



Full wwPDB NMR Structure Validation Report ⓘ

Feb 12, 2017 – 11:28 pm GMT

PDB ID : 2KWO
Title : Solution structure of the double PHD (plant homeodomain) fingers of human transcriptional protein DPF3b bound to a histone H4 peptide containing N-terminal acetylation at Serine 1
Authors : Zeng, L.; Zhang, Q.; Li, S.; Plotnikov, A.N.; Walsh, M.J.; Zhou, M.
Deposited on : 2010-04-14

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 : 1.7.2 (RC1), CSD as538be (2017)
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
ShiftChecker : trunk28760
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : recalc28949

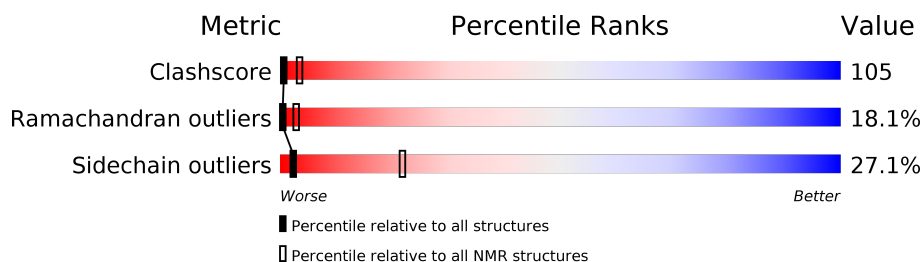
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 86%.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	NMR archive (#Entries)
Clashscore	125131	11601
Ramachandran outliers	121729	10391
Sidechain outliers	121581	10367

The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A cyan segment indicates the fraction of residues that are not part of the well-defined cores, and a grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	B	20	100%
2	A	114	11% 53% 25% 6% 6%

2 Ensemble composition and analysis ⓘ

This entry contains 20 models. Model 12 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *lowest energy*.

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

Well-defined (core) protein residues			
Well-defined core	Residue range (total)	Backbone RMSD (Å)	Medoid model
1	A:261-A:367 (107)	0.36	12

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. No single-model clusters were found.

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

3 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 1997 atoms, of which 970 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Histone peptide.

Mol	Chain	Residues	Atoms					Trace
1	B	20	Total	C	H	N	O	0
			303	84	160	36	23	

- Molecule 2 is a protein called Zinc finger protein DPF3.

Mol	Chain	Residues	Atoms					Trace
2	A	114	Total	C	H	N	O	S
			1690	542	810	147	174	17
								0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	259	GLY	-	EXPRESSION TAG	UNP Q92784
A	260	SER	-	EXPRESSION TAG	UNP Q92784

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

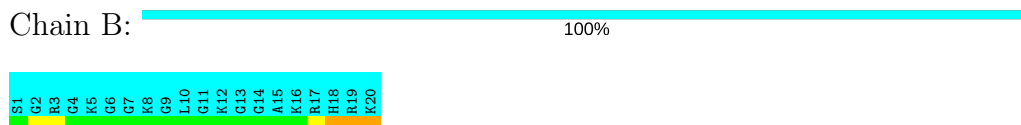
Mol	Chain	Residues	Atoms	
3	A	4	Total	Zn
			4	4

4 Residue-property plots

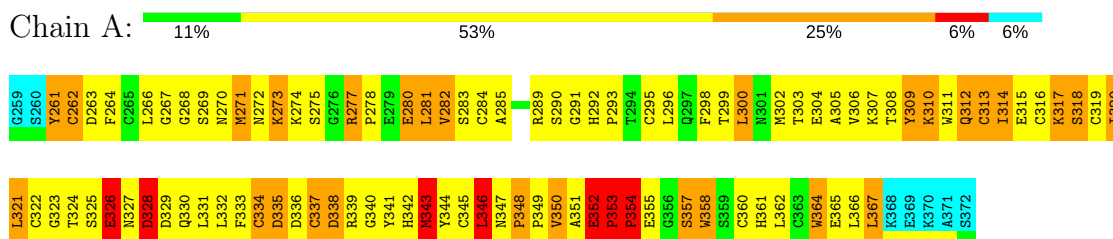
4.1 Average score per residue in the NMR ensemble

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: Histone peptide



- Molecule 2: Zinc finger protein DPF3

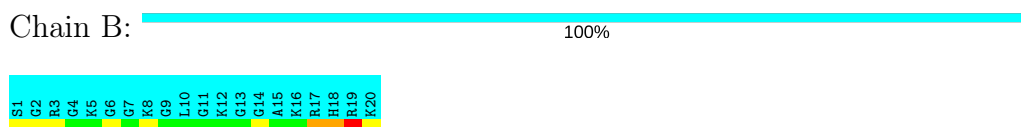


4.2 Scores per residue for each member of the ensemble

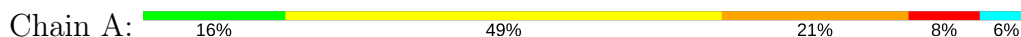
Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

- Molecule 1: Histone peptide



- Molecule 2: Zinc finger protein DPF3

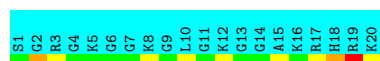




4.2.2 Score per residue for model 2

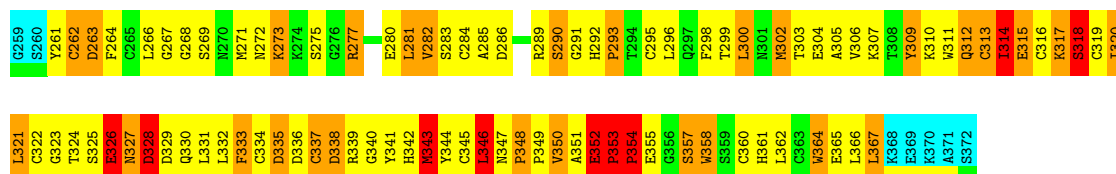
- Molecule 1: Histone peptide

Chain B: 100%



- Molecule 2: Zinc finger protein DPF3

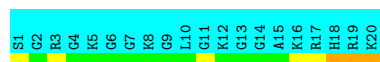
Chain A: 13% 48% 25% 8% 6%



4.2.3 Score per residue for model 3

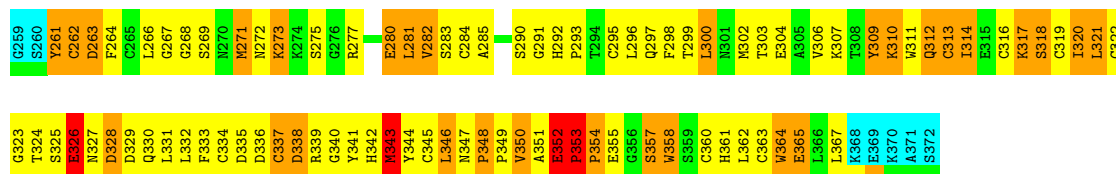
- Molecule 1: Histone peptide

Chain B: 100%



- Molecule 2: Zinc finger protein DPF3

Chain A: 16% 49% 25% 6%




4.2.4 Score per residue for model 4

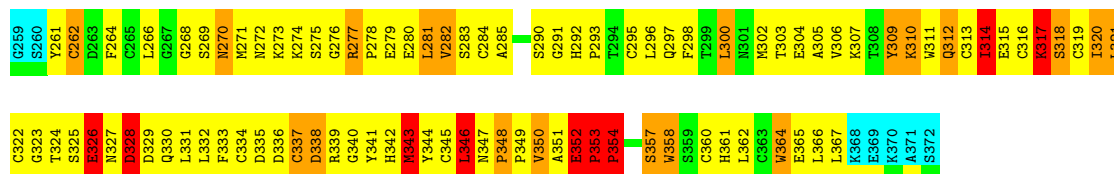
- Molecule 1: Histone peptide

Chain B:  100%



- Molecule 2: Zinc finger protein DPF3

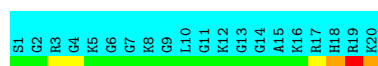
Chain A:  13% 56% 17% 8% 6%




4.2.5 Score per residue for model 5

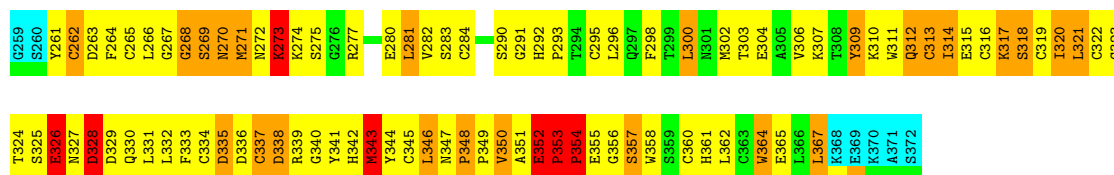
- Molecule 1: Histone peptide

Chain B:  100%



- Molecule 2: Zinc finger protein DPF3

Chain A:  15% 52% 21% 6% 6%



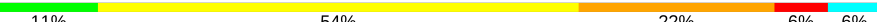
4.2.6 Score per residue for model 6

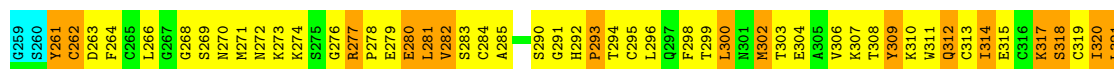
- Molecule 1: Histone peptide

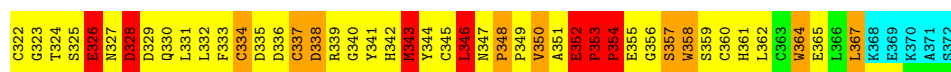
Chain B:  100%



- Molecule 2: Zinc finger protein DPF3

Chain A:  11% 54% 22% 6% 6%

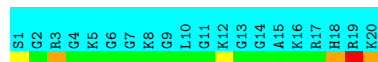




4.2.7 Score per residue for model 7

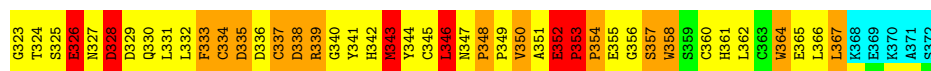
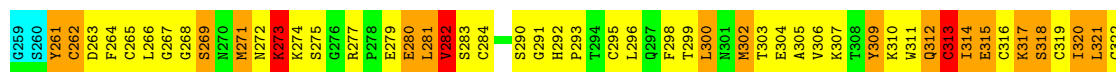
- Molecule 1: Histone peptide

