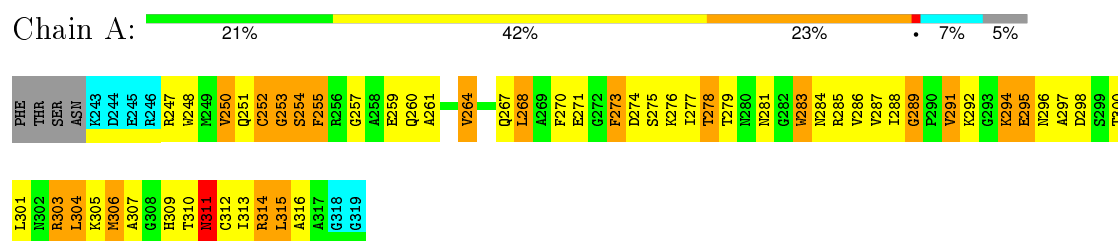
4.2.10 Score per residue for model 10

- Molecule 1: CELL DIVISION PROTEIN FTSN



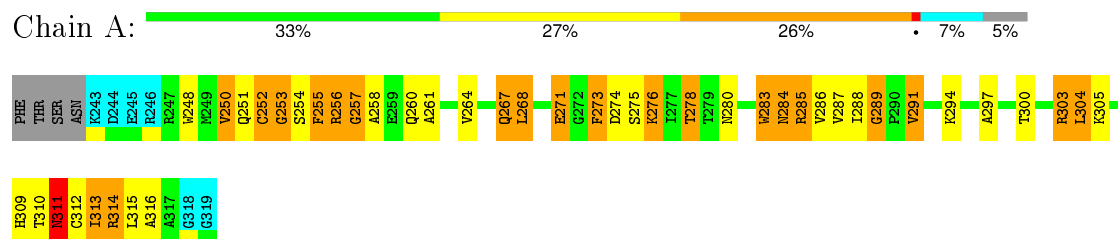
4.2.11 Score per residue for model 11

- Molecule 1: CELL DIVISION PROTEIN FTSN



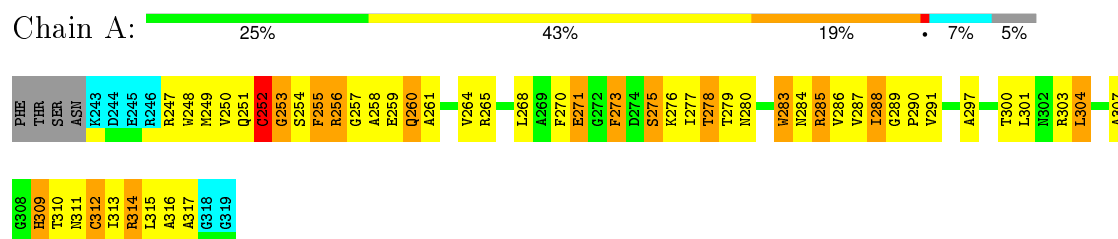
4.2.12 Score per residue for model 12

- Molecule 1: CELL DIVISION PROTEIN FTSN



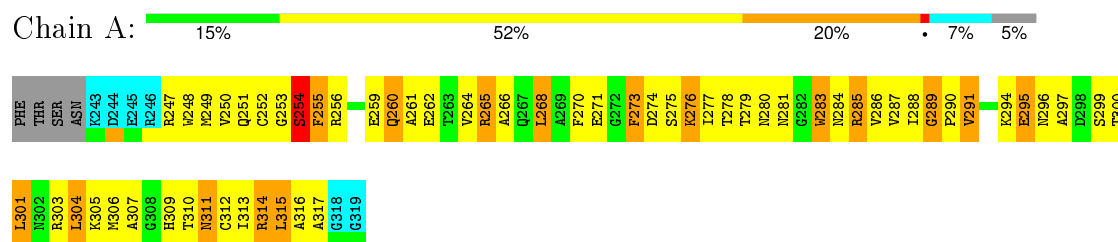
4.2.13 Score per residue for model 13

- Molecule 1: CELL DIVISION PROTEIN FTSN



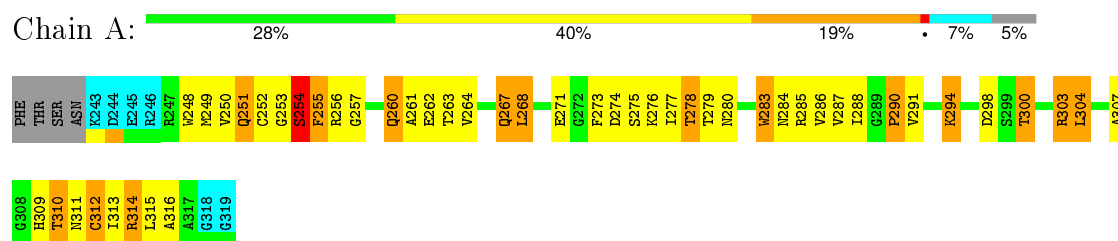
4.2.14 Score per residue for model 14

- Molecule 1: CELL DIVISION PROTEIN FTSN



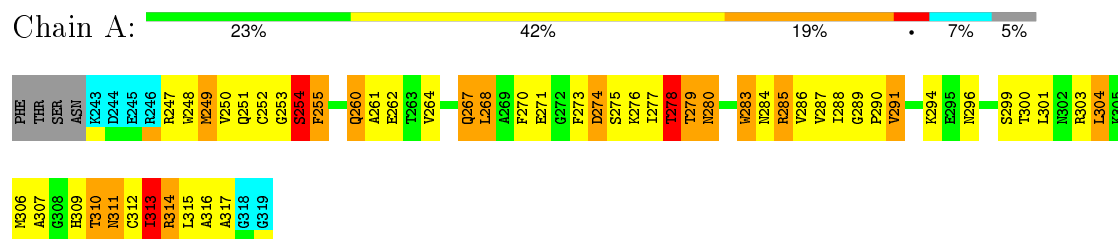
4.2.15 Score per residue for model 15

- Molecule 1: CELL DIVISION PROTEIN FTSN



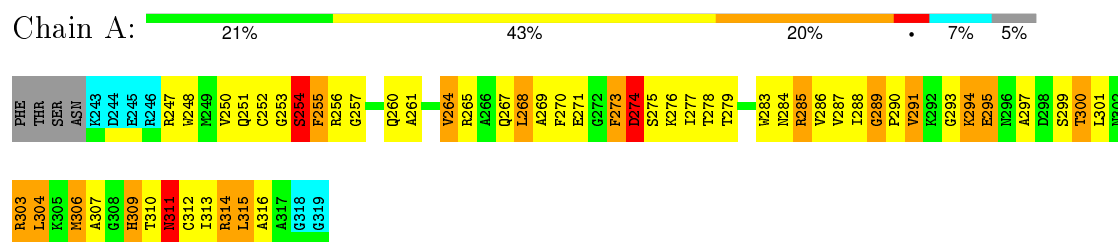
4.2.16 Score per residue for model 16

- Molecule 1: CELL DIVISION PROTEIN FTSN



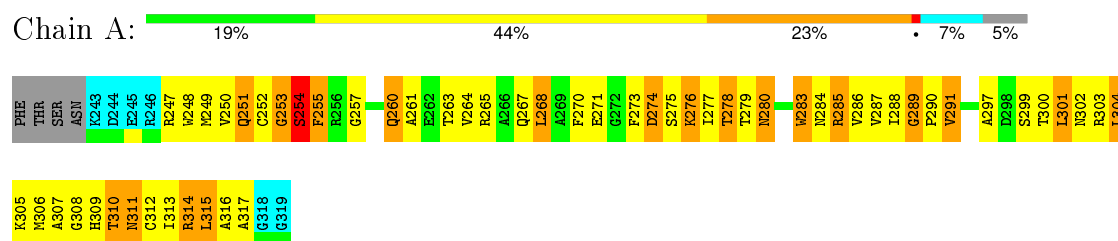
4.2.18 Score per residue for model 18

- Molecule 1: CELL DIVISION PROTEIN FTSN



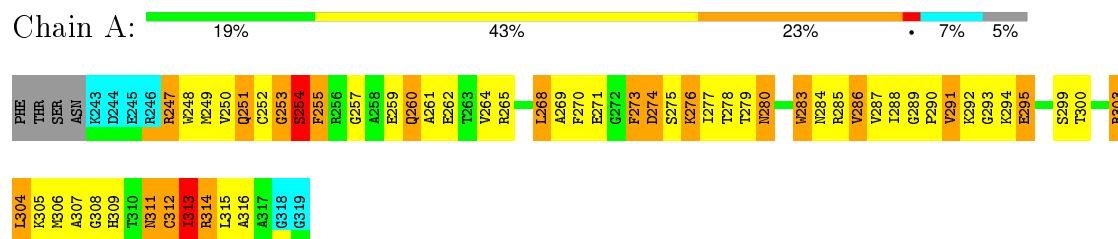
4.2.19 Score per residue for model 19

- Molecule 1: CELL DIVISION PROTEIN FTSN



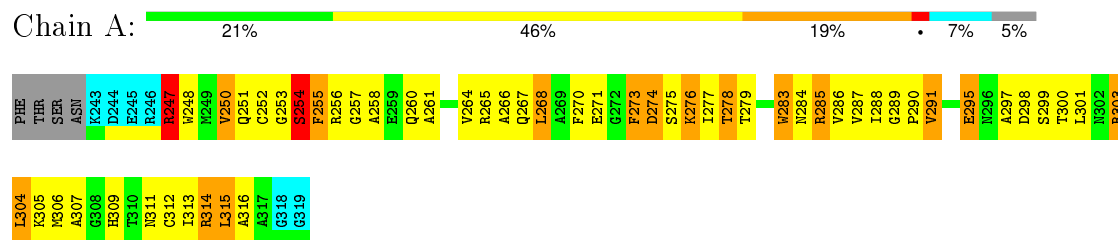
4.2.20 Score per residue for model 20

- Molecule 1: CELL DIVISION PROTEIN FTSN



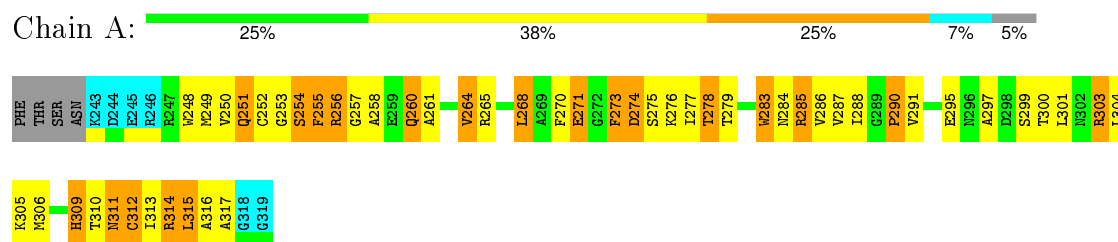
4.2.21 Score per residue for model 21

- Molecule 1: CELL DIVISION PROTEIN FTSN



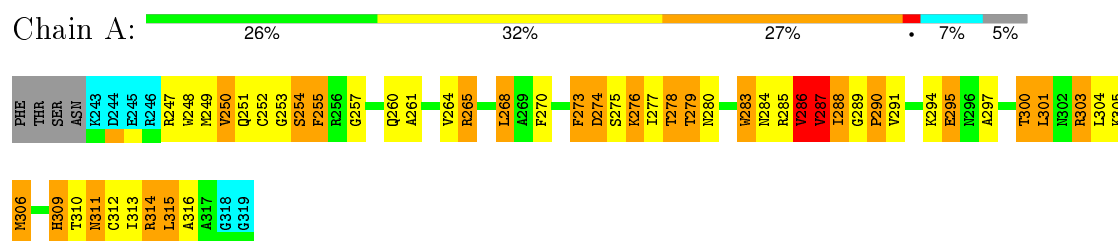
4.2.22 Score per residue for model 22

- Molecule 1: CELL DIVISION PROTEIN FTSN



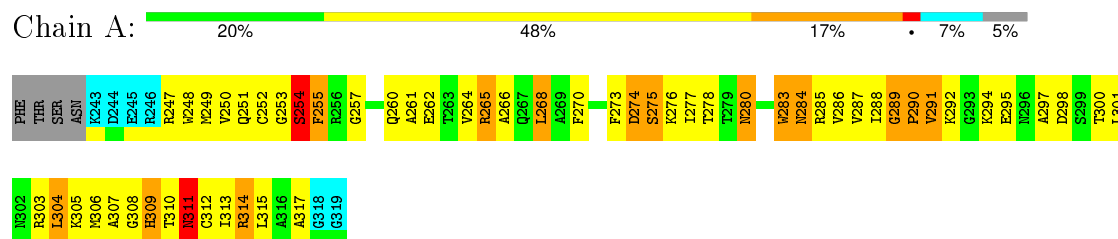
4.2.23 Score per residue for model 23

- Molecule 1: CELL DIVISION PROTEIN FTSN



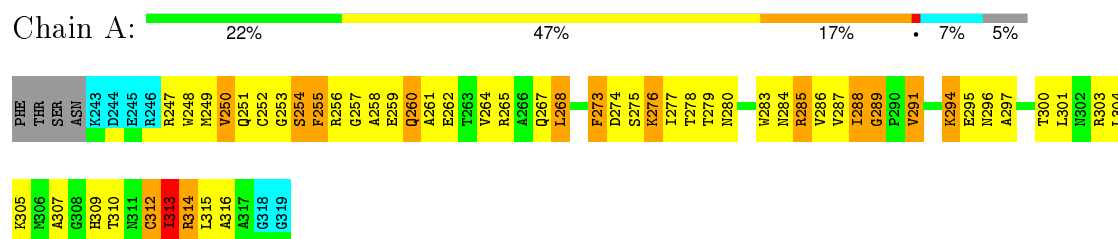
4.2.24 Score per residue for model 24

- Molecule 1: CELL DIVISION PROTEIN FTSN



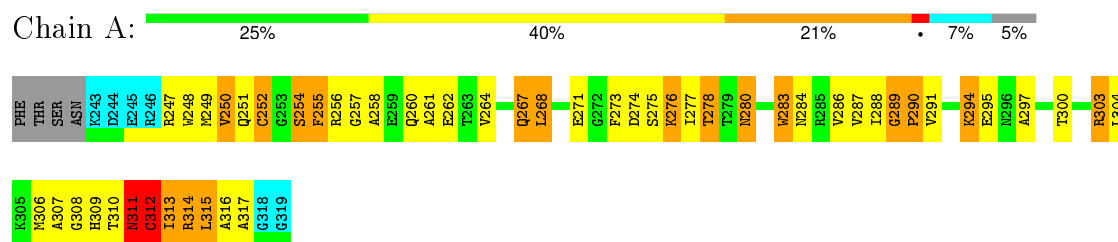
4.2.25 Score per residue for model 25

- Molecule 1: CELL DIVISION PROTEIN FTSN



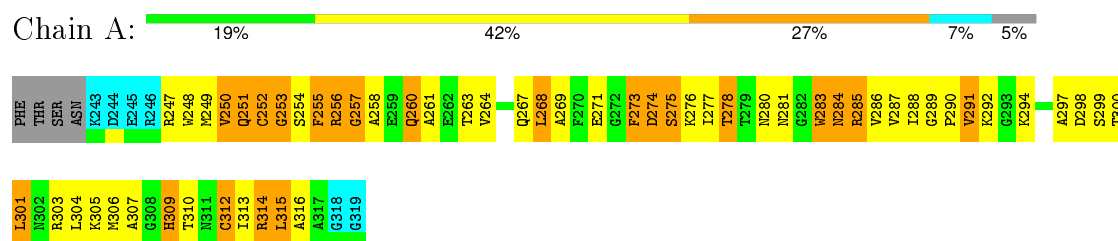
4.2.26 Score per residue for model 26

- Molecule 1: CELL DIVISION PROTEIN FTSN



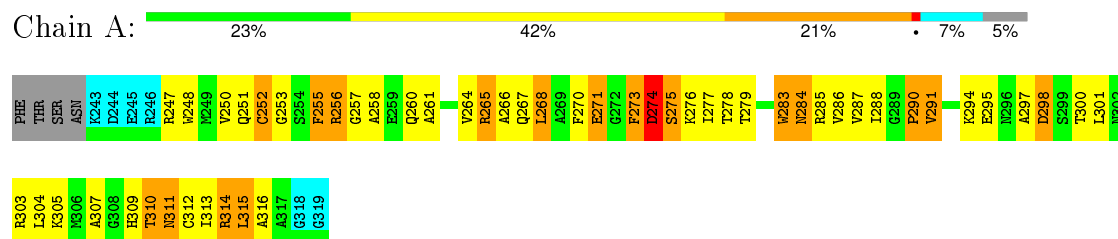
4.2.27 Score per residue for model 27

- Molecule 1: CELL DIVISION PROTEIN FTSN



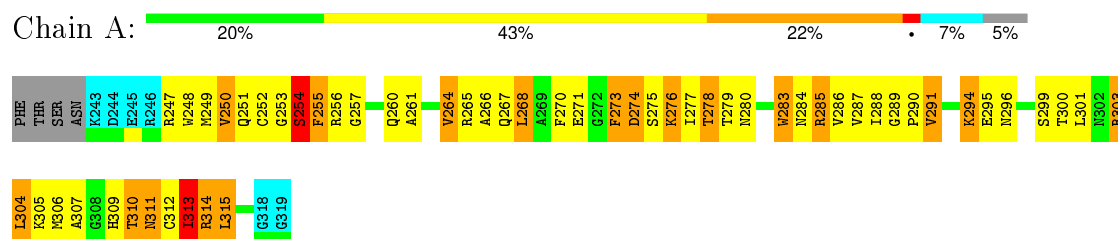
4.2.28 Score per residue for model 28

- Molecule 1: CELL DIVISION PROTEIN FTSN




4.2.29 Score per residue for model 29

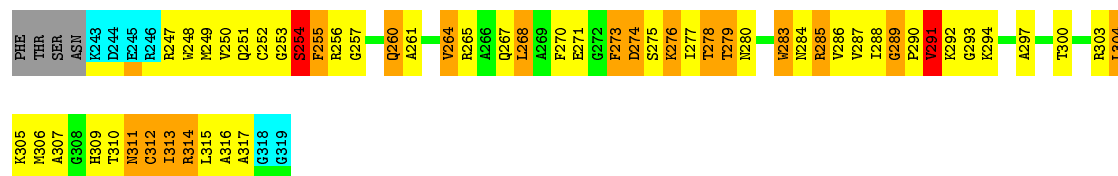
- Molecule 1: CELL DIVISION PROTEIN FTSN



4.2.30 Score per residue for model 30

- Molecule 1: CELL DIVISION PROTEIN FTSN

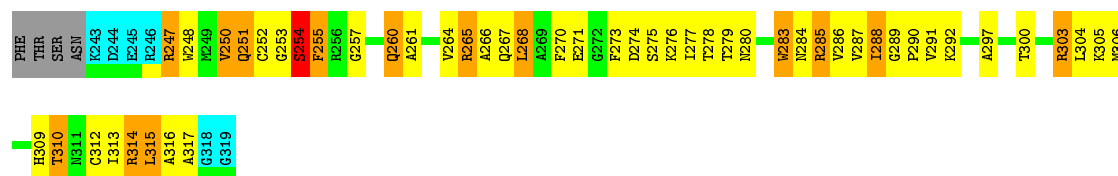
Chain A: 



4.2.31 Score per residue for model 31

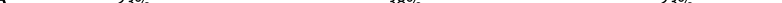
- Molecule 1: CELL DIVISION PROTEIN FTSN

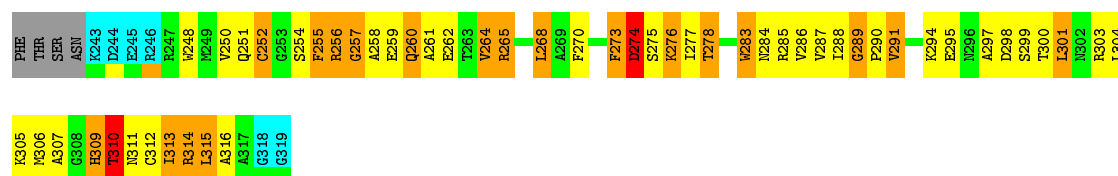
Chain A: 26% 43% 17% 7% 5%



4.2.32 Score per residue for model 32

- Molecule 1: CELL DIVISION PROTEIN FTSN

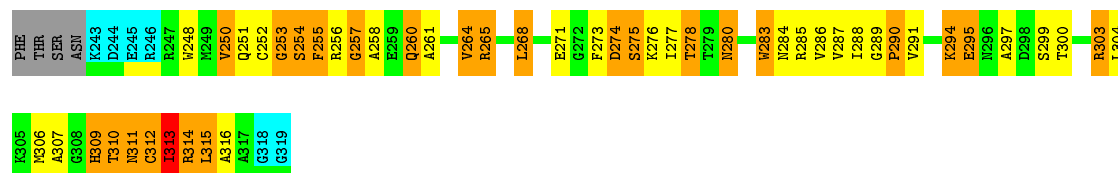
Chain A:  23% 38% 23% 7% 5%



4.2.33 Score per residue for model 33

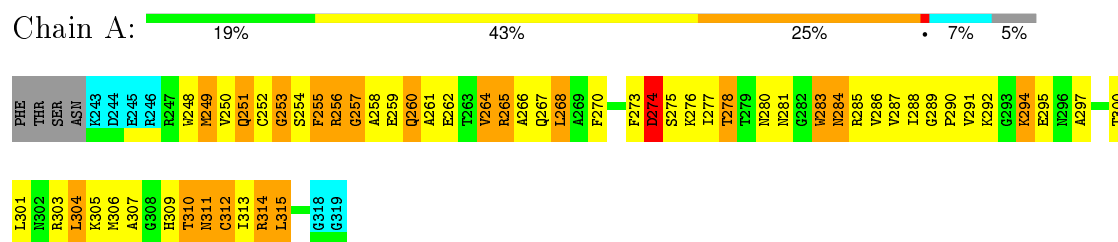
- Molecule 1: CELL DIVISION PROTEIN FTSN

Chain A:



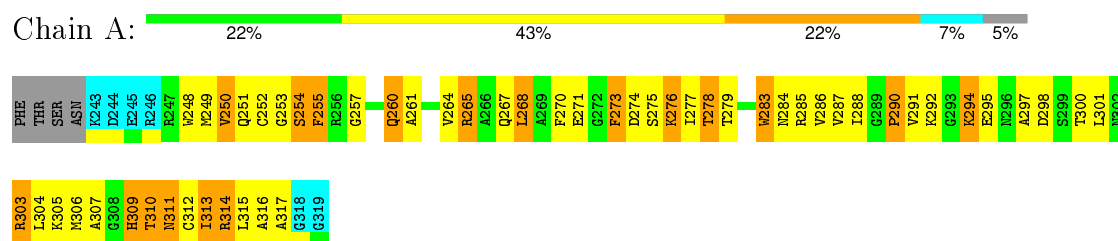
4.2.34 Score per residue for model 34

- Molecule 1: CELL DIVISION PROTEIN FTSN



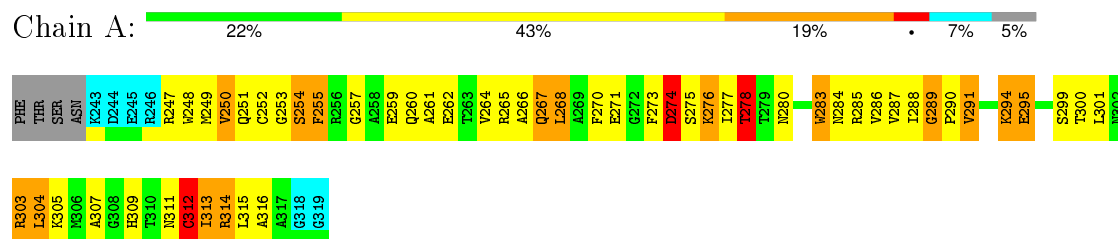
4.2.35 Score per residue for model 35

- Molecule 1: CELL DIVISION PROTEIN FTSN



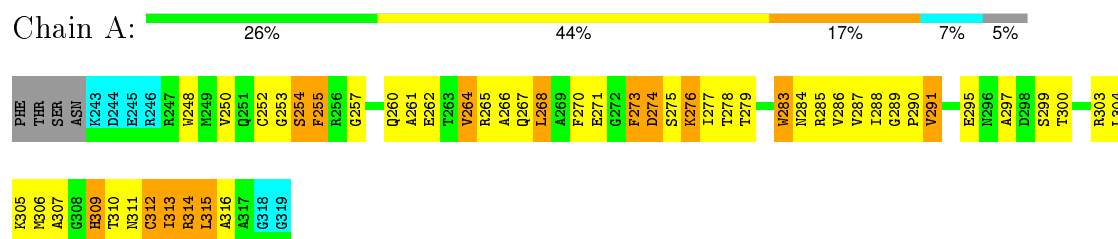
4.2.36 Score per residue for model 36

- Molecule 1: CELL DIVISION PROTEIN FTSN



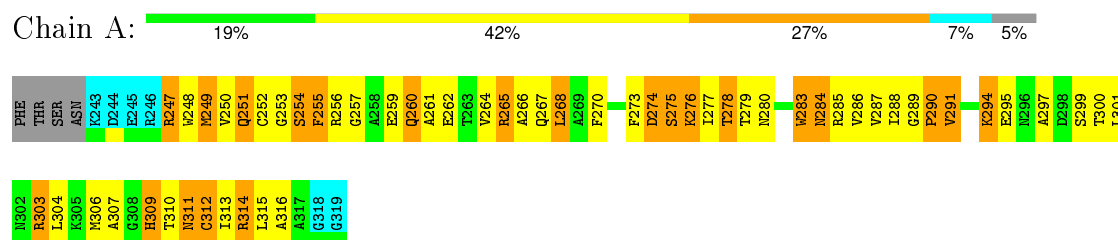
4.2.37 Score per residue for model 37

- Molecule 1: CELL DIVISION PROTEIN FTSN



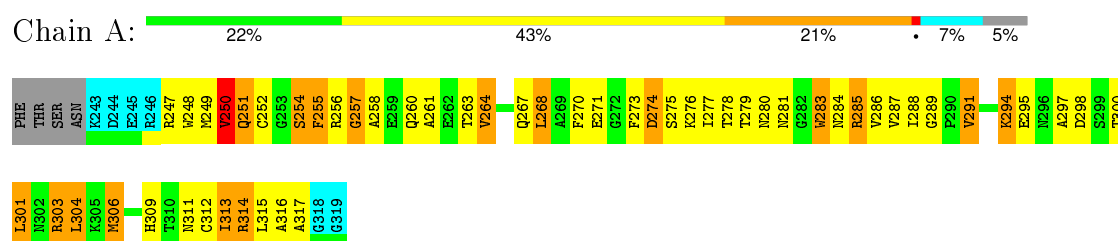
4.2.38 Score per residue for model 38

- Molecule 1: CELL DIVISION PROTEIN FTSN



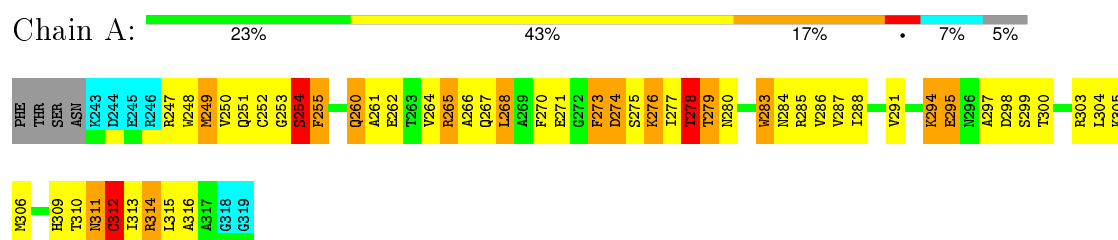
4.2.39 Score per residue for model 39

- Molecule 1: CELL DIVISION PROTEIN FTSN



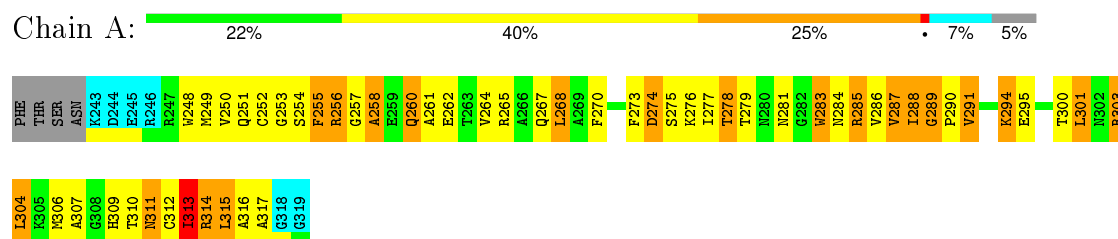
4.2.40 Score per residue for model 40

- Molecule 1: CELL DIVISION PROTEIN FTSN



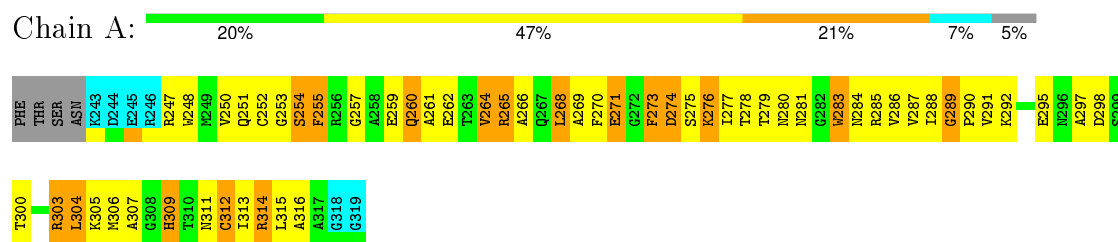
4.2.41 Score per residue for model 41

- Molecule 1: CELL DIVISION PROTEIN FTSN



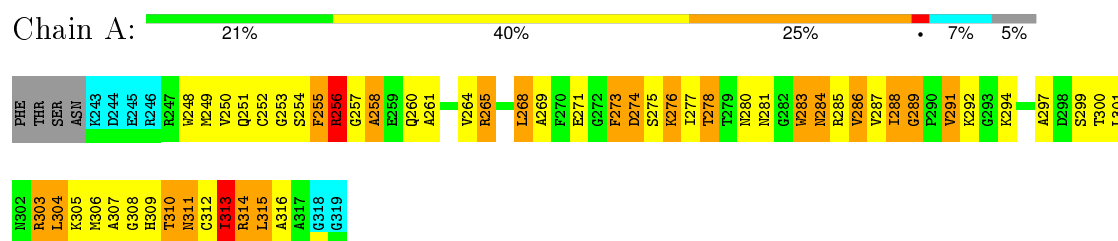
4.2.42 Score per residue for model 42

- Molecule 1: CELL DIVISION PROTEIN FTSN



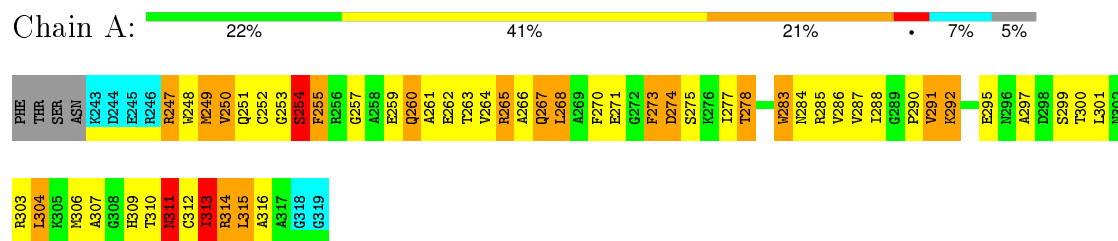
4.2.43 Score per residue for model 43

- Molecule 1: CELL DIVISION PROTEIN FTSN



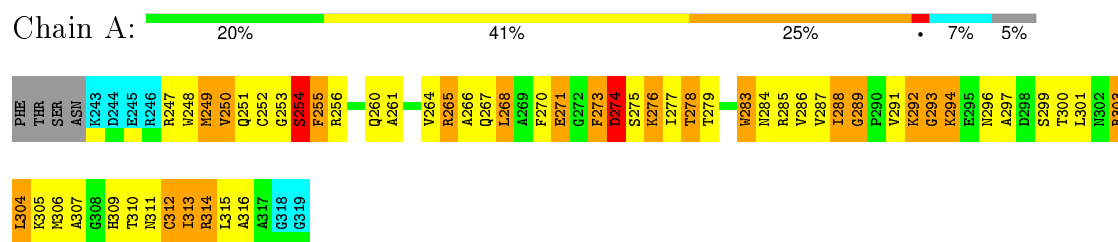
4.2.44 Score per residue for model 44

- Molecule 1: CELL DIVISION PROTEIN FTSN



4.2.45 Score per residue for model 45

- Molecule 1: CELL DIVISION PROTEIN FTSN



5 Refinement protocol and experimental data overview

The models were refined using the following method: *SIMULATED ANNEALING*.

Of the 50 calculated structures, 45 were deposited, based on the following criterion: *LOW NOE ENERGY*.

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

Software name	Classification	Version
CNS	refinement	
CNS	structure solution	

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	547	545	544	93±11
All	All	24615	24525	24480	4166

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 85.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:250:VAL:HG11	1:A:288:ILE:HD12	1.13	1.18	16	29
1:A:277:ILE:HG22	1:A:286:VAL:HG22	1.09	1.13	36	4
1:A:291:VAL:HG21	1:A:297:ALA:HB2	1.03	1.29	44	6
1:A:250:VAL:HG21	1:A:288:ILE:HD12	1.02	1.25	4	7
1:A:248:TRP:NE1	1:A:297:ALA:HB3	1.02	1.70	44	2
1:A:268:LEU:HD12	1:A:273:PHE:CD2	1.00	1.91	32	12
1:A:268:LEU:HD13	1:A:304:LEU:HD21	0.99	1.33	21	10
1:A:268:LEU:HD13	1:A:286:VAL:HG11	0.96	1.37	19	2
1:A:268:LEU:HD22	1:A:273:PHE:CZ	0.96	1.95	18	2
1:A:275:SER:HA	1:A:288:ILE:HG23	0.96	1.34	41	28
1:A:264:VAL:HG23	1:A:309:HIS:CE1	0.94	1.97	19	1
1:A:268:LEU:HD13	1:A:273:PHE:CE2	0.93	1.99	26	5
1:A:304:LEU:HD23	1:A:309:HIS:CE1	0.92	1.99	34	7
1:A:253:GLY:CA	1:A:286:VAL:HG12	0.92	1.94	38	8

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:250:VAL:HG23	1:A:291:VAL:HG21	0.92	1.41	5	8
1:A:288:ILE:HD11	1:A:300:THR:HG21	0.91	1.40	19	21
1:A:268:LEU:HD11	1:A:309:HIS:CE1	0.91	2.00	23	2
1:A:268:LEU:HD12	1:A:273:PHE:CE2	0.91	2.00	34	4
1:A:248:TRP:CB	1:A:291:VAL:HG23	0.90	1.97	28	40
1:A:248:TRP:HB2	1:A:291:VAL:HG23	0.90	1.41	35	28
1:A:268:LEU:HD22	1:A:304:LEU:CD2	0.90	1.97	26	2
1:A:251:GLN:HA	1:A:287:VAL:HG12	0.89	1.44	11	24
1:A:264:VAL:HG22	1:A:309:HIS:ND1	0.89	1.83	7	7
1:A:301:LEU:HD13	1:A:314:ARG:NH2	0.89	1.83	38	8
1:A:268:LEU:HD23	1:A:273:PHE:CD2	0.88	2.03	39	23
1:A:268:LEU:HD21	1:A:275:SER:CB	0.87	1.98	33	8
1:A:268:LEU:HD13	1:A:273:PHE:CD2	0.87	2.05	30	7
1:A:300:THR:HG22	1:A:304:LEU:HD12	0.87	1.47	21	13
1:A:253:GLY:HA2	1:A:255:PHE:CZ	0.87	2.05	20	11
1:A:268:LEU:O	1:A:273:PHE:O	0.87	1.91	36	16
1:A:268:LEU:HD22	1:A:275:SER:CB	0.86	1.99	3	23
1:A:276:LYS:N	1:A:287:VAL:O	0.86	2.08	20	42
1:A:268:LEU:HD22	1:A:275:SER:HB3	0.85	1.45	11	13
1:A:274:ASP:O	1:A:288:ILE:HG23	0.85	1.70	29	30
1:A:268:LEU:HD22	1:A:275:SER:HB2	0.85	1.49	39	11
1:A:255:PHE:CE1	1:A:309:HIS:HB3	0.84	2.07	30	12
1:A:250:VAL:HG11	1:A:288:ILE:CD1	0.84	2.02	9	28
1:A:253:GLY:HA2	1:A:255:PHE:CE1	0.84	2.08	37	23
1:A:273:PHE:CE1	1:A:303:ARG:HB3	0.83	2.09	16	22
1:A:260:GLN:O	1:A:264:VAL:HG23	0.83	1.73	7	32
1:A:288:ILE:CD1	1:A:300:THR:HG21	0.82	2.03	19	38
1:A:261:ALA:O	1:A:264:VAL:HG12	0.82	1.74	19	2
1:A:253:GLY:HA3	1:A:286:VAL:HG12	0.82	1.50	10	8
1:A:304:LEU:HD23	1:A:309:HIS:NE2	0.82	1.87	34	8
1:A:304:LEU:HD23	1:A:309:HIS:CD2	0.82	2.09	16	21
1:A:300:THR:HG22	1:A:304:LEU:CD1	0.82	2.04	21	11
1:A:261:ALA:HB3	1:A:284:ASN:HB2	0.82	1.49	43	4
1:A:301:LEU:HD13	1:A:314:ARG:NH1	0.82	1.88	18	3
1:A:257:GLY:O	1:A:261:ALA:N	0.82	2.13	34	30
1:A:301:LEU:HD22	1:A:314:ARG:NH2	0.81	1.90	1	9
1:A:248:TRP:HB3	1:A:291:VAL:HG23	0.81	1.53	43	31
1:A:255:PHE:CZ	1:A:309:HIS:HB3	0.81	2.09	37	12
1:A:268:LEU:HD11	1:A:275:SER:HB3	0.81	1.53	34	3
1:A:277:ILE:HD11	1:A:284:ASN:HB3	0.81	1.53	43	3
1:A:277:ILE:HD11	1:A:284:ASN:OD1	0.81	1.76	32	11

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:268:LEU:HD12	1:A:275:SER:CB	0.80	2.05	30	5
1:A:268:LEU:HD21	1:A:304:LEU:HD11	0.80	1.50	19	5
1:A:277:ILE:HG22	1:A:286:VAL:CG2	0.80	2.05	36	1
1:A:268:LEU:HD13	1:A:304:LEU:CD2	0.80	2.06	32	9
1:A:265:ARG:HA	1:A:268:LEU:HD23	0.79	1.53	28	4
1:A:301:LEU:CA	1:A:313:ILE:HD11	0.79	2.06	39	1
1:A:268:LEU:HD21	1:A:275:SER:HB3	0.79	1.52	32	4
1:A:268:LEU:HD23	1:A:273:PHE:HD2	0.79	1.37	39	6
1:A:288:ILE:HD13	1:A:300:THR:HG21	0.79	1.54	29	10
1:A:250:VAL:CG2	1:A:288:ILE:HD12	0.79	2.06	4	1
1:A:250:VAL:HG13	1:A:288:ILE:H	0.79	1.37	12	23
1:A:268:LEU:HD12	1:A:275:SER:HB3	0.79	1.55	18	3
1:A:268:LEU:CD1	1:A:286:VAL:HG11	0.79	2.07	19	1
1:A:264:VAL:HG23	1:A:309:HIS:NE2	0.78	1.91	19	1
1:A:250:VAL:HG22	1:A:314:ARG:HD3	0.78	1.56	25	3
1:A:250:VAL:HG21	1:A:288:ILE:HD11	0.78	1.55	13	1
1:A:268:LEU:HD21	1:A:275:SER:OG	0.78	1.79	28	3
1:A:268:LEU:HD13	1:A:275:SER:CB	0.77	2.09	13	1
1:A:255:PHE:CZ	1:A:264:VAL:HG11	0.77	2.14	10	13
1:A:264:VAL:HG13	1:A:309:HIS:CE1	0.77	2.15	16	17
1:A:250:VAL:HG22	1:A:314:ARG:HG3	0.77	1.55	19	12
1:A:264:VAL:O	1:A:268:LEU:HD12	0.77	1.77	11	16
1:A:286:VAL:O	1:A:287:VAL:HG13	0.77	1.79	42	28
1:A:264:VAL:HG12	1:A:268:LEU:HD12	0.77	1.55	10	1
1:A:304:LEU:CD1	1:A:313:ILE:HD13	0.77	2.10	39	1
1:A:301:LEU:HD12	1:A:314:ARG:NH2	0.77	1.94	14	1
1:A:273:PHE:CD2	1:A:300:THR:HG23	0.76	2.15	31	31
1:A:255:PHE:N	1:A:255:PHE:CD1	0.76	2.54	25	6
1:A:268:LEU:HA	1:A:273:PHE:CE2	0.76	2.15	40	14
1:A:250:VAL:HG22	1:A:314:ARG:CD	0.76	2.09	25	3
1:A:275:SER:CA	1:A:288:ILE:HG23	0.76	2.10	8	10
1:A:255:PHE:CE2	1:A:264:VAL:HG11	0.76	2.15	21	29
1:A:301:LEU:HD13	1:A:302:ASN:N	0.76	1.96	19	1
1:A:268:LEU:HD21	1:A:309:HIS:CE1	0.76	2.16	22	2
1:A:255:PHE:CE1	1:A:286:VAL:HG23	0.76	2.16	25	2
1:A:255:PHE:CE2	1:A:261:ALA:HA	0.75	2.17	25	6
1:A:268:LEU:HB2	1:A:273:PHE:CE2	0.75	2.16	28	5
1:A:250:VAL:CG1	1:A:288:ILE:HD12	0.75	2.09	20	12
1:A:277:ILE:CG2	1:A:286:VAL:HG22	0.75	2.10	25	3
1:A:268:LEU:HD13	1:A:304:LEU:HD11	0.75	1.55	36	1
1:A:268:LEU:HD23	1:A:273:PHE:CE2	0.75	2.17	13	17