Chain B: 100%



- Molecule 2: Zinc finger protein DPF3

Chain A: 12% 48% 25% 8% 6%



4.2.8 Score per residue for model 8

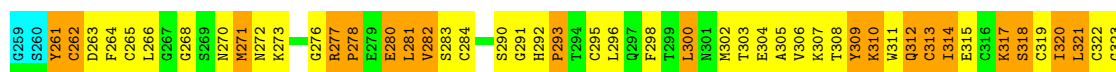
- Molecule 1: Histone peptide

Chain B: 100%



- Molecule 2: Zinc finger protein DPF3

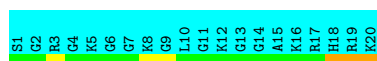
Chain A: 15% 45% 28% 6% 6%



4.2.9 Score per residue for model 9

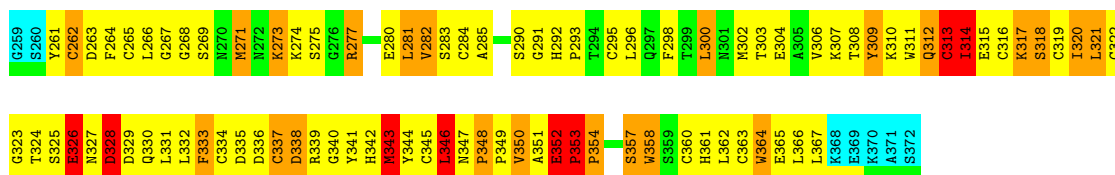
- Molecule 1: Histone peptide

Chain B: 100%



- Molecule 2: Zinc finger protein DPF3

Chain A: 15% 53% 19% 7% 6%



4.2.10 Score per residue for model 10

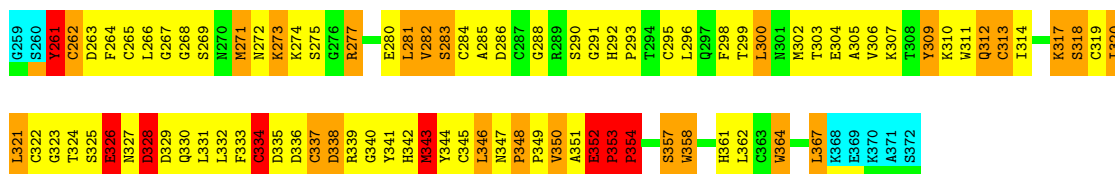
- Molecule 1: Histone peptide

Chain B: 100%



- Molecule 2: Zinc finger protein DPF3

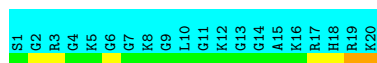
Chain A: 17% 49% 21% 7% 6%



4.2.11 Score per residue for model 11

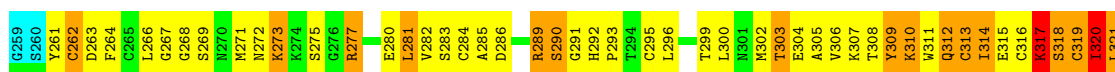
- Molecule 1: Histone peptide

Chain B: 100%



- Molecule 2: Zinc finger protein DPF3

Chain A: 12% 52% 23% 7% 6%

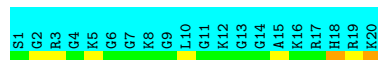




4.2.12 Score per residue for model 12 (medoid)

- Molecule 1: Histone peptide

Chain B:  100%



- Molecule 2: Zinc finger protein DPF3

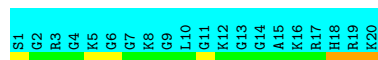
Chain A:  11% 50% 26% 6% 6%




4.2.13 Score per residue for model 13

- Molecule 1: Histone peptide

Chain B:  100%



- Molecule 2: Zinc finger protein DPF3

Chain A:  12% 54% 23% 6%



4.2.14 Score per residue for model 14

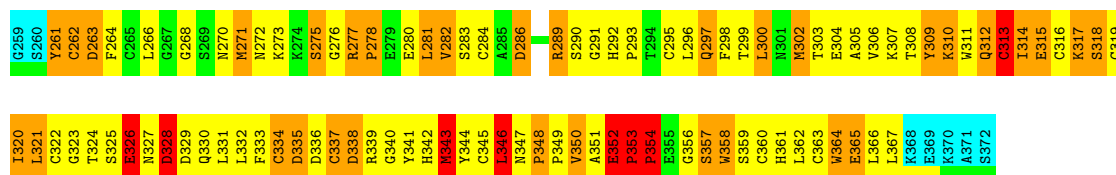
- Molecule 1: Histone peptide

Chain B:  100%



- Molecule 2: Zinc finger protein DPF3

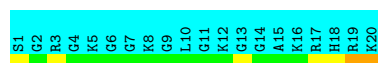
Chain A: 10% 48% 29% 7% 6%



4.2.15 Score per residue for model 15

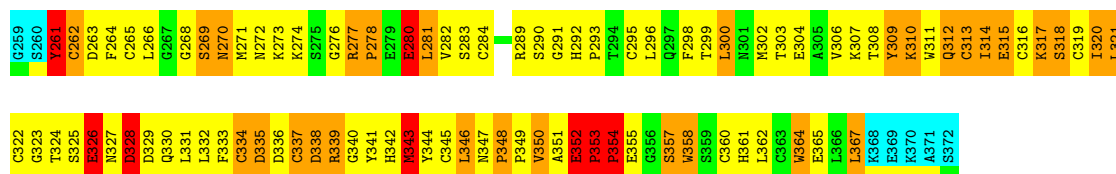
- Molecule 1: Histone peptide

Chain B: 100%



- Molecule 2: Zinc finger protein DPF3

Chain A: 13% 48% 25% 7% 6%



4.2.16 Score per residue for model 16

- Molecule 1: Histone peptide

Chain B: 100%



- Molecule 2: Zinc finger protein DPF3

Chain A: 11% 56% 20% 7% 6%

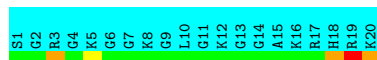




4.2.17 Score per residue for model 17

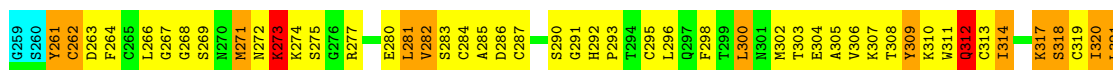
- Molecule 1: Histone peptide

Chain B: 100%



- Molecule 2: Zinc finger protein DPF3

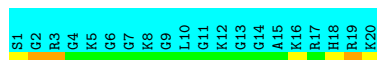
Chain A: 13% 55% 16% 10% 6%



4.2.18 Score per residue for model 18

- Molecule 1: Histone peptide

Chain B: 100%



- Molecule 2: Zinc finger protein DPF3

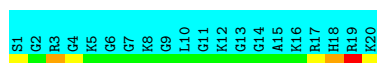
Chain A: 18% 47% 22% 7% 6%



4.2.19 Score per residue for model 19

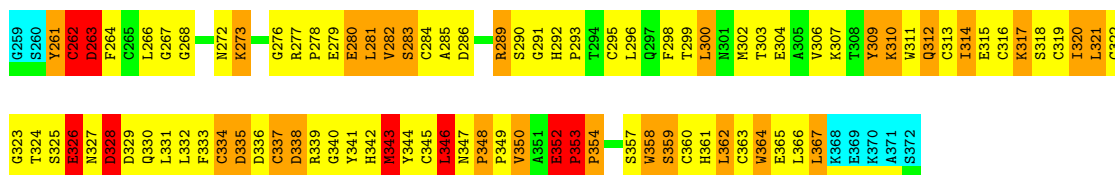
- Molecule 1: Histone peptide

Chain B: 100%



- Molecule 2: Zinc finger protein DPF3

Chain A: 14% 49% 24% 7% 6%



4.2.20 Score per residue for model 20

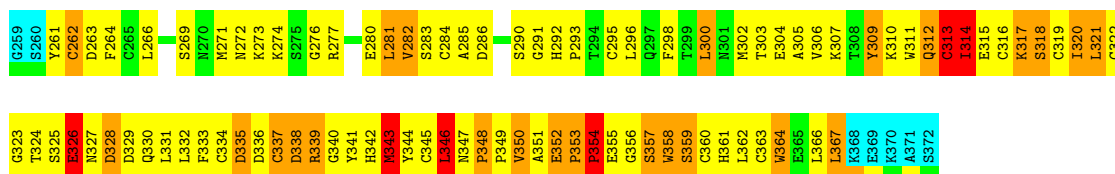
- Molecule 1: Histone peptide

Chain B: 100%



- Molecule 2: Zinc finger protein DPF3

Chain A: 14% 54% 21% 5% 6%



5 Refinement protocol and experimental data overview

The models were refined using the following method: *DGSA-distance geometry simulated annealing, torsion angle dynamics*.

Of the 200 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
ARIA	refinement	2.2
CNS	structure solution	1.2

The following table shows chemical shift validation statistics as aggregates over all chemical shift files. Detailed validation can be found in section 7 of this report.

Chemical shift file(s)	BMRB entry 16865
Number of chemical shift lists	1
Total number of shifts	1282
Number of shifts mapped to atoms	1282
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	86%

No validations of the models with respect to experimental NMR restraints is performed at this time.