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:264:VAL:O	1:A:307:ALA:HB1	0.75	1.82	24	3
1:A:307:ALA:HB3	1:A:309:HIS:NE2	0.74	1.97	24	21
1:A:300:THR:O	1:A:304:LEU:HD23	0.74	1.82	45	3
1:A:254:SER:N	1:A:285:ARG:HA	0.74	1.97	43	23
1:A:250:VAL:HG22	1:A:314:ARG:CG	0.74	2.12	43	5
1:A:255:PHE:CE2	1:A:264:VAL:HG21	0.74	2.18	19	6
1:A:250:VAL:HB	1:A:314:ARG:NH1	0.74	1.97	44	4
1:A:304:LEU:HB3	1:A:309:HIS:CD2	0.74	2.18	39	29
1:A:248:TRP:CZ3	1:A:316:ALA:HB2	0.74	2.18	40	39
1:A:268:LEU:HD12	1:A:275:SER:HB2	0.74	1.57	14	2
1:A:263:THR:HG22	1:A:267:GLN:HG3	0.73	1.59	19	3
1:A:268:LEU:HA	1:A:273:PHE:CE1	0.73	2.17	27	29
1:A:301:LEU:HA	1:A:313:ILE:HD11	0.73	1.60	39	1
1:A:253:GLY:N	1:A:286:VAL:HG12	0.73	1.98	16	3
1:A:268:LEU:O	1:A:268:LEU:HD12	0.73	1.83	26	2
1:A:247:ARG:HA	1:A:292:LYS:HA	0.73	1.61	44	5
1:A:252:CYS:SG	1:A:304:LEU:HD21	0.73	2.24	13	5
1:A:300:THR:O	1:A:304:LEU:HD12	0.73	1.84	7	15
1:A:250:VAL:HG12	1:A:291:VAL:CG2	0.72	2.13	39	4
1:A:291:VAL:CG2	1:A:297:ALA:HB2	0.72	2.12	44	6
1:A:297:ALA:HB1	1:A:314:ARG:HG3	0.72	1.61	4	10
1:A:273:PHE:HD2	1:A:300:THR:HG23	0.72	1.45	32	21
1:A:301:LEU:HD13	1:A:314:ARG:CZ	0.72	2.14	1	7
1:A:312:CYS:O	1:A:313:ILE:HG23	0.72	1.85	43	40
1:A:297:ALA:HB1	1:A:314:ARG:CG	0.72	2.15	26	12
1:A:301:LEU:HA	1:A:304:LEU:HD12	0.71	1.59	23	1
1:A:256:ARG:CG	1:A:264:VAL:HG21	0.71	2.15	41	2
1:A:252:CYS:SG	1:A:286:VAL:HG13	0.71	2.25	8	5
1:A:253:GLY:HA2	1:A:255:PHE:CE2	0.71	2.19	41	2
1:A:268:LEU:HD12	1:A:273:PHE:O	0.71	1.85	27	2
1:A:304:LEU:HD23	1:A:309:HIS:CG	0.71	2.20	13	4
1:A:261:ALA:HB1	1:A:284:ASN:HB3	0.70	1.63	22	33
1:A:268:LEU:HD13	1:A:273:PHE:HD2	0.70	1.46	22	2
1:A:313:ILE:CD1	1:A:315:LEU:HD12	0.70	2.15	27	2
1:A:268:LEU:HD12	1:A:273:PHE:HD2	0.70	1.46	36	6
1:A:255:PHE:CD1	1:A:255:PHE:N	0.70	2.59	18	14
1:A:250:VAL:HG23	1:A:291:VAL:CG2	0.70	2.15	29	7
1:A:256:ARG:HB3	1:A:260:GLN:HB3	0.70	1.64	43	2
1:A:309:HIS:CG	1:A:312:CYS:SG	0.70	2.84	39	1
1:A:277:ILE:O	1:A:278:THR:HG23	0.69	1.87	38	41
1:A:268:LEU:HD21	1:A:309:HIS:NE2	0.69	2.01	18	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:268:LEU:HD11	1:A:275:SER:HB2	0.69	1.63	38	6
1:A:265:ARG:HB2	1:A:277:ILE:HD13	0.69	1.65	43	2
1:A:248:TRP:CD1	1:A:297:ALA:HB3	0.69	2.21	45	2
1:A:277:ILE:HD11	1:A:284:ASN:CG	0.69	2.08	15	4
1:A:276:LYS:O	1:A:286:VAL:HG23	0.69	1.88	43	1
1:A:304:LEU:HD13	1:A:309:HIS:NE2	0.69	2.02	42	1
1:A:314:ARG:N	1:A:314:ARG:HD2	0.69	2.01	39	1
1:A:310:THR:HG22	1:A:311:ASN:OD1	0.69	1.88	1	1
1:A:251:GLN:HB3	1:A:315:LEU:HD13	0.69	1.65	22	6
1:A:304:LEU:HD13	1:A:312:CYS:SG	0.69	2.28	7	4
1:A:277:ILE:HG22	1:A:286:VAL:HB	0.69	1.63	17	5
1:A:268:LEU:HD21	1:A:275:SER:HB2	0.69	1.64	33	3
1:A:264:VAL:HG21	1:A:309:HIS:HB3	0.68	1.64	23	9
1:A:252:CYS:SG	1:A:304:LEU:HD11	0.68	2.28	35	7
1:A:268:LEU:HD21	1:A:304:LEU:CD1	0.68	2.18	19	7
1:A:291:VAL:HG11	1:A:314:ARG:NH2	0.68	2.02	39	1
1:A:264:VAL:HA	1:A:307:ALA:HB1	0.68	1.66	28	9
1:A:268:LEU:HD13	1:A:275:SER:OG	0.68	1.89	2	3
1:A:252:CYS:HB3	1:A:304:LEU:HD22	0.68	1.65	16	9
1:A:264:VAL:HG22	1:A:309:HIS:HD1	0.68	1.47	36	4
1:A:260:GLN:O	1:A:264:VAL:N	0.68	2.26	27	36
1:A:264:VAL:HG13	1:A:307:ALA:HB1	0.68	1.64	25	2
1:A:250:VAL:HB	1:A:314:ARG:HD3	0.68	1.64	33	2
1:A:250:VAL:HG13	1:A:314:ARG:CD	0.68	2.19	4	2
1:A:268:LEU:HD23	1:A:273:PHE:O	0.68	1.88	4	2
1:A:250:VAL:HG13	1:A:314:ARG:NE	0.68	2.03	4	1
1:A:250:VAL:HB	1:A:314:ARG:CZ	0.68	2.19	31	5
1:A:276:LYS:O	1:A:287:VAL:HG23	0.68	1.89	37	2
1:A:261:ALA:HB1	1:A:284:ASN:CB	0.67	2.19	40	42
1:A:300:THR:CG2	1:A:304:LEU:HD12	0.67	2.19	4	3
1:A:288:ILE:HD12	1:A:300:THR:HG21	0.67	1.65	13	3
1:A:268:LEU:HD21	1:A:304:LEU:CG	0.67	2.19	9	4
1:A:251:GLN:HG2	1:A:315:LEU:HD13	0.67	1.65	15	1
1:A:252:CYS:HA	1:A:312:CYS:HA	0.67	1.66	13	28
1:A:288:ILE:HD11	1:A:300:THR:CG2	0.67	2.20	43	5
1:A:253:GLY:HA2	1:A:286:VAL:N	0.66	2.04	23	1
1:A:248:TRP:HB2	1:A:316:ALA:HA	0.66	1.65	44	2
1:A:286:VAL:HG13	1:A:287:VAL:N	0.66	2.03	23	1
1:A:265:ARG:HB2	1:A:277:ILE:HD12	0.66	1.68	35	5
1:A:255:PHE:CE1	1:A:309:HIS:HB2	0.66	2.25	14	3
1:A:297:ALA:HB1	1:A:314:ARG:HG2	0.66	1.67	12	13

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:252:CYS:SG	1:A:304:LEU:HD13	0.66	2.30	22	7
1:A:297:ALA:HA	1:A:314:ARG:NH2	0.66	2.05	31	6
1:A:313:ILE:HD13	1:A:313:ILE:N	0.66	2.06	20	3
1:A:304:LEU:HB3	1:A:309:HIS:NE2	0.66	2.06	39	19
1:A:255:PHE:CD1	1:A:309:HIS:HB2	0.66	2.26	41	1
1:A:255:PHE:HE1	1:A:286:VAL:HG23	0.66	1.51	25	1
1:A:268:LEU:HD13	1:A:304:LEU:CD1	0.66	2.21	36	1
1:A:250:VAL:HG21	1:A:288:ILE:CD1	0.66	2.14	4	3
1:A:268:LEU:O	1:A:273:PHE:CD2	0.65	2.50	37	6
1:A:253:GLY:HA3	1:A:286:VAL:N	0.65	2.06	40	13
1:A:264:VAL:HG13	1:A:309:HIS:CD2	0.65	2.26	7	3
1:A:268:LEU:HD22	1:A:273:PHE:CE2	0.65	2.26	22	2
1:A:264:VAL:HG22	1:A:309:HIS:CE1	0.65	2.26	44	8
1:A:250:VAL:HB	1:A:288:ILE:HB	0.65	1.69	3	1
1:A:301:LEU:HD22	1:A:314:ARG:HH22	0.65	1.52	18	8
1:A:304:LEU:HD13	1:A:312:CYS:HB3	0.65	1.68	25	1
1:A:250:VAL:HG12	1:A:291:VAL:HG21	0.65	1.67	39	1
1:A:297:ALA:HA	1:A:314:ARG:CZ	0.65	2.21	40	6
1:A:268:LEU:HA	1:A:273:PHE:CZ	0.65	2.26	38	6
1:A:268:LEU:HD11	1:A:275:SER:CB	0.65	2.22	24	7
1:A:268:LEU:HD11	1:A:304:LEU:CD2	0.65	2.22	22	2
1:A:297:ALA:HB1	1:A:314:ARG:NH1	0.64	2.06	31	3
1:A:313:ILE:HD12	1:A:315:LEU:HD12	0.64	1.67	18	4
1:A:263:THR:HG22	1:A:267:GLN:CG	0.64	2.22	19	3
1:A:255:PHE:HB3	1:A:310:THR:HG22	0.64	1.68	22	2
1:A:313:ILE:HD12	1:A:314:ARG:HH11	0.64	1.53	39	1
1:A:268:LEU:CD1	1:A:273:PHE:CD2	0.64	2.81	28	5
1:A:261:ALA:CB	1:A:284:ASN:HB2	0.64	2.23	24	34
1:A:268:LEU:HG	1:A:273:PHE:CZ	0.64	2.28	3	14
1:A:268:LEU:O	1:A:273:PHE:CD1	0.64	2.51	27	22
1:A:268:LEU:HD21	1:A:304:LEU:HD21	0.64	1.68	10	2
1:A:313:ILE:O	1:A:313:ILE:HD12	0.64	1.93	27	2
1:A:273:PHE:CG	1:A:300:THR:HG23	0.63	2.28	22	7
1:A:250:VAL:HG22	1:A:288:ILE:H	0.63	1.53	26	1
1:A:275:SER:CB	1:A:288:ILE:HG22	0.63	2.23	27	1
1:A:269:ALA:HB2	1:A:274:ASP:OD1	0.63	1.91	3	1
1:A:268:LEU:CD1	1:A:304:LEU:HD21	0.63	2.22	40	1
1:A:250:VAL:HB	1:A:314:ARG:NE	0.63	2.09	42	3
1:A:265:ARG:HG3	1:A:277:ILE:HG23	0.63	1.71	5	6
1:A:268:LEU:HD22	1:A:275:SER:OG	0.63	1.94	8	6
1:A:250:VAL:O	1:A:287:VAL:HG12	0.63	1.94	39	10

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:279:THR:HG23	1:A:283:TRP:C	0.63	2.14	29	7
1:A:268:LEU:HD13	1:A:275:SER:HB3	0.63	1.71	13	1
1:A:256:ARG:O	1:A:258:ALA:N	0.63	2.31	34	13
1:A:273:PHE:CE2	1:A:304:LEU:HD22	0.62	2.29	31	2
1:A:268:LEU:HD22	1:A:304:LEU:HD21	0.62	1.70	27	1
1:A:301:LEU:HD12	1:A:304:LEU:HD12	0.62	1.69	22	1
1:A:275:SER:CB	1:A:288:ILE:HG12	0.62	2.24	22	32
1:A:255:PHE:CE1	1:A:309:HIS:ND1	0.62	2.68	38	10
1:A:251:GLN:CB	1:A:315:LEU:HD12	0.62	2.24	19	2
1:A:304:LEU:HD13	1:A:309:HIS:CE1	0.62	2.29	42	1
1:A:253:GLY:O	1:A:255:PHE:N	0.62	2.32	20	2
1:A:304:LEU:HD23	1:A:309:HIS:HD2	0.62	1.54	21	3
1:A:250:VAL:HA	1:A:315:LEU:H	0.62	1.54	27	10
1:A:248:TRP:HB2	1:A:291:VAL:CG2	0.62	2.24	34	4
1:A:300:THR:HG22	1:A:314:ARG:NH1	0.62	2.10	12	1
1:A:255:PHE:CE1	1:A:309:HIS:CG	0.61	2.88	38	7
1:A:255:PHE:CZ	1:A:286:VAL:HG21	0.61	2.30	1	7
1:A:273:PHE:HE2	1:A:304:LEU:HD22	0.61	1.55	31	1
1:A:268:LEU:HB3	1:A:273:PHE:O	0.61	1.95	31	16
1:A:250:VAL:HG11	1:A:288:ILE:HD11	0.61	1.71	27	1
1:A:304:LEU:HD12	1:A:313:ILE:HD13	0.61	1.71	39	1
1:A:268:LEU:O	1:A:273:PHE:CG	0.61	2.53	35	4
1:A:255:PHE:CZ	1:A:264:VAL:HG21	0.61	2.30	19	1
1:A:255:PHE:O	1:A:261:ALA:HB2	0.61	1.94	41	2
1:A:269:ALA:HB1	1:A:274:ASP:OD2	0.61	1.96	17	4
1:A:249:MET:HG3	1:A:317:ALA:HB2	0.61	1.73	39	8
1:A:268:LEU:HB2	1:A:273:PHE:CZ	0.61	2.30	24	5
1:A:251:GLN:HB3	1:A:315:LEU:HD12	0.61	1.73	11	2
1:A:251:GLN:CG	1:A:287:VAL:HG12	0.61	2.26	32	1
1:A:252:CYS:O	1:A:304:LEU:HD22	0.61	1.96	10	5
1:A:273:PHE:CB	1:A:300:THR:HG23	0.61	2.26	29	6
1:A:248:TRP:CE2	1:A:297:ALA:HB3	0.61	2.31	44	2
1:A:253:GLY:CA	1:A:286:VAL:HG13	0.61	2.26	43	1
1:A:291:VAL:HG11	1:A:314:ARG:HH22	0.60	1.56	39	3
1:A:255:PHE:N	1:A:255:PHE:HD1	0.60	1.92	25	1
1:A:263:THR:HG22	1:A:267:GLN:OE1	0.60	1.97	15	2
1:A:301:LEU:HD13	1:A:314:ARG:HH22	0.60	1.55	38	1
1:A:268:LEU:HD21	1:A:286:VAL:CG1	0.60	2.27	29	2
1:A:254:SER:HA	1:A:284:ASN:O	0.60	1.95	7	5
1:A:275:SER:HB3	1:A:288:ILE:HG22	0.60	1.74	27	1
1:A:310:THR:O	1:A:311:ASN:CB	0.60	2.50	19	24