6 Model quality

6.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SAC, ZN

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
2	A	0.58±0.02	0±0/853 (0.0±0.0%)	0.78±0.02	1±0/1157 (0.1±0.0%)
All	All	0.58	0/17060 (0.0%)	0.78	19/23140 (0.1%)

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
2	A	353	PRO	N-CA-CB	-6.34	95.62	102.60	13	18
2	A	354	PRO	N-CA-CB	-5.54	96.50	102.60	20	1

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	B	0	0	0	0±0
2	A	831	758	757	167±11
All	All	16700	15160	15140	3334

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 105.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:282:VAL:HG23	2:A:291:GLY:O	0.99	1.56	10	1
2:A:314:ILE:HD13	2:A:317:LYS:HD3	0.98	1.34	6	2
2:A:282:VAL:HG12	2:A:291:GLY:O	0.91	1.64	15	2
2:A:354:PRO:HB2	2:A:358:TRP:HB2	0.88	1.45	20	20
2:A:314:ILE:HG22	2:A:315:GLU:N	0.86	1.84	14	9
2:A:314:ILE:HD12	2:A:317:LYS:HE3	0.84	1.49	2	5
2:A:293:PRO:HG2	2:A:303:THR:HG23	0.83	1.48	10	14
2:A:352:GLU:H	2:A:353:PRO:HD2	0.82	1.34	20	20
2:A:320:ILE:HD12	2:A:339:ARG:HD3	0.82	1.50	17	8
2:A:282:VAL:HG13	2:A:291:GLY:O	0.82	1.73	11	1
2:A:352:GLU:N	2:A:353:PRO:HD2	0.82	1.89	20	20
2:A:350:VAL:HG21	2:A:354:PRO:HD2	0.82	1.51	12	19
2:A:282:VAL:HG22	2:A:291:GLY:O	0.81	1.76	3	16
2:A:303:THR:HG22	2:A:307:LYS:HE2	0.80	1.52	10	18
2:A:342:HIS:HB2	2:A:345:CYS:SG	0.79	2.18	11	20
2:A:346:LEU:HD13	2:A:346:LEU:H	0.79	1.38	9	1
2:A:364:TRP:HA	2:A:367:LEU:HB2	0.78	1.53	8	20
2:A:314:ILE:HA	2:A:317:LYS:CD	0.77	2.08	6	3
2:A:314:ILE:CG2	2:A:315:GLU:N	0.77	2.47	9	10
2:A:332:LEU:HG	2:A:343:MET:HG3	0.77	1.57	11	19
2:A:346:LEU:H	2:A:346:LEU:HD13	0.77	1.38	8	1
2:A:332:LEU:HD13	2:A:358:TRP:CE2	0.76	2.16	9	19
2:A:314:ILE:HD12	2:A:317:LYS:CE	0.75	2.10	10	8
2:A:325:SER:HA	2:A:331:LEU:HD11	0.75	1.57	5	20
2:A:346:LEU:H	2:A:346:LEU:CD1	0.74	1.96	9	2
2:A:314:ILE:O	2:A:317:LYS:HD2	0.74	1.82	20	11
2:A:314:ILE:HD13	2:A:317:LYS:CE	0.74	2.12	19	1
2:A:350:VAL:HG23	2:A:352:GLU:H	0.73	1.43	17	2
2:A:321:LEU:HD23	2:A:321:LEU:N	0.73	1.99	18	13
2:A:321:LEU:N	2:A:321:LEU:HD23	0.72	1.99	10	7
2:A:353:PRO:HB2	2:A:354:PRO:HD3	0.72	1.60	5	20
2:A:314:ILE:HD12	2:A:317:LYS:CD	0.72	2.14	10	1
2:A:292:HIS:HB2	2:A:295:CYS:SG	0.72	2.25	14	20
2:A:281:LEU:HD22	2:A:290:SER:HG	0.72	1.45	2	2
2:A:324:THR:HG23	2:A:326:GLU:H	0.72	1.44	20	19
2:A:317:LYS:HD3	2:A:318:SER:N	0.72	1.99	20	6
2:A:317:LYS:HD3	2:A:318:SER:H	0.71	1.45	3	10
2:A:332:LEU:HD12	2:A:346:LEU:HD21	0.71	1.60	9	2
2:A:337:CYS:SG	2:A:339:ARG:HG3	0.71	2.25	10	12
2:A:364:TRP:HA	2:A:367:LEU:CB	0.71	2.16	14	3
2:A:314:ILE:O	2:A:317:LYS:HB3	0.71	1.86	13	4

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:317:LYS:HG3	2:A:318:SER:N	0.71	2.00	8	4
2:A:341:TYR:HH	2:A:361:HIS:CG	0.71	2.04	18	2
2:A:272:ASN:N	2:A:277:ARG:O	0.70	2.24	5	10
2:A:314:ILE:HD12	2:A:317:LYS:HD3	0.70	1.62	10	1
2:A:333:PHE:CD1	2:A:333:PHE:N	0.70	2.60	15	8
2:A:317:LYS:CD	2:A:318:SER:N	0.70	2.54	4	9
2:A:314:ILE:O	2:A:316:CYS:N	0.70	2.25	7	10
2:A:334:CYS:HA	2:A:358:TRP:O	0.70	1.86	17	19
2:A:293:PRO:N	2:A:296:LEU:HD12	0.69	2.03	2	16
2:A:303:THR:O	2:A:306:VAL:HG22	0.69	1.87	11	2
2:A:314:ILE:HD13	2:A:317:LYS:CD	0.69	2.15	6	2
2:A:262:CYS:N	2:A:281:LEU:HD22	0.69	2.03	13	17
2:A:350:VAL:HB	2:A:353:PRO:HG2	0.69	1.63	20	1
2:A:317:LYS:HD2	2:A:318:SER:H	0.69	1.47	5	2
2:A:281:LEU:HD22	2:A:290:SER:OG	0.68	1.89	11	2
2:A:314:ILE:HA	2:A:317:LYS:HD2	0.68	1.64	19	4
2:A:332:LEU:HD22	2:A:343:MET:CG	0.68	2.18	5	1
2:A:272:ASN:O	2:A:274:LYS:N	0.68	2.27	1	4
2:A:314:ILE:O	2:A:317:LYS:HE3	0.68	1.89	3	6
2:A:353:PRO:HB2	2:A:354:PRO:CD	0.67	2.20	8	17
2:A:284:CYS:HB3	2:A:312:GLN:HA	0.67	1.64	17	1
2:A:332:LEU:HD13	2:A:358:TRP:CD2	0.67	2.25	7	19
2:A:284:CYS:SG	2:A:287:CYS:N	0.67	2.68	16	1
2:A:328:ASP:HA	2:A:331:LEU:HG	0.66	1.66	11	19
2:A:317:LYS:HD2	2:A:317:LYS:N	0.66	2.04	11	3
2:A:322:CYS:SG	2:A:324:THR:HG22	0.66	2.30	13	2
2:A:262:CYS:SG	2:A:264:PHE:HB2	0.66	2.30	1	20
2:A:317:LYS:N	2:A:317:LYS:HD2	0.66	2.05	9	5
2:A:350:VAL:CG2	2:A:351:ALA:N	0.66	2.58	17	1
2:A:302:MET:O	2:A:306:VAL:HG22	0.66	1.89	4	15
2:A:346:LEU:N	2:A:346:LEU:CD1	0.66	2.58	9	1
2:A:346:LEU:CD1	2:A:346:LEU:N	0.66	2.58	8	1
2:A:302:MET:SD	2:A:337:CYS:N	0.66	2.69	15	15
2:A:292:HIS:C	2:A:296:LEU:HD12	0.66	2.11	2	2
2:A:332:LEU:HB3	2:A:358:TRP:CZ3	0.66	2.26	8	19
2:A:298:PHE:CD2	2:A:302:MET:SD	0.66	2.89	7	1
2:A:293:PRO:CG	2:A:303:THR:HG23	0.65	2.21	15	18
2:A:333:PHE:N	2:A:333:PHE:CD1	0.65	2.63	2	11
2:A:343:MET:HB3	2:A:350:VAL:HG22	0.65	1.68	12	18
2:A:330:GLN:O	2:A:343:MET:SD	0.65	2.54	5	20
2:A:350:VAL:HG21	2:A:354:PRO:CD	0.65	2.22	5	4

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:332:LEU:HB3	2:A:358:TRP:CE3	0.65	2.27	11	18
2:A:283:SER:HA	2:A:290:SER:HA	0.65	1.69	16	20
2:A:343:MET:HG2	2:A:350:VAL:HG22	0.65	1.67	14	18
2:A:346:LEU:N	2:A:346:LEU:HD23	0.65	2.06	11	8
2:A:354:PRO:HG3	2:A:358:TRP:CD1	0.65	2.27	12	18
2:A:314:ILE:O	2:A:317:LYS:CD	0.64	2.44	14	13
2:A:350:VAL:HG11	2:A:354:PRO:HD3	0.64	1.68	11	1
2:A:350:VAL:HG11	2:A:353:PRO:HB2	0.64	1.69	11	1
2:A:321:LEU:HD11	2:A:341:TYR:CD2	0.64	2.27	1	19
2:A:332:LEU:HG	2:A:343:MET:CG	0.64	2.23	9	18
2:A:321:LEU:HD12	2:A:345:CYS:C	0.64	2.13	2	20
2:A:337:CYS:O	2:A:338:ASP:HB3	0.64	1.93	15	10
2:A:314:ILE:O	2:A:317:LYS:CE	0.64	2.45	5	11
2:A:354:PRO:CB	2:A:358:TRP:HB2	0.63	2.23	7	18
2:A:341:TYR:HB3	2:A:346:LEU:CD2	0.63	2.23	11	7
2:A:319:CYS:SG	2:A:321:LEU:HB2	0.63	2.33	8	20
2:A:332:LEU:O	2:A:340:GLY:HA2	0.63	1.93	1	16
2:A:317:LYS:CD	2:A:318:SER:H	0.63	2.05	7	8
2:A:269:SER:OG	2:A:281:LEU:N	0.63	2.31	3	3
2:A:320:ILE:HG22	2:A:340:GLY:O	0.63	1.94	1	20
2:A:339:ARG:NE	2:A:362:LEU:HD12	0.63	2.08	15	6
2:A:282:VAL:HG21	2:A:306:VAL:HG23	0.63	1.69	18	2
2:A:353:PRO:CB	2:A:354:PRO:CD	0.63	2.77	12	15
2:A:302:MET:HB2	2:A:335:ASP:O	0.63	1.93	11	18
2:A:298:PHE:CE2	2:A:302:MET:SD	0.63	2.92	7	1
2:A:346:LEU:HD23	2:A:346:LEU:N	0.63	2.08	5	10
2:A:262:CYS:O	2:A:266:LEU:HD23	0.62	1.95	13	18
2:A:353:PRO:CB	2:A:354:PRO:HD3	0.62	2.24	12	18
2:A:275:SER:HB3	2:A:277:ARG:HE	0.62	1.55	4	2
2:A:321:LEU:HD12	2:A:345:CYS:CB	0.62	2.25	14	18
2:A:262:CYS:HA	2:A:291:GLY:HA2	0.62	1.71	19	20
2:A:314:ILE:HD12	2:A:317:LYS:HE2	0.62	1.72	17	4
2:A:272:ASN:CG	2:A:277:ARG:H	0.62	1.97	13	2
2:A:334:CYS:O	2:A:338:ASP:N	0.62	2.33	17	13
2:A:346:LEU:H	2:A:346:LEU:HD23	0.62	1.55	2	10
2:A:364:TRP:HB3	2:A:367:LEU:HD12	0.61	1.72	9	1
2:A:313:CYS:O	2:A:317:LYS:HB3	0.61	1.94	12	2
2:A:319:CYS:HB3	2:A:323:GLY:H	0.61	1.54	1	17
2:A:296:LEU:HB3	2:A:298:PHE:CE1	0.61	2.30	3	18
2:A:282:VAL:CG2	2:A:296:LEU:HD11	0.61	2.25	19	16
2:A:350:VAL:HG12	2:A:351:ALA:H	0.61	1.55	11	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:339:ARG:HB2	2:A:341:TYR:OH	0.61	1.94	12	1
2:A:272:ASN:CB	2:A:277:ARG:N	0.61	2.63	13	2
2:A:284:CYS:SG	2:A:312:GLN:HA	0.61	2.35	19	11
2:A:314:ILE:O	2:A:317:LYS:N	0.61	2.32	18	10
2:A:263:ASP:HB3	2:A:289:ARG:HE	0.61	1.55	14	1
2:A:282:VAL:O	2:A:290:SER:HA	0.61	1.96	3	19
2:A:272:ASN:HB2	2:A:276:GLY:H	0.61	1.56	19	1
2:A:331:LEU:O	2:A:333:PHE:CE1	0.61	2.53	20	19
2:A:350:VAL:HG23	2:A:351:ALA:N	0.61	2.10	17	2
2:A:364:TRP:C	2:A:366:LEU:N	0.60	2.48	9	3
2:A:314:ILE:HG22	2:A:315:GLU:H	0.60	1.56	9	9
2:A:341:TYR:O	2:A:342:HIS:C	0.60	2.38	1	20
2:A:317:LYS:HZ3	2:A:338:ASP:C	0.60	1.99	13	2
2:A:320:ILE:HD12	2:A:339:ARG:HE	0.60	1.57	10	1
2:A:342:HIS:O	2:A:344:TYR:N	0.60	2.35	9	20
2:A:361:HIS:CD2	2:A:362:LEU:N	0.60	2.69	4	19
2:A:317:LYS:O	2:A:318:SER:O	0.60	2.19	4	9
2:A:314:ILE:HA	2:A:317:LYS:NZ	0.60	2.11	19	2
2:A:341:TYR:CB	2:A:346:LEU:HD12	0.60	2.27	9	2
2:A:269:SER:HB2	2:A:280:GLU:HA	0.60	1.72	7	12
2:A:334:CYS:SG	2:A:334:CYS:O	0.59	2.59	18	2
2:A:293:PRO:HA	2:A:296:LEU:HD12	0.59	1.74	18	16
2:A:346:LEU:HD23	2:A:346:LEU:H	0.59	1.55	7	8
2:A:302:MET:SD	2:A:306:VAL:HG11	0.59	2.38	7	1
2:A:321:LEU:HD12	2:A:345:CYS:HB3	0.59	1.74	1	17
2:A:341:TYR:HB3	2:A:346:LEU:HD12	0.59	1.73	9	2
2:A:272:ASN:HB3	2:A:277:ARG:N	0.59	2.12	12	6
2:A:334:CYS:H	2:A:341:TYR:HE1	0.59	1.41	12	1
2:A:293:PRO:CA	2:A:296:LEU:HD12	0.58	2.28	13	18
2:A:317:LYS:HE2	2:A:333:PHE:CE2	0.58	2.34	12	4
2:A:352:GLU:N	2:A:353:PRO:CD	0.58	2.65	20	20
2:A:284:CYS:HB2	2:A:313:CYS:HB3	0.58	1.75	15	13
2:A:320:ILE:HD12	2:A:339:ARG:NE	0.58	2.14	10	1
2:A:282:VAL:HG11	2:A:306:VAL:CG2	0.58	2.29	3	16
2:A:342:HIS:O	2:A:345:CYS:N	0.58	2.37	2	20
2:A:346:LEU:HD22	2:A:349:PRO:HA	0.58	1.76	9	2
2:A:304:GLU:O	2:A:308:THR:HG23	0.58	1.98	13	11
2:A:320:ILE:HG21	2:A:339:ARG:HB3	0.57	1.75	13	17
2:A:314:ILE:O	2:A:317:LYS:NZ	0.57	2.35	5	2
2:A:318:SER:HB2	2:A:325:SER:N	0.57	2.14	19	3
2:A:319:CYS:HB3	2:A:323:GLY:N	0.57	2.14	2	8