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:268:LEU:HD12	1:A:275:SER:OG	0.60	1.96	30	2
1:A:275:SER:OG	1:A:286:VAL:HG12	0.60	1.96	19	3
1:A:253:GLY:CA	1:A:255:PHE:CZ	0.60	2.85	20	1
1:A:264:VAL:HG23	1:A:309:HIS:CD2	0.60	2.32	19	1
1:A:253:GLY:O	1:A:254:SER:CB	0.60	2.50	23	9
1:A:268:LEU:CD2	1:A:273:PHE:CE2	0.59	2.85	8	17
1:A:250:VAL:CG2	1:A:288:ILE:HD11	0.59	2.26	13	1
1:A:268:LEU:HG	1:A:273:PHE:CE2	0.59	2.33	31	13
1:A:300:THR:O	1:A:304:LEU:N	0.59	2.32	23	22
1:A:250:VAL:HG13	1:A:314:ARG:HD3	0.59	1.73	29	7
1:A:301:LEU:HD22	1:A:301:LEU:O	0.59	1.97	19	1
1:A:248:TRP:N	1:A:291:VAL:O	0.59	2.35	42	6
1:A:301:LEU:N	1:A:313:ILE:HD11	0.59	2.13	39	1
1:A:250:VAL:CG2	1:A:313:ILE:HG22	0.59	2.28	39	1
1:A:311:ASN:O	1:A:312:CYS:CB	0.59	2.50	7	3
1:A:268:LEU:CD1	1:A:304:LEU:HD11	0.59	2.28	36	2
1:A:309:HIS:CE1	1:A:311:ASN:O	0.59	2.56	15	2
1:A:310:THR:HG22	1:A:311:ASN:ND2	0.59	2.13	7	1
1:A:254:SER:HB2	1:A:283:TRP:CD1	0.58	2.33	36	17
1:A:255:PHE:HE2	1:A:261:ALA:HA	0.58	1.58	24	5
1:A:253:GLY:HA2	1:A:286:VAL:HG13	0.58	1.75	43	1
1:A:312:CYS:C	1:A:313:ILE:HD13	0.58	2.18	29	3
1:A:261:ALA:CB	1:A:284:ASN:CB	0.58	2.81	36	32
1:A:251:GLN:CB	1:A:315:LEU:HD13	0.58	2.28	17	6
1:A:276:LYS:HB2	1:A:287:VAL:HG23	0.58	1.75	41	2
1:A:255:PHE:CE2	1:A:309:HIS:HB2	0.58	2.33	27	11
1:A:253:GLY:HA3	1:A:286:VAL:H	0.58	1.59	37	6
1:A:264:VAL:CG1	1:A:309:HIS:CE1	0.58	2.87	25	5
1:A:273:PHE:O	1:A:275:SER:N	0.58	2.36	40	8
1:A:253:GLY:HA3	1:A:286:VAL:HG23	0.58	1.74	19	6
1:A:250:VAL:CG2	1:A:314:ARG:NH1	0.58	2.67	40	1
1:A:301:LEU:HD12	1:A:314:ARG:HH21	0.57	1.57	32	2
1:A:250:VAL:HG23	1:A:251:GLN:N	0.57	2.13	26	3
1:A:250:VAL:HG12	1:A:288:ILE:H	0.57	1.58	7	1
1:A:255:PHE:CD2	1:A:309:HIS:CG	0.57	2.93	41	1
1:A:250:VAL:HG13	1:A:314:ARG:HD2	0.57	1.75	40	1
1:A:250:VAL:HB	1:A:314:ARG:HG3	0.57	1.76	32	6
1:A:254:SER:OG	1:A:254:SER:O	0.57	2.22	5	7
1:A:260:GLN:O	1:A:264:VAL:HB	0.57	1.99	42	11
1:A:248:TRP:CB	1:A:291:VAL:HG22	0.57	2.29	40	1
1:A:268:LEU:HD23	1:A:273:PHE:CZ	0.57	2.35	13	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:276:LYS:O	1:A:286:VAL:HG13	0.57	2.00	24	1
1:A:277:ILE:HA	1:A:286:VAL:HA	0.57	1.76	17	6
1:A:268:LEU:CD2	1:A:275:SER:OG	0.57	2.53	16	4
1:A:304:LEU:O	1:A:309:HIS:CD2	0.57	2.57	43	20
1:A:248:TRP:O	1:A:291:VAL:HG22	0.57	1.98	45	2
1:A:273:PHE:CZ	1:A:303:ARG:HB3	0.56	2.34	15	18
1:A:250:VAL:HB	1:A:314:ARG:HD2	0.56	1.77	34	2
1:A:255:PHE:CG	1:A:309:HIS:HB3	0.56	2.35	43	1
1:A:250:VAL:HG21	1:A:300:THR:HG21	0.56	1.77	3	1
1:A:248:TRP:O	1:A:290:PRO:HA	0.56	2.01	6	34
1:A:252:CYS:O	1:A:252:CYS:SG	0.56	2.63	23	1
1:A:278:THR:O	1:A:285:ARG:N	0.56	2.37	30	10
1:A:264:VAL:HG12	1:A:265:ARG:N	0.56	2.16	29	12
1:A:268:LEU:HD11	1:A:304:LEU:HD21	0.56	1.77	44	2
1:A:261:ALA:HB3	1:A:284:ASN:CB	0.56	2.29	43	1
1:A:275:SER:HA	1:A:288:ILE:HG22	0.56	1.78	27	2
1:A:253:GLY:HA3	1:A:286:VAL:CB	0.56	2.31	41	12
1:A:268:LEU:HD13	1:A:275:SER:HB2	0.56	1.78	13	1
1:A:255:PHE:CZ	1:A:309:HIS:HB2	0.56	2.35	28	12
1:A:301:LEU:HD22	1:A:301:LEU:C	0.56	2.21	19	1
1:A:250:VAL:CG2	1:A:251:GLN:N	0.56	2.69	44	24
1:A:268:LEU:HD22	1:A:273:PHE:HE2	0.56	1.61	22	1
1:A:275:SER:HB2	1:A:288:ILE:HG12	0.56	1.77	23	5
1:A:253:GLY:HA3	1:A:286:VAL:CG2	0.56	2.30	19	4
1:A:267:GLN:O	1:A:307:ALA:HB2	0.55	2.01	29	1
1:A:251:GLN:OE1	1:A:315:LEU:HD22	0.55	2.02	32	1
1:A:252:CYS:SG	1:A:255:PHE:CZ	0.55	2.99	7	2
1:A:301:LEU:HD22	1:A:314:ARG:CZ	0.55	2.31	1	2
1:A:275:SER:OG	1:A:288:ILE:HG13	0.55	2.01	19	1
1:A:252:CYS:CB	1:A:304:LEU:HG	0.55	2.31	31	2
1:A:261:ALA:HB1	1:A:284:ASN:HB2	0.55	1.77	19	9
1:A:268:LEU:HG	1:A:275:SER:OG	0.55	2.00	27	3
1:A:255:PHE:CE2	1:A:264:VAL:CG1	0.55	2.88	21	1
1:A:268:LEU:CD2	1:A:286:VAL:HG11	0.55	2.32	36	4
1:A:253:GLY:O	1:A:255:PHE:CE1	0.55	2.60	11	7
1:A:252:CYS:CB	1:A:304:LEU:HD13	0.55	2.32	10	12
1:A:278:THR:O	1:A:285:ARG:CB	0.55	2.54	9	14
1:A:255:PHE:CZ	1:A:309:HIS:CE1	0.55	2.94	43	1
1:A:273:PHE:CE1	1:A:303:ARG:CG	0.55	2.90	42	9
1:A:264:VAL:HG12	1:A:268:LEU:CD1	0.55	2.32	10	2
1:A:250:VAL:HB	1:A:288:ILE:H	0.55	1.61	40	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:255:PHE:CD2	1:A:309:HIS:HB3	0.55	2.36	43	1
1:A:252:CYS:CB	1:A:304:LEU:HD22	0.55	2.32	9	4
1:A:297:ALA:O	1:A:300:THR:HB	0.54	2.01	4	3
1:A:301:LEU:HB2	1:A:314:ARG:CZ	0.54	2.32	13	5
1:A:300:THR:HG22	1:A:304:LEU:CD2	0.54	2.33	42	2
1:A:250:VAL:HB	1:A:288:ILE:HG13	0.54	1.80	41	5
1:A:254:SER:CB	1:A:283:TRP:CD1	0.54	2.91	37	26
1:A:254:SER:HB3	1:A:283:TRP:CD1	0.54	2.37	31	11
1:A:250:VAL:CG2	1:A:291:VAL:HG21	0.54	2.28	29	3
1:A:275:SER:CB	1:A:288:ILE:HG23	0.54	2.32	13	1
1:A:250:VAL:HG22	1:A:314:ARG:HD2	0.54	1.79	40	1
1:A:250:VAL:CG1	1:A:288:ILE:HB	0.54	2.33	30	12
1:A:255:PHE:CZ	1:A:286:VAL:CG2	0.54	2.90	4	11
1:A:310:THR:HG22	1:A:311:ASN:N	0.54	2.16	15	1
1:A:297:ALA:HB1	1:A:314:ARG:HE	0.54	1.63	22	3
1:A:255:PHE:CZ	1:A:309:HIS:CB	0.54	2.91	20	4
1:A:313:ILE:N	1:A:314:ARG:NH2	0.54	2.55	27	3
1:A:264:VAL:CG2	1:A:309:HIS:ND1	0.54	2.70	42	11
1:A:275:SER:CA	1:A:288:ILE:HG22	0.54	2.33	27	1
1:A:304:LEU:CD2	1:A:309:HIS:CD2	0.54	2.90	1	9
1:A:311:ASN:O	1:A:312:CYS:O	0.54	2.26	22	4
1:A:291:VAL:HG21	1:A:314:ARG:HH22	0.54	1.60	11	1
1:A:267:GLN:O	1:A:271:GLU:N	0.54	2.41	39	10
1:A:304:LEU:HD22	1:A:309:HIS:NE2	0.54	2.18	40	3
1:A:250:VAL:HG22	1:A:288:ILE:N	0.54	2.18	26	1
1:A:268:LEU:CD2	1:A:275:SER:HB3	0.54	2.33	7	3
1:A:265:ARG:CG	1:A:277:ILE:HG23	0.54	2.33	37	4
1:A:268:LEU:HD21	1:A:304:LEU:HG	0.54	1.78	3	4
1:A:274:ASP:C	1:A:288:ILE:HG23	0.53	2.22	34	8
1:A:275:SER:HA	1:A:288:ILE:CG2	0.53	2.26	8	5
1:A:250:VAL:HB	1:A:288:ILE:HG12	0.53	1.80	13	1
1:A:307:ALA:HB3	1:A:309:HIS:HE2	0.53	1.62	32	1
1:A:252:CYS:CA	1:A:312:CYS:HA	0.53	2.33	13	13
1:A:250:VAL:HG23	1:A:313:ILE:CB	0.53	2.33	39	1
1:A:255:PHE:CZ	1:A:312:CYS:SG	0.53	2.94	39	1
1:A:250:VAL:HG11	1:A:288:ILE:HG13	0.53	1.79	40	1
1:A:265:ARG:CG	1:A:277:ILE:HB	0.53	2.33	14	5
1:A:264:VAL:CG2	1:A:309:HIS:HB3	0.53	2.32	27	1
1:A:314:ARG:CA	1:A:314:ARG:NE	0.53	2.71	4	2
1:A:264:VAL:HG22	1:A:268:LEU:CD1	0.53	2.33	19	1
1:A:273:PHE:N	1:A:273:PHE:CD1	0.53	2.76	40	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:274:ASP:O	1:A:288:ILE:HG12	0.53	2.03	24	2
1:A:253:GLY:HA2	1:A:286:VAL:HG12	0.53	1.78	5	4
1:A:301:LEU:HD22	1:A:314:ARG:HH21	0.53	1.63	28	2
1:A:297:ALA:HB1	1:A:314:ARG:NE	0.53	2.18	39	1
1:A:303:ARG:O	1:A:306:MET:HB2	0.53	2.04	39	8
1:A:252:CYS:HB3	1:A:314:ARG:NH1	0.53	2.19	36	2
1:A:250:VAL:HG12	1:A:251:GLN:N	0.53	2.19	24	13
1:A:252:CYS:HB3	1:A:304:LEU:HD13	0.53	1.80	40	3
1:A:266:ALA:O	1:A:270:PHE:CB	0.53	2.57	42	13
1:A:265:ARG:CB	1:A:277:ILE:HD12	0.53	2.34	35	3
1:A:248:TRP:CB	1:A:291:VAL:CG2	0.53	2.86	26	7
1:A:310:THR:O	1:A:311:ASN:HB2	0.53	2.03	35	8
1:A:264:VAL:HG12	1:A:309:HIS:CE1	0.53	2.38	35	1
1:A:252:CYS:C	1:A:286:VAL:HG12	0.52	2.25	23	1
1:A:275:SER:OG	1:A:288:ILE:HG12	0.52	2.05	16	6
1:A:251:GLN:CA	1:A:287:VAL:HG12	0.52	2.33	15	6
1:A:264:VAL:HG13	1:A:309:HIS:NE2	0.52	2.19	36	2
1:A:286:VAL:HG11	1:A:309:HIS:CE1	0.52	2.39	22	1
1:A:257:GLY:O	1:A:260:GLN:N	0.52	2.42	13	26
1:A:254:SER:O	1:A:254:SER:OG	0.52	2.26	10	3
1:A:273:PHE:O	1:A:273:PHE:CG	0.52	2.62	4	5
1:A:265:ARG:HG2	1:A:277:ILE:HG23	0.52	1.82	4	1
1:A:248:TRP:CZ3	1:A:314:ARG:HB3	0.52	2.39	40	31
1:A:286:VAL:HG22	1:A:287:VAL:N	0.52	2.20	15	8
1:A:255:PHE:HE2	1:A:264:VAL:HG11	0.52	1.63	7	7
1:A:251:GLN:HA	1:A:286:VAL:O	0.52	2.04	39	5
1:A:253:GLY:O	1:A:255:PHE:CG	0.52	2.63	20	2
1:A:297:ALA:O	1:A:314:ARG:HD2	0.52	2.04	12	6
1:A:255:PHE:HA	1:A:310:THR:HG22	0.52	1.80	25	1
1:A:268:LEU:HD13	1:A:304:LEU:CG	0.52	2.34	36	3
1:A:252:CYS:HB2	1:A:304:LEU:HD22	0.52	1.81	36	3
1:A:250:VAL:HG22	1:A:314:ARG:NH1	0.52	2.20	40	1
1:A:264:VAL:HG13	1:A:309:HIS:ND1	0.52	2.19	21	1
1:A:248:TRP:O	1:A:291:VAL:CG2	0.52	2.58	45	2
1:A:268:LEU:HD13	1:A:286:VAL:CG1	0.52	2.26	19	1
1:A:312:CYS:C	1:A:313:ILE:HD12	0.52	2.25	7	1
1:A:276:LYS:HG3	1:A:287:VAL:HG23	0.52	1.82	36	2
1:A:304:LEU:CD2	1:A:309:HIS:CE1	0.51	2.94	23	4
1:A:249:MET:O	1:A:315:LEU:O	0.51	2.28	44	10
1:A:309:HIS:CE1	1:A:312:CYS:HB3	0.51	2.39	9	9
1:A:264:VAL:HG21	1:A:309:HIS:CB	0.51	2.34	27	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:268:LEU:HD21	1:A:286:VAL:HG11	0.51	1.83	36	2
1:A:252:CYS:HB2	1:A:286:VAL:HB	0.51	1.82	34	3
1:A:300:THR:HA	1:A:303:ARG:HB2	0.51	1.82	42	7
1:A:251:GLN:CB	1:A:287:VAL:HG12	0.51	2.36	22	2
1:A:310:THR:HG23	1:A:310:THR:O	0.51	2.05	22	1
1:A:268:LEU:O	1:A:268:LEU:HG	0.51	2.06	21	4
1:A:300:THR:HB	1:A:314:ARG:NH1	0.51	2.21	39	1
1:A:250:VAL:HG13	1:A:288:ILE:N	0.51	2.20	34	12
1:A:275:SER:CB	1:A:288:ILE:CG1	0.51	2.89	10	11
1:A:253:GLY:O	1:A:255:PHE:CD2	0.51	2.63	19	1
1:A:304:LEU:HD22	1:A:309:HIS:CE1	0.51	2.40	26	3
1:A:264:VAL:HG21	1:A:308:GLY:O	0.51	2.06	24	2
1:A:253:GLY:C	1:A:284:ASN:O	0.51	2.48	20	1
1:A:268:LEU:HD11	1:A:309:HIS:NE2	0.51	2.20	25	2
1:A:252:CYS:SG	1:A:312:CYS:HB3	0.51	2.46	23	1
1:A:286:VAL:CG1	1:A:287:VAL:N	0.51	2.70	23	12
1:A:253:GLY:CA	1:A:255:PHE:CE1	0.51	2.94	20	6
1:A:288:ILE:HD12	1:A:314:ARG:NH2	0.51	2.20	22	6
1:A:268:LEU:CD1	1:A:273:PHE:CE2	0.51	2.86	34	4
1:A:291:VAL:HG21	1:A:314:ARG:HH21	0.51	1.66	39	1
1:A:255:PHE:CG	1:A:309:HIS:HB2	0.50	2.41	41	1
1:A:304:LEU:CD1	1:A:313:ILE:HG21	0.50	2.36	39	1
1:A:288:ILE:HD12	1:A:314:ARG:CZ	0.50	2.36	40	1
1:A:286:VAL:O	1:A:287:VAL:CG1	0.50	2.59	6	22
1:A:264:VAL:CG1	1:A:265:ARG:N	0.50	2.74	32	6
1:A:253:GLY:O	1:A:254:SER:O	0.50	2.30	7	1
1:A:254:SER:N	1:A:284:ASN:O	0.50	2.44	44	10
1:A:250:VAL:CG2	1:A:314:ARG:HD3	0.50	2.33	4	3
1:A:297:ALA:O	1:A:314:ARG:HG2	0.50	2.07	45	2
1:A:304:LEU:CD2	1:A:309:HIS:NE2	0.50	2.74	23	3
1:A:252:CYS:O	1:A:286:VAL:O	0.50	2.30	38	1
1:A:253:GLY:CA	1:A:286:VAL:HG23	0.50	2.37	41	2
1:A:250:VAL:CG1	1:A:251:GLN:N	0.50	2.75	13	11
1:A:275:SER:N	1:A:288:ILE:HG23	0.50	2.21	34	2
1:A:304:LEU:CD1	1:A:314:ARG:NH1	0.50	2.75	23	3
1:A:253:GLY:CA	1:A:286:VAL:HB	0.50	2.37	41	8
1:A:268:LEU:CG	1:A:273:PHE:CE2	0.50	2.95	31	2
1:A:250:VAL:HG23	1:A:314:ARG:NE	0.50	2.22	12	1
1:A:250:VAL:CB	1:A:288:ILE:HD12	0.50	2.37	24	3
1:A:250:VAL:HB	1:A:288:ILE:CB	0.50	2.35	3	1
1:A:248:TRP:HB2	1:A:291:VAL:HG22	0.50	1.82	40	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:251:GLN:HG3	1:A:287:VAL:HG12	0.50	1.84	32	1
1:A:264:VAL:HG13	1:A:309:HIS:CG	0.49	2.42	7	2
1:A:268:LEU:HD13	1:A:304:LEU:HD23	0.49	1.81	32	1
1:A:268:LEU:O	1:A:273:PHE:N	0.49	2.42	11	11
1:A:271:GLU:CB	1:A:273:PHE:CE1	0.49	2.94	10	9
1:A:255:PHE:C	1:A:257:GLY:N	0.49	2.64	43	2
1:A:256:ARG:CB	1:A:264:VAL:HG21	0.49	2.37	43	2
1:A:253:GLY:CA	1:A:286:VAL:CG1	0.49	2.90	43	4
1:A:252:CYS:HB2	1:A:286:VAL:HG12	0.49	1.84	33	1
1:A:260:GLN:C	1:A:264:VAL:HG23	0.49	2.26	7	2
1:A:250:VAL:HG23	1:A:314:ARG:HD2	0.49	1.83	22	1
1:A:255:PHE:CD2	1:A:309:HIS:ND1	0.49	2.81	41	1
1:A:255:PHE:CE2	1:A:309:HIS:HB3	0.49	2.41	42	4
1:A:314:ARG:NE	1:A:314:ARG:N	0.49	2.60	13	4
1:A:248:TRP:CH2	1:A:316:ALA:HB2	0.49	2.43	40	1
1:A:275:SER:HB3	1:A:288:ILE:HG12	0.49	1.83	17	9
1:A:252:CYS:O	1:A:304:LEU:CD2	0.49	2.60	20	5
1:A:304:LEU:HD11	1:A:313:ILE:HG21	0.49	1.83	39	1
1:A:252:CYS:HB2	1:A:286:VAL:CG1	0.49	2.38	32	2
1:A:314:ARG:N	1:A:314:ARG:NE	0.49	2.60	16	5
1:A:264:VAL:CG1	1:A:286:VAL:HG21	0.49	2.38	19	1
1:A:275:SER:HB3	1:A:288:ILE:CG1	0.49	2.38	15	3
1:A:273:PHE:CE2	1:A:304:LEU:HD23	0.49	2.43	26	1
1:A:250:VAL:CB	1:A:314:ARG:NH1	0.49	2.74	45	3
1:A:275:SER:CA	1:A:288:ILE:HG12	0.49	2.37	16	12
1:A:283:TRP:N	1:A:283:TRP:CD1	0.49	2.80	43	9
1:A:265:ARG:HG3	1:A:277:ILE:CG2	0.49	2.38	38	4
1:A:250:VAL:HG11	1:A:288:ILE:CG1	0.49	2.38	23	4
1:A:250:VAL:HG21	1:A:314:ARG:NH1	0.49	2.23	37	1
1:A:248:TRP:CZ3	1:A:316:ALA:N	0.48	2.81	12	21
1:A:297:ALA:HB1	1:A:314:ARG:CZ	0.48	2.38	31	4
1:A:286:VAL:C	1:A:287:VAL:HG22	0.48	2.28	23	1
1:A:250:VAL:HG22	1:A:251:GLN:N	0.48	2.23	38	8
1:A:249:MET:SD	1:A:317:ALA:HB2	0.48	2.48	16	3
1:A:250:VAL:HB	1:A:314:ARG:HH11	0.48	1.66	44	2
1:A:252:CYS:SG	1:A:288:ILE:HD11	0.48	2.48	24	2
1:A:286:VAL:HG12	1:A:287:VAL:N	0.48	2.23	29	16
1:A:273:PHE:CE2	1:A:304:LEU:HG	0.48	2.43	34	1
1:A:273:PHE:CG	1:A:273:PHE:O	0.48	2.66	3	2
1:A:251:GLN:NE2	1:A:313:ILE:HD11	0.48	2.23	4	1
1:A:301:LEU:CD2	1:A:314:ARG:NH2	0.48	2.76	41	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:311:ASN:O	1:A:312:CYS:HB3	0.48	2.09	8	2
1:A:255:PHE:CE2	1:A:309:HIS:CB	0.48	2.96	20	1
1:A:250:VAL:CG2	1:A:288:ILE:HG13	0.48	2.38	8	2
1:A:304:LEU:HD23	1:A:309:HIS:ND1	0.48	2.23	13	1
1:A:252:CYS:CB	1:A:312:CYS:HA	0.48	2.38	22	2
1:A:253:GLY:O	1:A:284:ASN:O	0.48	2.31	20	1
1:A:252:CYS:C	1:A:286:VAL:HB	0.48	2.29	36	1
1:A:275:SER:OG	1:A:286:VAL:HG21	0.48	2.08	15	2
1:A:309:HIS:CE1	1:A:312:CYS:N	0.48	2.81	31	1
1:A:250:VAL:HG22	1:A:288:ILE:HG13	0.48	1.85	8	1
1:A:253:GLY:HA2	1:A:286:VAL:CG1	0.48	2.38	43	1
1:A:268:LEU:HG	1:A:273:PHE:O	0.48	2.08	33	1
1:A:250:VAL:HB	1:A:288:ILE:HD12	0.48	1.86	24	1
1:A:303:ARG:O	1:A:306:MET:N	0.48	2.44	30	19
1:A:253:GLY:HA2	1:A:255:PHE:CD2	0.48	2.43	41	1
1:A:307:ALA:HB3	1:A:309:HIS:CE1	0.48	2.44	7	4
1:A:247:ARG:HD2	1:A:317:ALA:HB3	0.48	1.85	31	1
1:A:268:LEU:HD13	1:A:286:VAL:HG21	0.48	1.86	10	1
1:A:264:VAL:HG12	1:A:277:ILE:HD11	0.48	1.85	18	1
1:A:268:LEU:C	1:A:268:LEU:HD12	0.48	2.29	26	1
1:A:301:LEU:HD12	1:A:312:CYS:SG	0.48	2.49	13	1
1:A:268:LEU:CD1	1:A:273:PHE:O	0.48	2.60	27	1
1:A:271:GLU:HB3	1:A:273:PHE:CE1	0.48	2.44	42	12
1:A:255:PHE:CG	1:A:309:HIS:CG	0.48	3.02	41	1
1:A:254:SER:H	1:A:285:ARG:HA	0.48	1.68	25	1
1:A:304:LEU:CD1	1:A:309:HIS:CE1	0.47	2.96	42	1
1:A:301:LEU:HD13	1:A:314:ARG:HH21	0.47	1.65	2	2
1:A:255:PHE:CZ	1:A:286:VAL:HG11	0.47	2.44	43	1
1:A:271:GLU:HB2	1:A:273:PHE:CE1	0.47	2.43	39	4
1:A:265:ARG:HA	1:A:268:LEU:HD22	0.47	1.86	33	1
1:A:248:TRP:O	1:A:249:MET:HG2	0.47	2.09	8	1
1:A:255:PHE:CZ	1:A:286:VAL:HB	0.47	2.45	23	1
1:A:250:VAL:HG12	1:A:291:VAL:HG22	0.47	1.85	10	2
1:A:299:SER:O	1:A:303:ARG:N	0.47	2.45	37	13
1:A:297:ALA:CB	1:A:314:ARG:NH2	0.47	2.77	39	1
1:A:255:PHE:HE2	1:A:264:VAL:HG21	0.47	1.69	1	2
1:A:250:VAL:HG23	1:A:314:ARG:CD	0.47	2.39	7	1
1:A:255:PHE:HZ	1:A:286:VAL:HG21	0.47	1.68	28	1
1:A:252:CYS:SG	1:A:286:VAL:HG23	0.47	2.49	39	2
1:A:288:ILE:O	1:A:289:GLY:C	0.47	2.52	26	18
1:A:250:VAL:HG11	1:A:288:ILE:HB	0.47	1.85	39	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:264:VAL:HG22	1:A:307:ALA:O	0.47	2.10	25	2
1:A:254:SER:CA	1:A:283:TRP:CD1	0.47	2.97	5	8
1:A:271:GLU:HG3	1:A:307:ALA:HB2	0.47	1.85	10	2
1:A:255:PHE:CE2	1:A:286:VAL:CG1	0.47	2.97	43	1
1:A:256:ARG:HG2	1:A:308:GLY:O	0.47	2.10	43	1
1:A:255:PHE:O	1:A:283:TRP:HB2	0.47	2.10	19	12
1:A:268:LEU:CG	1:A:275:SER:HB3	0.47	2.40	35	1
1:A:286:VAL:HG21	1:A:309:HIS:CE1	0.47	2.45	25	1
1:A:314:ARG:NE	1:A:314:ARG:HA	0.47	2.24	4	1
1:A:301:LEU:HB2	1:A:314:ARG:NE	0.47	2.25	7	2
1:A:267:GLN:HG2	1:A:307:ALA:HB1	0.47	1.86	36	1
1:A:273:PHE:CZ	1:A:303:ARG:C	0.47	2.88	43	15
1:A:253:GLY:HA3	1:A:286:VAL:HB	0.47	1.86	20	7
1:A:298:ASP:HA	1:A:314:ARG:NH2	0.47	2.24	32	2
1:A:255:PHE:CE1	1:A:261:ALA:HA	0.47	2.45	43	1
1:A:255:PHE:CE2	1:A:286:VAL:HG21	0.47	2.45	3	2
1:A:283:TRP:CD1	1:A:283:TRP:N	0.47	2.82	1	3
1:A:253:GLY:CA	1:A:286:VAL:N	0.47	2.78	23	1
1:A:268:LEU:CD1	1:A:275:SER:HB3	0.47	2.35	34	1
1:A:300:THR:O	1:A:304:LEU:CD2	0.47	2.63	31	1
1:A:288:ILE:CD1	1:A:314:ARG:NH2	0.46	2.78	44	3
1:A:268:LEU:HD22	1:A:286:VAL:HG11	0.46	1.86	42	1
1:A:268:LEU:CD2	1:A:304:LEU:HD11	0.46	2.32	19	2
1:A:253:GLY:CA	1:A:286:VAL:CG2	0.46	2.92	41	1
1:A:255:PHE:C	1:A:255:PHE:CD1	0.46	2.89	41	1
1:A:256:ARG:HG2	1:A:264:VAL:HG21	0.46	1.86	41	1
1:A:273:PHE:CE1	1:A:303:ARG:CB	0.46	2.98	36	5
1:A:264:VAL:HG13	1:A:309:HIS:HE1	0.46	1.70	45	2
1:A:252:CYS:HB3	1:A:312:CYS:CB	0.46	2.41	31	1
1:A:251:GLN:O	1:A:253:GLY:N	0.46	2.47	13	1
1:A:255:PHE:CD2	1:A:309:HIS:HB2	0.46	2.44	40	3
1:A:253:GLY:O	1:A:285:ARG:CB	0.46	2.64	22	1
1:A:264:VAL:O	1:A:268:LEU:N	0.46	2.48	37	4
1:A:261:ALA:CB	1:A:284:ASN:HB3	0.46	2.41	27	1
1:A:252:CYS:CB	1:A:286:VAL:HG13	0.46	2.40	32	1
1:A:260:GLN:O	1:A:264:VAL:CG2	0.46	2.64	39	17
1:A:254:SER:OG	1:A:283:TRP:CD1	0.46	2.67	35	4
1:A:265:ARG:O	1:A:268:LEU:HD23	0.46	2.11	24	1
1:A:268:LEU:HD21	1:A:304:LEU:HD23	0.46	1.86	23	1
1:A:278:THR:O	1:A:285:ARG:CG	0.46	2.64	15	4
1:A:255:PHE:CD1	1:A:284:ASN:O	0.46	2.69	25	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:273:PHE:CD1	1:A:273:PHE:N	0.46	2.84	7	3
1:A:297:ALA:O	1:A:314:ARG:NE	0.46	2.49	11	5
1:A:252:CYS:HB3	1:A:312:CYS:HA	0.46	1.86	33	2
1:A:279:THR:HG23	1:A:283:TRP:O	0.46	2.10	29	1
1:A:248:TRP:O	1:A:249:MET:CG	0.46	2.64	34	2
1:A:252:CYS:SG	1:A:301:LEU:HD13	0.46	2.51	44	1
1:A:264:VAL:HG11	1:A:286:VAL:HG21	0.46	1.87	4	1
1:A:268:LEU:CD2	1:A:273:PHE:CD2	0.45	2.96	23	2
1:A:254:SER:CB	1:A:283:TRP:NE1	0.45	2.79	19	10
1:A:263:THR:O	1:A:267:GLN:N	0.45	2.45	19	1
1:A:253:GLY:O	1:A:285:ARG:HA	0.45	2.11	22	1
1:A:264:VAL:HG12	1:A:309:HIS:ND1	0.45	2.26	24	1
1:A:252:CYS:HB2	1:A:304:LEU:HD13	0.45	1.88	43	2
1:A:268:LEU:CA	1:A:273:PHE:CE2	0.45	2.97	42	3
1:A:278:THR:N	1:A:285:ARG:O	0.45	2.49	16	5
1:A:252:CYS:O	1:A:253:GLY:O	0.45	2.34	12	3
1:A:275:SER:HA	1:A:288:ILE:CB	0.45	2.41	27	1
1:A:274:ASP:O	1:A:288:ILE:CG2	0.45	2.64	40	11
1:A:268:LEU:HD21	1:A:304:LEU:CD2	0.45	2.42	25	2
1:A:250:VAL:HG23	1:A:313:ILE:HG22	0.45	1.88	39	1
1:A:253:GLY:N	1:A:311:ASN:O	0.45	2.50	11	2
1:A:300:THR:O	1:A:304:LEU:HG	0.45	2.11	27	3
1:A:256:ARG:O	1:A:260:GLN:CB	0.45	2.64	41	2
1:A:278:THR:O	1:A:285:ARG:HB3	0.45	2.12	21	6
1:A:252:CYS:HA	1:A:313:ILE:H	0.45	1.71	18	2
1:A:264:VAL:CG1	1:A:309:HIS:ND1	0.45	2.79	21	1
1:A:303:ARG:O	1:A:306:MET:CB	0.45	2.65	43	14
1:A:255:PHE:CE1	1:A:309:HIS:CB	0.45	3.00	44	3
1:A:273:PHE:CE2	1:A:300:THR:HG23	0.45	2.46	4	2
1:A:252:CYS:HB2	1:A:304:LEU:CD1	0.45	2.41	43	2
1:A:269:ALA:HA	1:A:273:PHE:O	0.45	2.10	42	1
1:A:255:PHE:CD1	1:A:310:THR:O	0.45	2.70	27	1
1:A:249:MET:O	1:A:315:LEU:HB3	0.45	2.12	27	1
1:A:304:LEU:CD1	1:A:309:HIS:NE2	0.45	2.77	42	1
1:A:273:PHE:CD2	1:A:300:THR:CG2	0.45	3.00	22	1
1:A:273:PHE:O	1:A:274:ASP:O	0.45	2.34	28	3
1:A:250:VAL:CG2	1:A:313:ILE:CG2	0.45	2.94	39	1
1:A:268:LEU:CD2	1:A:275:SER:HB2	0.45	2.35	1	3
1:A:300:THR:HG22	1:A:304:LEU:HD21	0.45	1.88	31	1
1:A:253:GLY:HA2	1:A:255:PHE:HE1	0.45	1.68	29	3
1:A:314:ARG:HB2	1:A:314:ARG:CZ	0.45	2.42	16	4