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:334:CYS:SG	2:A:359:SER:O	0.57	2.62	19	1
2:A:337:CYS:O	2:A:338:ASP:CB	0.57	2.51	11	14
2:A:282:VAL:O	2:A:282:VAL:HG13	0.57	2.00	18	2
2:A:319:CYS:HA	2:A:340:GLY:O	0.57	1.98	14	20
2:A:262:CYS:O	2:A:264:PHE:HD1	0.57	1.81	19	1
2:A:303:THR:O	2:A:307:LYS:HE2	0.57	2.00	11	2
2:A:341:TYR:CD1	2:A:341:TYR:N	0.57	2.70	12	1
2:A:284:CYS:HB3	2:A:288:GLY:CA	0.57	2.30	16	1
2:A:309:TYR:CG	2:A:310:LYS:N	0.56	2.73	16	20
2:A:341:TYR:CZ	2:A:360:CYS:HB2	0.56	2.35	16	17
2:A:331:LEU:O	2:A:333:PHE:CE2	0.56	2.58	8	1
2:A:268:GLY:HA2	2:A:281:LEU:HD11	0.56	1.77	10	19
2:A:332:LEU:HD12	2:A:346:LEU:HD11	0.56	1.75	4	17
2:A:303:THR:O	2:A:307:LYS:HE3	0.56	2.00	8	16
2:A:296:LEU:HD13	2:A:298:PHE:CE2	0.56	2.35	7	16
2:A:334:CYS:O	2:A:334:CYS:SG	0.56	2.63	17	2
2:A:332:LEU:HD21	2:A:354:PRO:HG2	0.56	1.76	7	3
2:A:341:TYR:CE1	2:A:358:TRP:HZ3	0.56	2.18	12	1
2:A:354:PRO:O	2:A:356:GLY:N	0.56	2.39	6	4
2:A:314:ILE:HD13	2:A:317:LYS:HG3	0.56	1.77	4	2
2:A:350:VAL:HG21	2:A:354:PRO:HD3	0.56	1.77	20	2
2:A:262:CYS:HA	2:A:290:SER:O	0.56	2.01	14	7
2:A:298:PHE:CG	2:A:302:MET:SD	0.56	2.99	6	4
2:A:312:GLN:HB3	2:A:316:CYS:SG	0.56	2.41	18	4
2:A:359:SER:O	2:A:360:CYS:SG	0.56	2.64	19	1
2:A:342:HIS:HB3	2:A:344:TYR:CE1	0.55	2.36	6	18
2:A:280:GLU:HG2	2:A:307:LYS:HD2	0.55	1.79	8	13
2:A:318:SER:HB3	2:A:325:SER:N	0.55	2.17	8	3
2:A:318:SER:O	2:A:319:CYS:C	0.55	2.45	11	1
2:A:330:GLN:HA	2:A:343:MET:SD	0.55	2.41	10	14
2:A:314:ILE:C	2:A:317:LYS:HD2	0.55	2.21	3	2
2:A:293:PRO:HG3	2:A:303:THR:HG23	0.55	1.78	15	4
2:A:347:ASN:N	2:A:348:PRO:CD	0.55	2.69	4	20
2:A:302:MET:SD	2:A:335:ASP:HA	0.55	2.42	14	2
2:A:272:ASN:HB3	2:A:276:GLY:C	0.55	2.21	12	4
2:A:343:MET:HE3	2:A:350:VAL:HG22	0.55	1.79	17	1
2:A:332:LEU:HG	2:A:358:TRP:CD2	0.55	2.36	5	1
2:A:343:MET:HA	2:A:346:LEU:HD21	0.55	1.78	5	13
2:A:320:ILE:HD12	2:A:339:ARG:CD	0.55	2.29	17	2
2:A:321:LEU:CD2	2:A:321:LEU:N	0.55	2.70	3	14
2:A:363:CYS:O	2:A:366:LEU:HB3	0.55	2.02	17	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:285:ALA:HB3	2:A:310:LYS:HG3	0.55	1.79	18	2
2:A:302:MET:HG3	2:A:306:VAL:HG13	0.55	1.78	2	2
2:A:364:TRP:HA	2:A:367:LEU:HG	0.55	1.77	9	1
2:A:302:MET:SD	2:A:338:ASP:N	0.55	2.80	14	6
2:A:282:VAL:H	2:A:291:GLY:H	0.54	1.44	1	7
2:A:315:GLU:HA	2:A:317:LYS:HZ1	0.54	1.61	15	3
2:A:298:PHE:HB3	2:A:302:MET:HG2	0.54	1.80	6	1
2:A:320:ILE:HG21	2:A:341:TYR:CE2	0.54	2.37	12	1
2:A:321:LEU:N	2:A:321:LEU:CD2	0.54	2.71	1	6
2:A:352:GLU:H	2:A:353:PRO:CD	0.54	2.12	20	19
2:A:346:LEU:HD13	2:A:358:TRP:CZ2	0.54	2.37	12	16
2:A:346:LEU:HG	2:A:358:TRP:CZ2	0.54	2.37	8	2
2:A:339:ARG:HD2	2:A:362:LEU:HD23	0.54	1.79	16	1
2:A:332:LEU:HD11	2:A:354:PRO:HG2	0.54	1.78	5	1
2:A:298:PHE:HZ	2:A:311:TRP:NE1	0.54	2.00	17	10
2:A:262:CYS:HA	2:A:291:GLY:CA	0.54	2.32	19	2
2:A:283:SER:HA	2:A:289:ARG:O	0.54	2.02	16	2
2:A:343:MET:CG	2:A:350:VAL:HG22	0.54	2.32	12	18
2:A:300:LEU:O	2:A:304:GLU:HG3	0.54	2.03	2	18
2:A:328:ASP:H	2:A:342:HIS:HE2	0.54	1.46	2	2
2:A:314:ILE:O	2:A:315:GLU:C	0.54	2.46	14	10
2:A:314:ILE:HD12	2:A:317:LYS:HG2	0.54	1.80	8	2
2:A:289:ARG:HG3	2:A:289:ARG:O	0.54	2.03	19	1
2:A:328:ASP:HA	2:A:331:LEU:CG	0.54	2.33	3	18
2:A:343:MET:HB3	2:A:350:VAL:HG13	0.54	1.80	17	1
2:A:313:CYS:O	2:A:316:CYS:SG	0.54	2.66	18	1
2:A:303:THR:HG22	2:A:307:LYS:CE	0.54	2.33	13	2
2:A:310:LYS:HG2	2:A:312:GLN:HG3	0.53	1.78	18	1
2:A:314:ILE:CA	2:A:317:LYS:HD2	0.53	2.33	19	3
2:A:361:HIS:CD2	2:A:362:LEU:HD22	0.53	2.39	16	2
2:A:272:ASN:O	2:A:276:GLY:N	0.53	2.42	4	2
2:A:275:SER:HB3	2:A:277:ARG:NE	0.53	2.19	11	2
2:A:302:MET:SD	2:A:337:CYS:C	0.53	2.87	20	6
2:A:327:ASN:C	2:A:329:ASP:H	0.53	2.06	16	19
2:A:330:GLN:O	2:A:331:LEU:C	0.53	2.45	5	20
2:A:282:VAL:HG21	2:A:296:LEU:CD1	0.53	2.33	19	10
2:A:272:ASN:HB2	2:A:277:ARG:N	0.53	2.18	6	2
2:A:334:CYS:HB2	2:A:360:CYS:N	0.53	2.19	8	4
2:A:303:THR:HG22	2:A:307:LYS:NZ	0.53	2.19	13	1
2:A:284:CYS:HB2	2:A:313:CYS:H	0.53	1.63	18	6
2:A:317:LYS:HD2	2:A:318:SER:N	0.53	2.18	4	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:262:CYS:O	2:A:291:GLY:HA2	0.53	2.03	19	1
2:A:289:ARG:HH22	2:A:291:GLY:HA3	0.53	1.62	14	1
2:A:312:GLN:O	2:A:316:CYS:SG	0.53	2.67	15	2
2:A:364:TRP:HA	2:A:367:LEU:CG	0.53	2.33	9	1
2:A:350:VAL:HG23	2:A:352:GLU:N	0.53	2.19	20	2
2:A:346:LEU:CD1	2:A:350:VAL:HG23	0.53	2.34	11	1
2:A:292:HIS:O	2:A:296:LEU:HG	0.53	2.03	10	4
2:A:343:MET:CB	2:A:350:VAL:HG22	0.52	2.32	12	18
2:A:282:VAL:CG2	2:A:291:GLY:O	0.52	2.57	7	13
2:A:364:TRP:HA	2:A:367:LEU:H	0.52	1.64	9	1
2:A:303:THR:CG2	2:A:307:LYS:HE2	0.52	2.34	18	2
2:A:314:ILE:CD1	2:A:317:LYS:HE3	0.52	2.34	5	3
2:A:283:SER:HB3	2:A:290:SER:OG	0.52	2.03	17	10
2:A:327:ASN:O	2:A:329:ASP:N	0.52	2.43	19	20
2:A:272:ASN:HB2	2:A:276:GLY:C	0.52	2.24	6	2
2:A:364:TRP:O	2:A:367:LEU:N	0.52	2.42	17	8
2:A:319:CYS:O	2:A:323:GLY:HA2	0.52	2.04	20	16
2:A:341:TYR:CD1	2:A:358:TRP:CZ3	0.52	2.98	12	1
2:A:357:SER:O	2:A:358:TRP:HB3	0.52	2.04	17	16
2:A:325:SER:O	2:A:328:ASP:N	0.52	2.43	14	12
2:A:334:CYS:SG	2:A:336:ASP:HB3	0.52	2.45	20	16
2:A:298:PHE:CE2	2:A:306:VAL:HG21	0.52	2.40	18	4
2:A:313:CYS:SG	2:A:314:ILE:N	0.52	2.82	11	3
2:A:276:GLY:O	2:A:277:ARG:HB2	0.52	2.05	8	3
2:A:312:GLN:HB2	2:A:317:LYS:HA	0.51	1.82	19	2
2:A:306:VAL:HB	2:A:311:TRP:HB2	0.51	1.82	5	5
2:A:332:LEU:HD21	2:A:355:GLU:H	0.51	1.65	7	1
2:A:361:HIS:O	2:A:365:GLU:HG3	0.51	2.05	16	3
2:A:334:CYS:HB3	2:A:341:TYR:OH	0.51	2.05	12	1
2:A:284:CYS:SG	2:A:313:CYS:N	0.51	2.83	9	3
2:A:277:ARG:HB3	2:A:278:PRO:HD2	0.51	1.80	14	5
2:A:285:ALA:HB3	2:A:310:LYS:CG	0.51	2.35	18	1
2:A:298:PHE:CZ	2:A:311:TRP:NE1	0.51	2.78	17	12
2:A:262:CYS:CA	2:A:291:GLY:HA2	0.51	2.35	19	1
2:A:341:TYR:HB2	2:A:346:LEU:CD2	0.51	2.35	19	11
2:A:339:ARG:HD3	2:A:362:LEU:HD12	0.51	1.82	14	3
2:A:269:SER:C	2:A:271:MET:H	0.51	2.08	1	3
2:A:339:ARG:CD	2:A:362:LEU:HD23	0.51	2.35	19	1
2:A:282:VAL:HG11	2:A:306:VAL:HG23	0.51	1.82	13	13
2:A:292:HIS:O	2:A:295:CYS:N	0.51	2.44	7	8