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:301:LEU:HD13	1:A:314:ARG:NE	0.45	2.27	1	1
1:A:313:ILE:HD12	1:A:313:ILE:N	0.45	2.27	7	1
1:A:250:VAL:CG1	1:A:288:ILE:HG13	0.45	2.42	23	2
1:A:314:ARG:CZ	1:A:314:ARG:HB2	0.45	2.42	30	1
1:A:257:GLY:O	1:A:258:ALA:HB2	0.45	2.12	41	1
1:A:252:CYS:SG	1:A:286:VAL:N	0.45	2.90	39	1
1:A:275:SER:OG	1:A:288:ILE:HG23	0.45	2.11	13	1
1:A:264:VAL:O	1:A:268:LEU:HB3	0.45	2.11	40	2
1:A:267:GLN:HB3	1:A:307:ALA:HB1	0.45	1.87	21	1
1:A:268:LEU:HB3	1:A:275:SER:HB3	0.45	1.89	7	1
1:A:260:GLN:O	1:A:264:VAL:CB	0.44	2.66	33	14
1:A:265:ARG:HB2	1:A:277:ILE:CG2	0.44	2.42	44	1
1:A:275:SER:OG	1:A:286:VAL:CG2	0.44	2.65	43	1
1:A:275:SER:HB3	1:A:286:VAL:CG1	0.44	2.42	13	1
1:A:254:SER:OG	1:A:285:ARG:CB	0.44	2.65	27	1
1:A:275:SER:OG	1:A:286:VAL:CG1	0.44	2.63	19	2
1:A:253:GLY:HA3	1:A:286:VAL:O	0.44	2.13	23	1
1:A:293:GLY:O	1:A:294:LYS:CB	0.44	2.65	30	3
1:A:255:PHE:C	1:A:257:GLY:H	0.44	2.14	43	1
1:A:297:ALA:O	1:A:314:ARG:CZ	0.44	2.65	22	3
1:A:304:LEU:HD13	1:A:313:ILE:HD13	0.44	1.88	39	1
1:A:252:CYS:CB	1:A:286:VAL:HB	0.44	2.43	13	2
1:A:273:PHE:HE2	1:A:304:LEU:HD12	0.44	1.73	13	1
1:A:288:ILE:HG22	1:A:288:ILE:O	0.44	2.12	29	1
1:A:268:LEU:CD1	1:A:275:SER:HB2	0.44	2.39	38	3
1:A:254:SER:O	1:A:283:TRP:CG	0.44	2.71	11	1
1:A:304:LEU:CD1	1:A:313:ILE:CG2	0.44	2.95	39	1
1:A:268:LEU:CB	1:A:273:PHE:O	0.44	2.65	4	1
1:A:314:ARG:NE	1:A:314:ARG:CA	0.44	2.81	23	2
1:A:249:MET:O	1:A:315:LEU:CB	0.44	2.65	23	5
1:A:249:MET:O	1:A:315:LEU:N	0.44	2.50	40	2
1:A:251:GLN:CD	1:A:315:LEU:HD12	0.44	2.33	5	1
1:A:286:VAL:CG2	1:A:287:VAL:N	0.44	2.80	44	8
1:A:297:ALA:CB	1:A:314:ARG:CZ	0.44	2.96	34	2
1:A:299:SER:O	1:A:303:ARG:HB2	0.44	2.13	16	4
1:A:268:LEU:CD2	1:A:273:PHE:CZ	0.44	2.87	18	1
1:A:266:ALA:O	1:A:270:PHE:N	0.44	2.49	31	1
1:A:301:LEU:HG	1:A:313:ILE:HG13	0.44	1.89	39	1
1:A:264:VAL:CG1	1:A:268:LEU:HD12	0.44	2.43	16	1
1:A:268:LEU:HD11	1:A:275:SER:OG	0.44	2.13	33	1
1:A:273:PHE:CE2	1:A:303:ARG:CB	0.44	3.01	13	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:252:CYS:HB3	1:A:286:VAL:HB	0.44	1.88	2	1
1:A:307:ALA:CB	1:A:309:HIS:CE1	0.44	2.99	7	2
1:A:248:TRP:CZ3	1:A:314:ARG:O	0.44	2.71	41	12
1:A:261:ALA:C	1:A:264:VAL:HG12	0.44	2.33	19	1
1:A:301:LEU:HD13	1:A:301:LEU:C	0.44	2.32	19	1
1:A:303:ARG:O	1:A:306:MET:HB3	0.44	2.13	10	3
1:A:298:ASP:HA	1:A:314:ARG:NH1	0.44	2.28	10	1
1:A:268:LEU:CD2	1:A:286:VAL:CG1	0.44	2.96	42	2
1:A:309:HIS:ND1	1:A:312:CYS:SG	0.44	2.91	39	1
1:A:252:CYS:O	1:A:309:HIS:CE1	0.44	2.70	15	1
1:A:304:LEU:HD11	1:A:314:ARG:NH1	0.44	2.27	27	1
1:A:268:LEU:HG	1:A:286:VAL:HG21	0.44	1.89	22	1
1:A:258:ALA:HA	1:A:283:TRP:HA	0.44	1.89	43	2
1:A:314:ARG:N	1:A:314:ARG:CZ	0.44	2.81	33	2
1:A:252:CYS:HB2	1:A:312:CYS:CB	0.44	2.43	35	1
1:A:273:PHE:CE2	1:A:303:ARG:HB3	0.44	2.48	2	1
1:A:285:ARG:HG3	1:A:285:ARG:O	0.43	2.13	17	1
1:A:276:LYS:CG	1:A:287:VAL:O	0.43	2.66	15	4
1:A:249:MET:HA	1:A:289:GLY:O	0.43	2.14	19	2
1:A:281:ASN:ND2	1:A:283:TRP:CZ2	0.43	2.85	42	1
1:A:250:VAL:CG2	1:A:314:ARG:NE	0.43	2.80	12	1
1:A:301:LEU:HD13	1:A:314:ARG:HE	0.43	1.72	28	1
1:A:255:PHE:O	1:A:257:GLY:N	0.43	2.51	43	1
1:A:252:CYS:O	1:A:286:VAL:HB	0.43	2.13	35	1
1:A:250:VAL:CB	1:A:288:ILE:HD11	0.43	2.43	13	1
1:A:273:PHE:CE1	1:A:303:ARG:HG2	0.43	2.48	22	5
1:A:250:VAL:CG2	1:A:288:ILE:HB	0.43	2.42	40	1
1:A:273:PHE:CE1	1:A:303:ARG:HG3	0.43	2.48	5	1
1:A:294:LYS:O	1:A:298:ASP:CB	0.43	2.67	7	1
1:A:268:LEU:CD2	1:A:309:HIS:CE1	0.43	3.00	18	2
1:A:256:ARG:CB	1:A:260:GLN:HB3	0.43	2.43	41	1
1:A:288:ILE:O	1:A:288:ILE:HG22	0.43	2.14	37	1
1:A:269:ALA:HB2	1:A:275:SER:OG	0.43	2.12	27	1
1:A:304:LEU:HD22	1:A:312:CYS:HB3	0.43	1.88	2	1
1:A:291:VAL:HG21	1:A:314:ARG:NH2	0.43	2.28	39	2
1:A:273:PHE:HB2	1:A:300:THR:HG23	0.43	1.90	10	1
1:A:289:GLY:O	1:A:291:VAL:HG13	0.43	2.14	34	2
1:A:252:CYS:O	1:A:286:VAL:CG1	0.43	2.67	18	1
1:A:255:PHE:HB3	1:A:310:THR:HG23	0.43	1.89	31	1
1:A:264:VAL:CA	1:A:307:ALA:HB1	0.43	2.40	28	1
1:A:270:PHE:CD1	1:A:270:PHE:O	0.43	2.72	30	12