2:A:334:CYS:CB	2:A:360:CYS:HB3	0.51	2.36	19	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:361:HIS:CD2	2:A:362:LEU:HD13	0.51	2.40	19	1
2:A:322:CYS:CB	2:A:324:THR:HG22	0.50	2.36	1	18
2:A:317:LYS:HZ3	2:A:333:PHE:HE2	0.50	1.49	14	3
2:A:268:GLY:O	2:A:270:ASN:N	0.50	2.44	1	1
2:A:331:LEU:N	2:A:342:HIS:HA	0.50	2.21	16	15
2:A:285:ALA:CB	2:A:310:LYS:HD3	0.50	2.37	3	12
2:A:321:LEU:CB	2:A:345:CYS:HB3	0.50	2.37	11	20
2:A:341:TYR:CB	2:A:346:LEU:CD2	0.50	2.89	1	10
2:A:280:GLU:O	2:A:281:LEU:O	0.50	2.29	7	1
2:A:359:SER:O	2:A:363:CYS:HB2	0.50	2.07	19	1
2:A:282:VAL:CG1	2:A:296:LEU:HD11	0.50	2.36	15	2
2:A:314:ILE:O	2:A:314:ILE:HD12	0.50	2.06	13	1
2:A:302:MET:HB2	2:A:335:ASP:C	0.50	2.27	2	3
2:A:272:ASN:ND2	2:A:277:ARG:HA	0.50	2.22	19	1
2:A:282:VAL:HG21	2:A:306:VAL:CG2	0.50	2.36	18	2
2:A:272:ASN:CG	2:A:277:ARG:N	0.50	2.65	13	1
2:A:332:LEU:CG	2:A:343:MET:HG3	0.50	2.33	11	1
2:A:314:ILE:HD12	2:A:314:ILE:O	0.50	2.06	8	1
2:A:269:SER:N	2:A:281:LEU:HD11	0.50	2.22	13	3
2:A:311:TRP:O	2:A:312:GLN:O	0.50	2.30	18	9
2:A:332:LEU:CD2	2:A:354:PRO:HG2	0.50	2.37	7	1
2:A:322:CYS:SG	2:A:324:THR:CG2	0.50	3.00	13	2
2:A:281:LEU:HB3	2:A:290:SER:HB3	0.50	1.82	16	6
2:A:311:TRP:O	2:A:313:CYS:N	0.50	2.45	15	4
2:A:334:CYS:SG	2:A:337:CYS:N	0.50	2.85	16	3
2:A:302:MET:HA	2:A:336:ASP:C	0.50	2.27	11	11
2:A:284:CYS:CB	2:A:313:CYS:H	0.50	2.19	6	5
2:A:363:CYS:O	2:A:367:LEU:HB2	0.49	2.06	3	1
2:A:302:MET:SD	2:A:335:ASP:HB2	0.49	2.47	6	2
2:A:338:ASP:O	2:A:339:ARG:C	0.49	2.50	7	3
2:A:262:CYS:O	2:A:266:LEU:N	0.49	2.45	1	19
2:A:320:ILE:HG21	2:A:341:TYR:CE1	0.49	2.42	20	17
2:A:347:ASN:HB2	2:A:348:PRO:HD3	0.49	1.83	9	6
2:A:339:ARG:HD2	2:A:362:LEU:HD12	0.49	1.83	17	1
2:A:306:VAL:HG12	2:A:337:CYS:O	0.49	2.07	15	2
2:A:346:LEU:H	2:A:346:LEU:CD2	0.49	2.19	14	8
2:A:321:LEU:HD21	2:A:341:TYR:CZ	0.49	2.42	11	6
2:A:324:THR:C	2:A:326:GLU:H	0.49	2.11	2	6
2:A:302:MET:HG2	2:A:303:THR:N	0.49	2.22	6	1
2:A:302:MET:O	2:A:303:THR:C	0.49	2.51	14	7
2:A:271:MET:N	2:A:278:PRO:HA	0.49	2.23	14	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:280:GLU:O	2:A:307:LYS:HD3	0.49	2.07	13	2
2:A:269:SER:N	2:A:281:LEU:CD1	0.49	2.76	13	3
2:A:343:MET:CB	2:A:350:VAL:HG13	0.49	2.36	17	1
2:A:314:ILE:HD11	2:A:333:PHE:CD2	0.49	2.43	16	1
2:A:327:ASN:C	2:A:329:ASP:N	0.49	2.66	19	19
2:A:305:ALA:HB1	2:A:337:CYS:HB2	0.49	1.85	17	2
2:A:339:ARG:HB2	2:A:360:CYS:SG	0.49	2.48	8	3
2:A:277:ARG:O	2:A:279:GLU:N	0.49	2.46	19	2
2:A:270:ASN:N	2:A:270:ASN:HD22	0.49	2.05	15	1
2:A:317:LYS:O	2:A:318:SER:C	0.49	2.50	11	1
2:A:320:ILE:N	2:A:340:GLY:O	0.49	2.46	12	1
2:A:341:TYR:HB2	2:A:346:LEU:HD22	0.49	1.84	2	5
2:A:283:SER:CA	2:A:290:SER:HA	0.49	2.36	16	1
2:A:275:SER:O	2:A:277:ARG:HD3	0.48	2.08	14	4
2:A:317:LYS:HG2	2:A:318:SER:N	0.48	2.22	14	1
2:A:324:THR:HG21	2:A:326:GLU:HG3	0.48	1.86	15	17
2:A:341:TYR:HB3	2:A:346:LEU:HD22	0.48	1.84	11	6
2:A:289:ARG:HD2	2:A:289:ARG:O	0.48	2.08	11	2
2:A:334:CYS:N	2:A:338:ASP:O	0.48	2.47	17	1
2:A:314:ILE:HA	2:A:317:LYS:CE	0.48	2.37	6	1
2:A:285:ALA:HB3	2:A:310:LYS:HB3	0.48	1.85	19	2
2:A:269:SER:HB2	2:A:281:LEU:H	0.48	1.67	18	2
2:A:296:LEU:HD13	2:A:298:PHE:CZ	0.48	2.44	19	3
2:A:318:SER:HB2	2:A:325:SER:H	0.48	1.68	10	1
2:A:343:MET:O	2:A:350:VAL:N	0.48	2.47	12	19
2:A:282:VAL:CG2	2:A:296:LEU:CD1	0.48	2.91	13	10
2:A:332:LEU:CD2	2:A:354:PRO:O	0.48	2.61	17	13
2:A:364:TRP:CA	2:A:367:LEU:H	0.48	2.20	9	1
2:A:324:THR:HG23	2:A:326:GLU:N	0.48	2.24	4	16
2:A:325:SER:O	2:A:326:GLU:C	0.48	2.52	6	14
2:A:346:LEU:HD11	2:A:350:VAL:HG23	0.48	1.86	11	1
2:A:342:HIS:C	2:A:344:TYR:N	0.48	2.66	12	20
2:A:268:GLY:O	2:A:271:MET:O	0.48	2.31	17	2
2:A:317:LYS:NZ	2:A:333:PHE:HE2	0.48	2.06	14	1
2:A:318:SER:O	2:A:323:GLY:HA2	0.48	2.09	11	1
2:A:339:ARG:HD2	2:A:360:CYS:SG	0.48	2.49	20	2
2:A:366:LEU:O	2:A:366:LEU:HD22	0.48	2.09	14	1
2:A:269:SER:C	2:A:271:MET:N	0.48	2.67	1	3
2:A:269:SER:CA	2:A:281:LEU:HG	0.48	2.39	1	1
2:A:262:CYS:HB2	2:A:281:LEU:CD2	0.48	2.38	1	14
2:A:364:TRP:CA	2:A:367:LEU:HB2	0.48	2.36	17	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:331:LEU:HD21	2:A:342:HIS:CE1	0.47	2.44	2	4
2:A:310:LYS:O	2:A:311:TRP:HB3	0.47	2.08	8	10
2:A:284:CYS:SG	2:A:286:ASP:HB3	0.47	2.48	2	6
2:A:282:VAL:CG1	2:A:306:VAL:HG23	0.47	2.40	3	7
2:A:320:ILE:CG2	2:A:341:TYR:CE1	0.47	2.97	20	19
2:A:334:CYS:C	2:A:336:ASP:H	0.47	2.13	12	11
2:A:346:LEU:CD2	2:A:346:LEU:H	0.47	2.20	20	4
2:A:261:TYR:HA	2:A:281:LEU:HD13	0.47	1.85	15	1
2:A:293:PRO:CG	2:A:307:LYS:NZ	0.47	2.77	11	1
2:A:284:CYS:HA	2:A:311:TRP:O	0.47	2.09	19	3
2:A:265:CYS:SG	2:A:272:ASN:ND2	0.47	2.87	5	1
2:A:346:LEU:HB2	2:A:348:PRO:HD2	0.47	1.85	10	6
2:A:331:LEU:HD23	2:A:342:HIS:N	0.47	2.24	12	2
2:A:280:GLU:CG	2:A:307:LYS:HD2	0.47	2.39	18	1
2:A:272:ASN:HA	2:A:292:HIS:CE1	0.47	2.45	7	3
2:A:305:ALA:HB3	2:A:337:CYS:HA	0.47	1.87	10	6
2:A:314:ILE:HA	2:A:317:LYS:HZ3	0.47	1.69	19	1
2:A:306:VAL:HG11	2:A:311:TRP:CD1	0.47	2.45	14	2
2:A:347:ASN:HB3	2:A:348:PRO:HD3	0.47	1.86	6	9
2:A:311:TRP:O	2:A:311:TRP:CE3	0.47	2.68	19	1
2:A:272:ASN:CB	2:A:277:ARG:H	0.47	2.23	19	1
2:A:263:ASP:HB3	2:A:289:ARG:NE	0.47	2.22	14	1
2:A:332:LEU:HB2	2:A:341:TYR:O	0.47	2.10	5	1
2:A:366:LEU:HD22	2:A:366:LEU:O	0.47	2.10	4	3
2:A:315:GLU:HA	2:A:317:LYS:NZ	0.47	2.25	7	4
2:A:314:ILE:C	2:A:316:CYS:N	0.47	2.68	14	1
2:A:346:LEU:CD2	2:A:350:VAL:HG13	0.46	2.40	8	2
2:A:324:THR:HG23	2:A:326:GLU:HB2	0.46	1.87	13	1
2:A:346:LEU:HG	2:A:349:PRO:HA	0.46	1.87	10	14
2:A:289:ARG:NH1	2:A:311:TRP:CH2	0.46	2.83	14	1
2:A:277:ARG:HD3	2:A:277:ARG:N	0.46	2.26	12	1
2:A:326:GLU:HB2	2:A:342:HIS:CE1	0.46	2.45	4	11
2:A:314:ILE:C	2:A:317:LYS:HB3	0.46	2.30	8	3
2:A:265:CYS:SG	2:A:272:ASN:OD1	0.46	2.73	15	2
2:A:267:GLY:HA3	2:A:273:LYS:HG3	0.46	1.87	18	12
2:A:317:LYS:CD	2:A:317:LYS:N	0.46	2.78	3	1
2:A:261:TYR:CD1	2:A:266:LEU:HA	0.46	2.46	15	5
2:A:282:VAL:CG1	2:A:282:VAL:O	0.46	2.64	18	1
2:A:316:CYS:C	2:A:318:SER:N	0.46	2.69	11	1
2:A:332:LEU:HD22	2:A:343:MET:HG3	0.46	1.84	5	1
2:A:303:THR:O	2:A:307:LYS:CE	0.46	2.63	12	6

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:296:LEU:O	2:A:297:GLN:OE1	0.46	2.33	14	1
2:A:303:THR:HG22	2:A:307:LYS:HE3	0.46	1.86	11	1
2:A:332:LEU:HD13	2:A:343:MET:CG	0.46	2.41	5	1
2:A:313:CYS:O	2:A:317:LYS:N	0.46	2.47	17	1
2:A:289:ARG:NH2	2:A:291:GLY:HA3	0.46	2.26	14	1
2:A:342:HIS:C	2:A:344:TYR:H	0.46	2.13	1	20
2:A:346:LEU:CD1	2:A:350:VAL:HG13	0.46	2.40	7	4
2:A:334:CYS:SG	2:A:359:SER:HA	0.46	2.51	20	1
2:A:318:SER:O	2:A:319:CYS:O	0.46	2.33	11	1
2:A:285:ALA:CB	2:A:310:LYS:HA	0.46	2.41	18	1
2:A:364:TRP:O	2:A:365:GLU:C	0.46	2.54	14	3
2:A:299:THR:O	2:A:300:LEU:C	0.45	2.54	2	3
2:A:269:SER:OG	2:A:270:ASN:N	0.45	2.48	18	1
2:A:262:CYS:SG	2:A:264:PHE:N	0.45	2.87	9	12
2:A:281:LEU:HD23	2:A:292:HIS:CD2	0.45	2.46	2	8
2:A:315:GLU:CA	2:A:317:LYS:HZ1	0.45	2.23	15	3
2:A:272:ASN:CG	2:A:276:GLY:HA3	0.45	2.31	8	2
2:A:341:TYR:CE1	2:A:360:CYS:HB2	0.45	2.46	8	2
2:A:275:SER:C	2:A:277:ARG:HD3	0.45	2.32	12	1
2:A:360:CYS:O	2:A:364:TRP:NE1	0.45	2.50	14	2
2:A:289:ARG:HD3	2:A:289:ARG:O	0.45	2.11	14	1
2:A:319:CYS:C	2:A:320:ILE:HG22	0.45	2.31	11	1
2:A:293:PRO:HA	2:A:296:LEU:HB2	0.45	1.88	3	6
2:A:284:CYS:SG	2:A:286:ASP:HB2	0.45	2.51	14	1
2:A:332:LEU:O	2:A:341:TYR:CD1	0.45	2.70	12	1
2:A:284:CYS:HB3	2:A:288:GLY:HA3	0.45	1.88	16	1
2:A:320:ILE:HD11	2:A:362:LEU:HD21	0.45	1.87	16	1
2:A:302:MET:O	2:A:305:ALA:N	0.45	2.50	14	4
2:A:320:ILE:CG2	2:A:340:GLY:O	0.45	2.64	12	3
2:A:325:SER:O	2:A:328:ASP:HB3	0.45	2.12	9	1
2:A:341:TYR:CB	2:A:346:LEU:CD1	0.45	2.95	9	2
2:A:320:ILE:CG2	2:A:341:TYR:CD1	0.45	3.00	9	10
2:A:314:ILE:C	2:A:317:LYS:HE3	0.45	2.32	15	2
2:A:314:ILE:HA	2:A:317:LYS:HB2	0.45	1.88	1	2
2:A:303:THR:CG2	2:A:307:LYS:NZ	0.45	2.79	13	2
2:A:346:LEU:CD2	2:A:346:LEU:N	0.45	2.79	19	3
2:A:356:GLY:O	2:A:357:SER:HB2	0.45	2.11	8	2
2:A:320:ILE:CG2	2:A:341:TYR:CE2	0.45	3.00	12	1
2:A:319:CYS:HB2	2:A:331:LEU:HD21	0.45	1.88	12	11
2:A:279:GLU:O	2:A:280:GLU:HB2	0.45	2.11	19	2
2:A:300:LEU:O	2:A:303:THR:HB	0.45	2.12	2	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:262:CYS:HB2	2:A:281:LEU:HD23	0.45	1.88	1	2
2:A:282:VAL:CG2	2:A:306:VAL:HG23	0.45	2.41	18	1
2:A:332:LEU:HD11	2:A:350:VAL:HG11	0.45	1.89	17	1
2:A:327:ASN:N	2:A:327:ASN:HD22	0.44	2.10	6	3
2:A:317:LYS:CE	2:A:333:PHE:CE2	0.44	3.00	14	3
2:A:334:CYS:HB2	2:A:360:CYS:HB3	0.44	1.89	19	1
2:A:264:PHE:CE1	2:A:289:ARG:NH2	0.44	2.86	14	1
2:A:284:CYS:C	2:A:286:ASP:H	0.44	2.16	10	2
2:A:262:CYS:C	2:A:264:PHE:N	0.44	2.71	15	2
2:A:291:GLY:O	2:A:296:LEU:HD11	0.44	2.12	10	1
2:A:320:ILE:HD13	2:A:341:TYR:CE1	0.44	2.48	13	5
2:A:317:LYS:CE	2:A:333:PHE:HE2	0.44	2.25	14	1
2:A:263:ASP:N	2:A:290:SER:O	0.44	2.49	13	1
2:A:332:LEU:CD2	2:A:346:LEU:HD11	0.44	2.42	5	1
2:A:317:LYS:CG	2:A:318:SER:N	0.44	2.80	14	4
2:A:273:LYS:C	2:A:275:SER:N	0.44	2.71	7	3
2:A:364:TRP:CD1	2:A:367:LEU:HD22	0.44	2.47	19	3
2:A:262:CYS:O	2:A:264:PHE:CD1	0.44	2.67	19	1
2:A:350:VAL:CG1	2:A:353:PRO:HG2	0.44	2.42	11	1
2:A:312:GLN:O	2:A:313:CYS:C	0.44	2.56	15	6
2:A:363:CYS:O	2:A:367:LEU:HG	0.44	2.13	9	1
2:A:366:LEU:HD13	2:A:366:LEU:O	0.44	2.13	8	2
2:A:332:LEU:HD22	2:A:354:PRO:O	0.44	2.13	11	1
2:A:333:PHE:CD2	2:A:333:PHE:N	0.44	2.85	8	1
2:A:351:ALA:C	2:A:352:GLU:CG	0.44	2.86	8	17
2:A:265:CYS:SG	2:A:274:LYS:HG3	0.44	2.52	9	2
2:A:280:GLU:HB3	2:A:307:LYS:HD3	0.44	1.89	6	2
2:A:317:LYS:NZ	2:A:338:ASP:OD2	0.44	2.50	10	1
2:A:262:CYS:C	2:A:264:PHE:H	0.44	2.15	15	4
2:A:347:ASN:C	2:A:349:PRO:CD	0.43	2.86	5	18
2:A:330:GLN:O	2:A:343:MET:HG3	0.43	2.13	7	4
2:A:343:MET:HG2	2:A:350:VAL:HB	0.43	1.89	11	1
2:A:284:CYS:HA	2:A:312:GLN:HA	0.43	1.90	6	1
2:A:262:CYS:O	2:A:262:CYS:SG	0.43	2.76	19	1
2:A:289:ARG:HH12	2:A:291:GLY:HA3	0.43	1.74	14	1
2:A:272:ASN:HD22	2:A:272:ASN:C	0.43	2.15	12	1
2:A:341:TYR:CD1	2:A:358:TRP:HZ3	0.43	2.31	12	1
2:A:325:SER:O	2:A:328:ASP:OD1	0.43	2.36	13	2
2:A:283:SER:OG	2:A:288:GLY:C	0.43	2.57	13	2
2:A:282:VAL:C	2:A:290:SER:HA	0.43	2.34	16	1
2:A:322:CYS:HB3	2:A:324:THR:HG22	0.43	1.91	4	5