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:250:VAL:CG2	1:A:314:ARG:HD2	0.43	2.43	44	1
1:A:255:PHE:CE2	1:A:261:ALA:CA	0.43	2.97	25	2
1:A:275:SER:HA	1:A:288:ILE:CG1	0.43	2.43	24	2
1:A:273:PHE:CD1	1:A:303:ARG:HG2	0.43	2.48	41	3
1:A:276:LYS:O	1:A:287:VAL:HG22	0.43	2.13	4	1
1:A:250:VAL:HG21	1:A:288:ILE:HB	0.43	1.91	40	1
1:A:314:ARG:HG3	1:A:314:ARG:HH11	0.43	1.73	44	1
1:A:255:PHE:HZ	1:A:286:VAL:HG12	0.43	1.73	22	1
1:A:304:LEU:HB3	1:A:309:HIS:HE2	0.43	1.74	9	1
1:A:254:SER:C	1:A:283:TRP:HB2	0.43	2.34	11	3
1:A:288:ILE:O	1:A:289:GLY:O	0.43	2.37	30	8
1:A:255:PHE:CD1	1:A:255:PHE:C	0.43	2.92	43	1
1:A:255:PHE:CZ	1:A:309:HIS:ND1	0.43	2.87	43	2
1:A:275:SER:HA	1:A:288:ILE:HA	0.43	1.90	28	4
1:A:309:HIS:O	1:A:311:ASN:N	0.43	2.51	26	1
1:A:264:VAL:O	1:A:267:GLN:N	0.43	2.51	29	1
1:A:274:ASP:O	1:A:275:SER:HB2	0.43	2.13	36	1
1:A:251:GLN:O	1:A:252:CYS:O	0.43	2.37	7	1
1:A:313:ILE:HG22	1:A:314:ARG:N	0.43	2.29	7	1
1:A:301:LEU:CB	1:A:314:ARG:CZ	0.43	2.97	7	1
1:A:267:GLN:CB	1:A:307:ALA:HB1	0.43	2.44	9	1
1:A:250:VAL:CG1	1:A:288:ILE:CG1	0.43	2.97	23	1
1:A:301:LEU:HG	1:A:314:ARG:NH1	0.43	2.28	23	1
1:A:288:ILE:CD1	1:A:300:THR:CG2	0.43	2.97	34	4
1:A:288:ILE:HD12	1:A:300:THR:CG2	0.43	2.44	3	1
1:A:300:THR:HG22	1:A:313:ILE:HD13	0.43	1.90	39	1
1:A:277:ILE:HG22	1:A:286:VAL:HG13	0.43	1.91	1	1
1:A:267:GLN:O	1:A:271:GLU:CG	0.43	2.67	40	3
1:A:250:VAL:CB	1:A:288:ILE:CD1	0.43	2.97	13	1
1:A:301:LEU:HD12	1:A:301:LEU:O	0.43	2.14	27	1
1:A:300:THR:HB	1:A:314:ARG:CZ	0.43	2.44	22	1
1:A:253:GLY:CA	1:A:255:PHE:HE1	0.42	2.27	18	1
1:A:248:TRP:CE3	1:A:316:ALA:CA	0.42	3.03	40	5
1:A:250:VAL:CB	1:A:314:ARG:HD2	0.42	2.44	34	1
1:A:268:LEU:CD2	1:A:275:SER:CB	0.42	2.95	28	2
1:A:248:TRP:CE3	1:A:316:ALA:HA	0.42	2.49	26	1
1:A:300:THR:O	1:A:304:LEU:CD1	0.42	2.67	37	1
1:A:252:CYS:O	1:A:253:GLY:C	0.42	2.56	13	1
1:A:268:LEU:CD2	1:A:273:PHE:O	0.42	2.67	2	3
1:A:268:LEU:CD1	1:A:275:SER:OG	0.42	2.67	40	1
1:A:278:THR:O	1:A:285:ARG:HG3	0.42	2.14	17	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:253:GLY:O	1:A:254:SER:HB2	0.42	2.14	30	2
1:A:297:ALA:O	1:A:314:ARG:CD	0.42	2.67	34	1
1:A:252:CYS:HB3	1:A:312:CYS:HB3	0.42	1.91	18	1
1:A:270:PHE:C	1:A:270:PHE:CD1	0.42	2.92	1	1
1:A:266:ALA:O	1:A:270:PHE:HB3	0.42	2.14	38	1
1:A:250:VAL:HG13	1:A:252:CYS:SG	0.42	2.55	5	1
1:A:250:VAL:HG21	1:A:314:ARG:CZ	0.42	2.44	9	1
1:A:297:ALA:CB	1:A:314:ARG:NH1	0.42	2.81	45	2
1:A:264:VAL:CG1	1:A:309:HIS:CG	0.42	3.02	26	1
1:A:255:PHE:C	1:A:283:TRP:CB	0.42	2.87	12	3
1:A:270:PHE:O	1:A:270:PHE:CD1	0.42	2.72	29	5
1:A:248:TRP:CZ3	1:A:316:ALA:CB	0.42	2.97	40	1
1:A:253:GLY:N	1:A:312:CYS:HA	0.42	2.29	7	1
1:A:277:ILE:CG2	1:A:286:VAL:HG23	0.42	2.45	38	1
1:A:250:VAL:CG1	1:A:314:ARG:NH1	0.42	2.83	34	1
1:A:248:TRP:CE3	1:A:316:ALA:N	0.42	2.87	39	1
1:A:310:THR:OG1	1:A:310:THR:O	0.42	2.35	26	1
1:A:267:GLN:O	1:A:271:GLU:CB	0.42	2.67	26	3
1:A:250:VAL:CG1	1:A:314:ARG:HD3	0.42	2.44	27	2
1:A:276:LYS:O	1:A:287:VAL:CG2	0.42	2.65	25	1
1:A:255:PHE:CD1	1:A:309:HIS:HB3	0.42	2.50	45	2
1:A:265:ARG:HG3	1:A:277:ILE:HB	0.42	1.90	42	3
1:A:297:ALA:CA	1:A:314:ARG:CZ	0.42	2.98	39	1
1:A:288:ILE:O	1:A:288:ILE:HG13	0.42	2.14	27	1
1:A:247:ARG:HG2	1:A:248:TRP:N	0.42	2.29	38	1
1:A:254:SER:OG	1:A:283:TRP:O	0.42	2.37	34	1
1:A:275:SER:OG	1:A:286:VAL:HG22	0.42	2.15	43	1
1:A:261:ALA:HA	1:A:264:VAL:HB	0.42	1.90	42	2
1:A:268:LEU:HD21	1:A:286:VAL:HG13	0.42	1.91	29	2
1:A:265:ARG:HB2	1:A:277:ILE:CD1	0.42	2.45	40	1
1:A:251:GLN:CG	1:A:287:VAL:CG1	0.42	2.98	22	1
1:A:253:GLY:CA	1:A:311:ASN:O	0.42	2.68	24	1
1:A:296:ASN:O	1:A:300:THR:N	0.42	2.52	11	1
1:A:286:VAL:HG22	1:A:287:VAL:H	0.42	1.74	10	2
1:A:251:GLN:OE1	1:A:313:ILE:HD11	0.42	2.15	10	1
1:A:250:VAL:CB	1:A:288:ILE:HG13	0.42	2.45	41	1
1:A:255:PHE:O	1:A:283:TRP:CB	0.42	2.68	42	1
1:A:277:ILE:HG21	1:A:286:VAL:HG22	0.42	1.89	25	1
1:A:275:SER:OG	1:A:286:VAL:HG13	0.42	2.14	2	1
1:A:275:SER:HA	1:A:288:ILE:HG12	0.42	1.91	9	1
1:A:252:CYS:SG	1:A:286:VAL:CG1	0.42	3.08	22	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:300:THR:HG22	1:A:304:LEU:HD11	0.42	1.85	37	1
1:A:314:ARG:HB2	1:A:314:ARG:NH1	0.42	2.30	14	1
1:A:252:CYS:HA	1:A:312:CYS:CA	0.42	2.45	24	1
1:A:301:LEU:CD1	1:A:314:ARG:NH2	0.41	2.81	3	3
1:A:268:LEU:CD1	1:A:304:LEU:CD2	0.41	2.98	33	1
1:A:275:SER:OG	1:A:287:VAL:C	0.41	2.58	13	1
1:A:309:HIS:CE1	1:A:312:CYS:SG	0.41	3.13	14	2
1:A:248:TRP:O	1:A:291:VAL:N	0.41	2.53	7	2
1:A:265:ARG:CB	1:A:277:ILE:HD13	0.41	2.40	43	1
1:A:251:GLN:H	1:A:313:ILE:HA	0.41	1.75	39	1
1:A:313:ILE:N	1:A:313:ILE:CD1	0.41	2.77	20	1
1:A:271:GLU:HB3	1:A:273:PHE:CD1	0.41	2.50	13	1
1:A:255:PHE:CE1	1:A:284:ASN:O	0.41	2.74	25	1
1:A:249:MET:N	1:A:315:LEU:O	0.41	2.53	19	3
1:A:264:VAL:O	1:A:268:LEU:HD23	0.41	2.15	14	1
1:A:248:TRP:CD1	1:A:297:ALA:CB	0.41	3.02	44	1
1:A:285:ARG:O	1:A:285:ARG:HG3	0.41	2.15	18	2
1:A:297:ALA:HB1	1:A:314:ARG:HH11	0.41	1.74	43	1
1:A:255:PHE:HB3	1:A:310:THR:OG1	0.41	2.14	26	1
1:A:268:LEU:CG	1:A:275:SER:CB	0.41	2.98	40	1
1:A:250:VAL:HG23	1:A:313:ILE:CG2	0.41	2.45	39	1
1:A:253:GLY:O	1:A:255:PHE:CD1	0.41	2.73	20	1
1:A:273:PHE:CE2	1:A:303:ARG:HB2	0.41	2.50	13	1
1:A:252:CYS:SG	1:A:304:LEU:CD2	0.41	3.09	32	2
1:A:312:CYS:O	1:A:313:ILE:CG2	0.41	2.68	37	4
1:A:277:ILE:HG22	1:A:278:THR:N	0.41	2.30	18	1
1:A:312:CYS:O	1:A:313:ILE:O	0.41	2.38	39	1
1:A:314:ARG:N	1:A:314:ARG:CD	0.41	2.80	39	1
1:A:257:GLY:O	1:A:261:ALA:HB2	0.41	2.15	25	1
1:A:267:GLN:O	1:A:271:GLU:HB2	0.41	2.15	28	2
1:A:252:CYS:O	1:A:304:LEU:HD21	0.41	2.16	19	1
1:A:289:GLY:O	1:A:291:VAL:N	0.41	2.53	24	1
1:A:256:ARG:HG3	1:A:264:VAL:HG11	0.41	1.91	43	1
1:A:268:LEU:HG	1:A:275:SER:CB	0.41	2.46	42	1
1:A:255:PHE:C	1:A:283:TRP:HB2	0.41	2.35	4	1
1:A:308:GLY:O	1:A:309:HIS:ND1	0.41	2.53	19	1
1:A:249:MET:CB	1:A:315:LEU:O	0.41	2.68	40	1
1:A:311:ASN:O	1:A:312:CYS:HB2	0.41	2.16	7	1
1:A:300:THR:O	1:A:303:ARG:N	0.41	2.54	31	1
1:A:268:LEU:HD22	1:A:309:HIS:HE1	0.41	1.75	35	1
1:A:250:VAL:CG1	1:A:291:VAL:HG21	0.41	2.46	27	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:250:VAL:CG1	1:A:288:ILE:CB	0.41	2.98	34	1
1:A:248:TRP:CE3	1:A:315:LEU:O	0.41	2.73	44	2
1:A:265:ARG:HB2	1:A:277:ILE:HG21	0.41	1.91	44	1
1:A:256:ARG:HB3	1:A:260:GLN:CB	0.41	2.40	43	1
1:A:250:VAL:HG13	1:A:288:ILE:HG13	0.41	1.92	8	1
1:A:311:ASN:O	1:A:312:CYS:SG	0.41	2.78	20	1
1:A:248:TRP:O	1:A:249:MET:O	0.41	2.39	45	1
1:A:250:VAL:CG1	1:A:288:ILE:H	0.41	2.26	45	1
1:A:268:LEU:CD2	1:A:304:LEU:HG	0.41	2.46	9	1
1:A:279:THR:HG23	1:A:284:ASN:N	0.41	2.31	23	2
1:A:285:ARG:CG	1:A:285:ARG:O	0.41	2.68	17	1
1:A:268:LEU:O	1:A:273:PHE:C	0.41	2.59	18	2
1:A:288:ILE:CD1	1:A:300:THR:OG1	0.41	2.69	43	1
1:A:248:TRP:HB3	1:A:291:VAL:CG2	0.41	2.44	12	1
1:A:251:GLN:CG	1:A:285:ARG:NH1	0.41	2.84	13	1
1:A:254:SER:HB3	1:A:285:ARG:HA	0.41	1.92	4	1
1:A:254:SER:CA	1:A:285:ARG:HB3	0.41	2.46	22	1
1:A:270:PHE:CD1	1:A:270:PHE:C	0.41	2.94	23	1
1:A:252:CYS:SG	1:A:304:LEU:CD1	0.41	3.07	14	2
1:A:277:ILE:HG12	1:A:278:THR:N	0.41	2.31	45	1
1:A:264:VAL:CG1	1:A:286:VAL:CG2	0.41	2.99	19	1
1:A:277:ILE:HG12	1:A:286:VAL:HG23	0.40	1.93	18	1
1:A:313:ILE:HD12	1:A:314:ARG:H	0.40	1.76	8	1
1:A:250:VAL:HG23	1:A:314:ARG:HD3	0.40	1.93	16	1
1:A:250:VAL:CG1	1:A:288:ILE:HG12	0.40	2.47	27	1
1:A:257:GLY:O	1:A:261:ALA:CB	0.40	2.69	25	1
1:A:298:ASP:O	1:A:301:LEU:HB2	0.40	2.15	4	1
1:A:310:THR:O	1:A:311:ASN:ND2	0.40	2.54	40	1
1:A:268:LEU:HD23	1:A:307:ALA:HB2	0.40	1.93	14	1
1:A:251:GLN:NE2	1:A:315:LEU:CD1	0.40	2.84	41	1
1:A:264:VAL:CG2	1:A:308:GLY:O	0.40	2.69	20	1
1:A:254:SER:O	1:A:311:ASN:ND2	0.40	2.54	40	1
1:A:273:PHE:HE2	1:A:304:LEU:HG	0.40	1.77	14	1
1:A:268:LEU:HD13	1:A:304:LEU:HG	0.40	1.92	24	1
1:A:309:HIS:C	1:A:309:HIS:ND1	0.40	2.75	41	1
1:A:248:TRP:CD1	1:A:293:GLY:HA2	0.40	2.51	18	2
1:A:255:PHE:CB	1:A:309:HIS:HB3	0.40	2.47	43	1
1:A:314:ARG:HA	1:A:314:ARG:HD2	0.40	1.73	31	1
1:A:253:GLY:C	1:A:254:SER:OG	0.40	2.59	3	1
1:A:250:VAL:HG13	1:A:288:ILE:HG12	0.40	1.93	27	1
1:A:250:VAL:CG2	1:A:314:ARG:HG3	0.40	2.41	43	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:309:HIS:O	1:A:310:THR:C	0.40	2.59	31	1
1:A:258:ALA:O	1:A:261:ALA:HB3	0.40	2.17	21	1
1:A:314:ARG:HA	1:A:314:ARG:NE	0.40	2.31	23	1
1:A:267:GLN:CB	1:A:307:ALA:HA	0.40	2.47	34	1
1:A:277:ILE:HB	1:A:285:ARG:O	0.40	2.16	31	1
1:A:253:GLY:C	1:A:255:PHE:CD1	0.40	2.94	25	1
1:A:264:VAL:HG22	1:A:268:LEU:HD12	0.40	1.92	19	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	71/81 (88%)	49±2 (69±3%)	15±3 (22±4%)	7±2 (10±3%)	2	11
All	All	3195/3645 (88%)	2194 (69%)	695 (22%)	306 (10%)	2	11