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:273:LYS:O	2:A:274:LYS:HB2	0.43	2.14	6	5
2:A:320:ILE:HG13	2:A:320:ILE:O	0.43	2.14	8	2
2:A:339:ARG:NH1	2:A:362:LEU:HB2	0.43	2.28	1	1
2:A:284:CYS:HB3	2:A:288:GLY:N	0.43	2.28	16	1
2:A:328:ASP:HB3	2:A:331:LEU:HD12	0.43	1.90	10	1
2:A:267:GLY:CA	2:A:273:LYS:HG3	0.43	2.43	9	4
2:A:332:LEU:HD21	2:A:354:PRO:O	0.43	2.14	17	1
2:A:262:CYS:SG	2:A:265:CYS:N	0.43	2.92	7	2
2:A:306:VAL:CG1	2:A:311:TRP:CD1	0.43	3.02	12	4
2:A:314:ILE:CD1	2:A:317:LYS:HG2	0.43	2.42	8	2
2:A:351:ALA:O	2:A:352:GLU:HB3	0.43	2.13	20	1
2:A:303:THR:O	2:A:307:LYS:HB2	0.43	2.14	13	1
2:A:270:ASN:HD22	2:A:270:ASN:H	0.43	1.57	15	1
2:A:261:TYR:C	2:A:290:SER:HB2	0.43	2.33	15	2
2:A:261:TYR:CE1	2:A:266:LEU:HD22	0.43	2.48	1	5
2:A:264:PHE:CD1	2:A:264:PHE:N	0.43	2.87	7	1
2:A:331:LEU:HA	2:A:342:HIS:HA	0.43	1.91	19	3
2:A:269:SER:CB	2:A:281:LEU:H	0.43	2.27	18	1
2:A:302:MET:SD	2:A:335:ASP:CB	0.43	3.06	13	1
2:A:262:CYS:O	2:A:264:PHE:N	0.43	2.52	2	1
2:A:314:ILE:HD13	2:A:317:LYS:HE2	0.43	1.90	19	1
2:A:282:VAL:HG11	2:A:296:LEU:CD1	0.43	2.44	15	2
2:A:327:ASN:ND2	2:A:344:TYR:OH	0.42	2.52	12	6
2:A:327:ASN:HD22	2:A:327:ASN:N	0.42	2.12	19	1
2:A:317:LYS:NZ	2:A:331:LEU:CD1	0.42	2.82	20	1
2:A:269:SER:O	2:A:270:ASN:ND2	0.42	2.52	5	1
2:A:330:GLN:O	2:A:343:MET:CG	0.42	2.67	15	8
2:A:317:LYS:NZ	2:A:333:PHE:CE2	0.42	2.86	14	1
2:A:269:SER:H	2:A:281:LEU:CG	0.42	2.27	1	1
2:A:272:ASN:ND2	2:A:292:HIS:ND1	0.42	2.67	11	1
2:A:272:ASN:HD22	2:A:275:SER:H	0.42	1.56	3	1
2:A:316:CYS:O	2:A:317:LYS:C	0.42	2.58	3	2
2:A:317:LYS:HZ3	2:A:331:LEU:HD12	0.42	1.74	4	2
2:A:362:LEU:HD22	2:A:362:LEU:N	0.42	2.30	16	1
2:A:346:LEU:HG	2:A:358:TRP:HZ2	0.42	1.74	8	1
2:A:364:TRP:C	2:A:367:LEU:H	0.42	2.18	9	1
2:A:292:HIS:O	2:A:294:THR:N	0.42	2.53	6	1
2:A:359:SER:HB2	2:A:363:CYS:SG	0.42	2.55	20	1
2:A:314:ILE:HD12	2:A:317:LYS:CB	0.42	2.44	13	1
2:A:320:ILE:HG23	2:A:321:LEU:HD23	0.42	1.91	3	5
2:A:335:ASP:OD2	2:A:357:SER:HA	0.42	2.14	7	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:262:CYS:SG	2:A:264:PHE:CB	0.42	3.06	1	3
2:A:271:MET:SD	2:A:278:PRO:HD3	0.42	2.54	15	1
2:A:273:LYS:O	2:A:274:LYS:CB	0.42	2.67	13	1
2:A:351:ALA:O	2:A:352:GLU:CD	0.42	2.58	11	1
2:A:332:LEU:HD22	2:A:343:MET:HG2	0.42	1.87	5	1
2:A:285:ALA:HB1	2:A:310:LYS:HD3	0.42	1.92	19	1
2:A:312:GLN:O	2:A:313:CYS:SG	0.42	2.77	12	1
2:A:331:LEU:HG	2:A:342:HIS:CD2	0.42	2.49	13	1
2:A:291:GLY:HA3	2:A:296:LEU:HD21	0.42	1.92	11	1
2:A:296:LEU:O	2:A:297:GLN:HB2	0.42	2.15	3	2
2:A:339:ARG:CD	2:A:362:LEU:HD12	0.42	2.45	3	2
2:A:317:LYS:HZ1	2:A:338:ASP:CG	0.42	2.18	10	1
2:A:316:CYS:O	2:A:318:SER:N	0.42	2.52	11	1
2:A:334:CYS:O	2:A:338:ASP:CA	0.42	2.68	18	1
2:A:346:LEU:N	2:A:346:LEU:CD2	0.41	2.79	3	2
2:A:350:VAL:CG2	2:A:353:PRO:HB2	0.41	2.45	17	1
2:A:284:CYS:HB2	2:A:313:CYS:N	0.41	2.30	16	1
2:A:302:MET:CG	2:A:303:THR:N	0.41	2.83	6	1
2:A:281:LEU:O	2:A:282:VAL:HG13	0.41	2.14	7	1
2:A:311:TRP:CZ2	2:A:313:CYS:HA	0.41	2.50	14	2
2:A:262:CYS:N	2:A:281:LEU:CD2	0.41	2.81	13	2
2:A:269:SER:HB2	2:A:281:LEU:N	0.41	2.30	15	1
2:A:350:VAL:CG2	2:A:352:GLU:H	0.41	2.20	17	1
2:A:319:CYS:SG	2:A:341:TYR:HA	0.41	2.56	12	1
2:A:341:TYR:OH	2:A:361:HIS:CG	0.41	2.74	8	1
2:A:300:LEU:O	2:A:301:ASN:C	0.41	2.58	12	2
2:A:318:SER:HB3	2:A:325:SER:HB3	0.41	1.93	13	1
2:A:317:LYS:NZ	2:A:331:LEU:HD12	0.41	2.31	20	1
2:A:272:ASN:CB	2:A:277:ARG:O	0.41	2.69	15	2
2:A:337:CYS:SG	2:A:339:ARG:NH1	0.41	2.93	1	1
2:A:310:LYS:CG	2:A:312:GLN:HG3	0.41	2.45	18	1
2:A:314:ILE:HA	2:A:317:LYS:HB3	0.41	1.91	5	1
2:A:270:ASN:C	2:A:278:PRO:HA	0.41	2.36	14	3
2:A:314:ILE:C	2:A:317:LYS:CE	0.41	2.89	15	1
2:A:282:VAL:HG11	2:A:293:PRO:HG3	0.41	1.93	11	1
2:A:314:ILE:C	2:A:317:LYS:NZ	0.41	2.74	5	1
2:A:339:ARG:O	2:A:341:TYR:CE1	0.41	2.74	12	1
2:A:312:GLN:O	2:A:313:CYS:O	0.41	2.38	15	3
2:A:364:TRP:O	2:A:367:LEU:CB	0.41	2.69	17	1
2:A:320:ILE:O	2:A:320:ILE:HG13	0.41	2.16	6	1
2:A:314:ILE:CD1	2:A:317:LYS:HD3	0.41	2.42	19	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:310:LYS:C	2:A:312:GLN:H	0.41	2.19	18	2
2:A:299:THR:O	2:A:303:THR:OG1	0.41	2.33	18	1
2:A:325:SER:O	2:A:328:ASP:OD2	0.41	2.39	18	2
2:A:306:VAL:CB	2:A:311:TRP:HB2	0.41	2.46	2	1
2:A:366:LEU:O	2:A:366:LEU:HD13	0.41	2.16	2	1
2:A:302:MET:SD	2:A:338:ASP:HB2	0.41	2.56	2	1
2:A:275:SER:HB3	2:A:277:ARG:HH11	0.41	1.75	9	1
2:A:330:GLN:HG3	2:A:344:TYR:CE1	0.41	2.51	7	1
2:A:337:CYS:SG	2:A:339:ARG:NE	0.41	2.94	2	1
2:A:262:CYS:CB	2:A:281:LEU:CD2	0.40	2.99	1	1
2:A:356:GLY:O	2:A:357:SER:O	0.40	2.39	16	1
2:A:277:ARG:CD	2:A:277:ARG:N	0.40	2.84	13	1
2:A:359:SER:OG	2:A:360:CYS:N	0.40	2.54	6	1
2:A:352:GLU:CG	2:A:353:PRO:CD	0.40	2.99	20	1
2:A:277:ARG:HB3	2:A:278:PRO:CD	0.40	2.46	14	1
2:A:289:ARG:HB3	2:A:289:ARG:NH1	0.40	2.31	12	1
2:A:341:TYR:OH	2:A:361:HIS:ND1	0.40	2.54	16	1
2:A:324:THR:C	2:A:326:GLU:N	0.40	2.75	13	1
2:A:272:ASN:HD22	2:A:275:SER:N	0.40	2.15	3	1
2:A:354:PRO:CG	2:A:358:TRP:CD1	0.40	3.04	9	1
2:A:273:LYS:C	2:A:275:SER:H	0.40	2.19	4	1
2:A:272:ASN:H	2:A:277:ARG:C	0.40	2.18	15	1
2:A:343:MET:HG2	2:A:350:VAL:CG2	0.40	2.44	14	1
2:A:311:TRP:O	2:A:312:GLN:C	0.40	2.59	15	1
2:A:262:CYS:H	2:A:281:LEU:CD2	0.40	2.30	1	1
2:A:281:LEU:HA	2:A:291:GLY:O	0.40	2.17	1	1
2:A:314:ILE:CG1	2:A:317:LYS:HE3	0.40	2.47	5	1