All 27 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	311	ASN	36
1	A	289	GLY	31
1	A	274	ASP	25
1	A	294	LYS	25
1	A	295	GLU	24
1	A	280	ASN	23
1	A	313	ILE	23
1	A	254	SER	22
1	A	290	PRO	17
1	A	253	GLY	13
1	A	312	CYS	12
1	A	247	ARG	7
1	A	250	VAL	7
1	A	257	GLY	6
1	A	278	THR	6

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Mol	Chain	Res	Type	Models (Total)
1	A	249	MET	5
1	A	310	THR	4
1	A	284	ASN	4
1	A	317	ALA	3
1	A	286	VAL	3
1	A	258	ALA	2
1	A	291	VAL	2
1	A	252	CYS	2
1	A	293	GLY	1
1	A	256	ARG	1
1	A	275	SER	1
1	A	287	VAL	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	56/64 (88%)	34±3 (61±6%)	22±3 (39±6%)	1	6
All	All	2520/2880 (88%)	1538 (61%)	982 (39%)	1	6

All 52 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	283	TRP	45
1	A	255	PHE	45
1	A	314	ARG	45
1	A	268	LEU	44
1	A	315	LEU	39
1	A	278	THR	36
1	A	304	LEU	32
1	A	305	LYS	31
1	A	254	SER	31
1	A	273	PHE	29
1	A	303	ARG	28
1	A	279	THR	28
1	A	291	VAL	28

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Mol	Chain	Res	Type	Models (Total)
1	A	247	ARG	26
1	A	260	GLN	24
1	A	256	ARG	24
1	A	285	ARG	23
1	A	265	ARG	22
1	A	294	LYS	22
1	A	276	LYS	22
1	A	262	GLU	20
1	A	295	GLU	18
1	A	310	THR	17
1	A	271	GLU	17
1	A	313	ILE	17
1	A	298	ASP	16
1	A	292	LYS	16
1	A	301	LEU	15
1	A	259	GLU	15
1	A	267	GLN	15
1	A	280	ASN	14
1	A	274	ASP	14
1	A	264	VAL	14
1	A	251	GLN	14
1	A	309	HIS	13
1	A	250	VAL	12
1	A	312	CYS	11
1	A	288	ILE	10
1	A	252	CYS	10
1	A	296	ASN	9
1	A	299	SER	9
1	A	311	ASN	9
1	A	306	MET	9
1	A	270	PHE	8
1	A	284	ASN	8
1	A	281	ASN	7
1	A	300	THR	6
1	A	249	MET	5
1	A	275	SER	5
1	A	287	VAL	2
1	A	286	VAL	2
1	A	277	ILE	1

6.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

6.5 Carbohydrates [i](#)

There are no 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