6.3 Torsion angles ⓘ

6.3.1 Protein backbone ⓘ

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	B	0	-	-	-	-
2	A	107/114 (94%)	62±3 (57±3%)	26±4 (24±3%)	19±3 (18±2%)	0 3

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	2140/2680 (80%)	1230 (57%)	522 (24%)	388 (18%)	0 3

All 44 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
2	A	337	CYS	20
2	A	357	SER	20
2	A	353	PRO	20
2	A	348	PRO	20
2	A	352	GLU	20
2	A	328	ASP	20
2	A	326	GLU	20
2	A	343	MET	20
2	A	358	TRP	19
2	A	318	SER	19
2	A	281	LEU	18
2	A	338	ASP	17
2	A	312	GLN	16
2	A	354	PRO	15
2	A	346	LEU	13
2	A	313	CYS	13
2	A	271	MET	10
2	A	355	GLU	10
2	A	280	GLU	10
2	A	314	ILE	7
2	A	339	ARG	7
2	A	278	PRO	7
2	A	310	LYS	6
2	A	315	GLU	5
2	A	334	CYS	5
2	A	273	LYS	4
2	A	293	PRO	3
2	A	279	GLU	3
2	A	317	LYS	2
2	A	261	TYR	2
2	A	269	SER	2
2	A	268	GLY	2
2	A	263	ASP	2
2	A	303	THR	1
2	A	320	ILE	1
2	A	282	VAL	1

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Mol	Chain	Res	Type	Models (Total)
2	A	311	TRP	1
2	A	356	GLY	1
2	A	270	ASN	1
2	A	275	SER	1
2	A	319	CYS	1
2	A	287	CYS	1
2	A	262	CYS	1
2	A	277	ARG	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	B	0	-	-	-	
2	A	96/101 (95%)	70±3 (73±3%)	26±3 (27±3%)	2	22
All	All	1920/2220 (86%)	1400 (73%)	520 (27%)	2	22

All 55 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)
2	A	321	LEU	20
2	A	261	TYR	20
2	A	320	ILE	20
2	A	346	LEU	20
2	A	309	TYR	20
2	A	262	CYS	20
2	A	326	GLU	20
2	A	343	MET	20
2	A	364	TRP	19
2	A	350	VAL	19
2	A	353	PRO	19
2	A	352	GLU	19
2	A	354	PRO	19
2	A	263	ASP	19
2	A	317	LYS	17
2	A	314	ILE	17

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Mol	Chain	Res	Type	Models (Total)
2	A	300	LEU	17
2	A	328	ASP	17
2	A	282	VAL	16
2	A	367	LEU	15
2	A	273	LYS	15
2	A	335	ASP	12
2	A	365	GLU	10
2	A	271	MET	10
2	A	277	ARG	10
2	A	299	THR	9
2	A	334	CYS	9
2	A	289	ARG	6
2	A	302	MET	5
2	A	359	SER	5
2	A	270	ASN	5
2	A	310	LYS	5
2	A	283	SER	4
2	A	363	CYS	4
2	A	313	CYS	4
2	A	333	PHE	3
2	A	286	ASP	3
2	A	337	CYS	2
2	A	269	SER	2
2	A	290	SER	2
2	A	312	GLN	2
2	A	275	SER	2
2	A	287	CYS	2
2	A	341	TYR	2
2	A	327	ASN	2
2	A	284	CYS	2
2	A	280	GLU	2
2	A	339	ARG	1
2	A	362	LEU	1
2	A	316	CYS	1
2	A	366	LEU	1
2	A	355	GLU	1
2	A	318	SER	1
2	A	297	GLN	1
2	A	272	ASN	1

6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

In the following table, the Counts columns list the number of bonds for which Mogul statistics could be retrieved, the number of bonds that are observed in the model and the number of bonds that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length is the number of standard deviations the observed value is removed from the expected value. A bond length with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond lengths.

Mol	Type	Chain	Res	Link	Bond lengths		
					Counts	RMSZ	#Z>2
1	SAC	B	1	1	8,8,9	0.90±0.06	0±0 (0±0%)

In the following table, the Counts columns list the number of angles for which Mogul statistics could be retrieved, the number of angles that are observed in the model and the number of angles that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond angle is the number of standard deviations the observed value is removed from the expected value. A bond angle with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond angles.

Mol	Type	Chain	Res	Link	Bond angles		
					Counts	RMSZ	#Z>2
1	SAC	B	1	1	6,9,11	1.26±0.07	0±0 (0±0%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	SAC	B	1	1	-	0±0,6,8,10	0±0,0,0,0

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

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

The completeness of assignment taking into account all chemical shift lists is 86% for the well-defined parts and 79% for the entire structure.

7.1 Chemical shift list 1

File name: BMRB entry 16865

Chemical shift list name: *assigned_chem_shift_list_1*

7.1.1 Bookkeeping

The following table shows the results of parsing the chemical shift list and reports the number of nuclei with statistically unusual chemical shifts.

Total number of shifts	1282
Number of shifts mapped to atoms	1282
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	3

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	113	-0.67 ± 0.27	Should be applied
$^{13}\text{C}_\beta$	105	-0.56 ± 0.16	Should be applied
$^{13}\text{C}'$	0	—	None (insufficient data)
^{15}N	106	1.02 ± 0.58	None needed (imprecise)

7.1.3 Completeness of resonance assignments

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 86%, i.e. 1076 atoms were assigned a chemical shift out of a possible 1252. 14 out of 14 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	416/523 (80%)	208/208 (100%)	107/214 (50%)	101/101 (100%)
Sidechain	547/612 (89%)	345/365 (95%)	194/225 (86%)	8/22 (36%)

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	Total	¹H	¹³C	¹⁵N
Aromatic	113/117 (97%)	61/61 (100%)	49/49 (100%)	3/7 (43%)
Overall	1076/1252 (86%)	614/634 (97%)	350/488 (72%)	112/130 (86%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 79%, i.e. 1241 atoms were assigned a chemical shift out of a possible 1564. 14 out of 15 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Backbone	476/653 (73%)	257/260 (99%)	113/266 (42%)	106/127 (83%)
Sidechain	648/786 (82%)	433/471 (92%)	207/277 (75%)	8/38 (21%)
Aromatic	117/125 (94%)	65/65 (100%)	49/51 (96%)	3/9 (33%)
Overall	1241/1564 (79%)	755/796 (95%)	369/594 (62%)	117/174 (67%)

7.1.4 Statistically unusual chemical shifts ⓘ

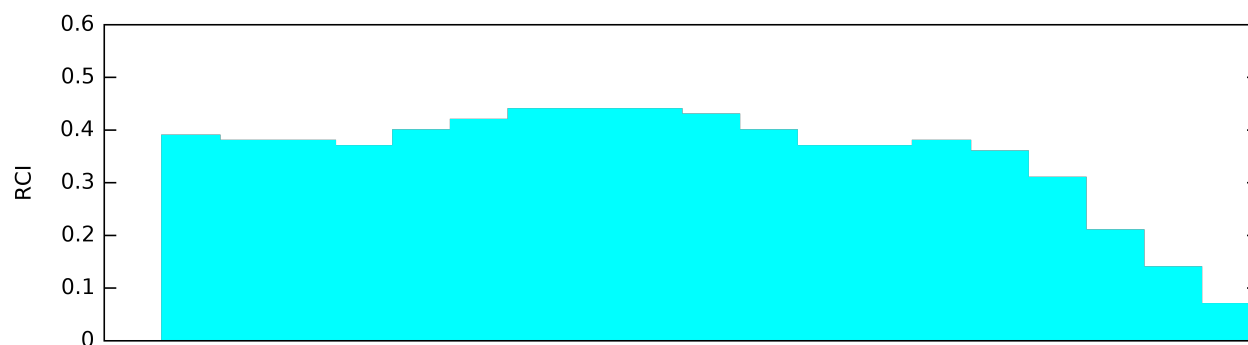
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

Mol	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	358	TRP	NE1	112.37	139.19 – 119.59	-8.7
1	A	364	TRP	NE1	112.73	139.19 – 119.59	-8.5
1	A	311	TRP	NE1	115.60	139.19 – 119.59	-7.0

7.1.5 Random Coil Index (RCI) plots ⓘ

The images below report *random coil index* values for the protein chains in the structure. The height of each bar gives a probability of a given residue to be disordered, as predicted from the available chemical shifts and the amino acid sequence. A value above 0.2 is an indication of significant predicted disorder. The colour of the bar shows whether the residue is in the well-defined core (black) or in the ill-defined residue ranges (cyan), as described in section 2 on ensemble composition.

Random coil index (RCI) for chain B:



Random coil index (RCI) for chain A:

