



Full wwPDB NMR Structure Validation Report ⓘ

Jun 22, 2024 – 11:34 PM EDT

PDB ID : 6D6S
BMRB ID : 30456
Title : Solution structure of Trigger Factor dimer
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Deposited on : 2018-04-22

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/NMRValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
wwPDB-RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
wwPDB-ShiftChecker : v1.2
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.37.1

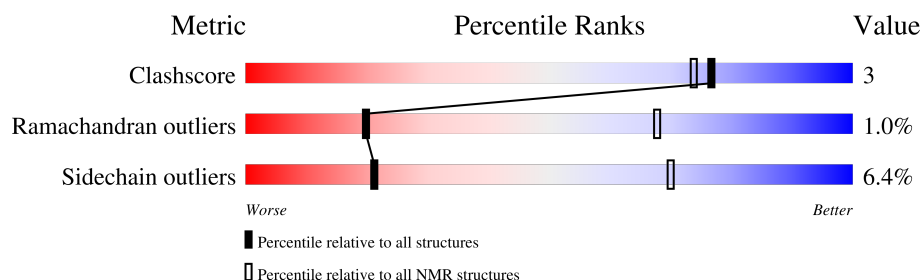
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 14%.

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	158937	12864
Ramachandran outliers	154571	11451
Sidechain outliers	154315	11428

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	443	
1	B	443	

2 Ensemble composition and analysis

This entry contains 20 models. Model 5 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *target function*.

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:2-A:111, B:109-B:429 (431)	1.53	5
2	A:112-A:430, B:2-B:108 (426)	1.51	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 3 clusters. No single-model clusters were found.

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

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 13578 atoms, of which 6806 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Trigger factor.

Mol	Chain	Residues	Atoms						Trace
1	A	432	Total	C	H	N	O	S	0
			6789	2119	3403	582	674	11	
1	B	432	Total	C	H	N	O	S	0
			6789	2119	3403	582	674	11	

There are 22 discrepancies between the modelled and reference sequences:

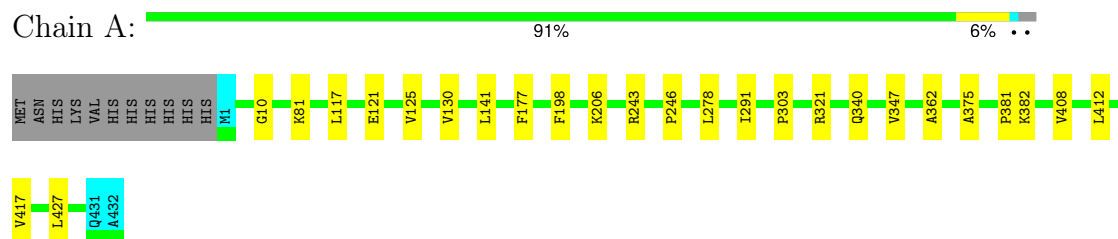
Chain	Residue	Modelled	Actual	Comment	Reference
A	-10	MET	-	initiating methionine	UNP P0A850
A	-9	ASN	-	expression tag	UNP P0A850
A	-8	HIS	-	expression tag	UNP P0A850
A	-7	LYS	-	expression tag	UNP P0A850
A	-6	VAL	-	expression tag	UNP P0A850
A	-5	HIS	-	expression tag	UNP P0A850
A	-4	HIS	-	expression tag	UNP P0A850
A	-3	HIS	-	expression tag	UNP P0A850
A	-2	HIS	-	expression tag	UNP P0A850
A	-1	HIS	-	expression tag	UNP P0A850
A	0	HIS	-	expression tag	UNP P0A850
B	-10	MET	-	initiating methionine	UNP P0A850
B	-9	ASN	-	expression tag	UNP P0A850
B	-8	HIS	-	expression tag	UNP P0A850
B	-7	LYS	-	expression tag	UNP P0A850
B	-6	VAL	-	expression tag	UNP P0A850
B	-5	HIS	-	expression tag	UNP P0A850
B	-4	HIS	-	expression tag	UNP P0A850
B	-3	HIS	-	expression tag	UNP P0A850
B	-2	HIS	-	expression tag	UNP P0A850
B	-1	HIS	-	expression tag	UNP P0A850
B	0	HIS	-	expression tag	UNP P0A850

4 Residue-property plots

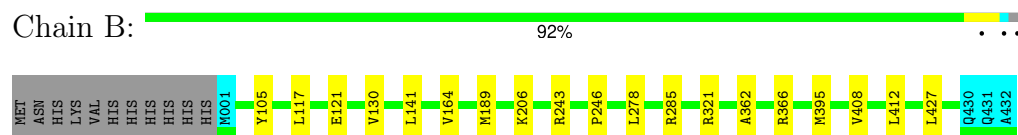
4.1 Average score per residue in the NMR ensemble

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

- Molecule 1: Trigger factor



- Molecule 1: Trigger factor

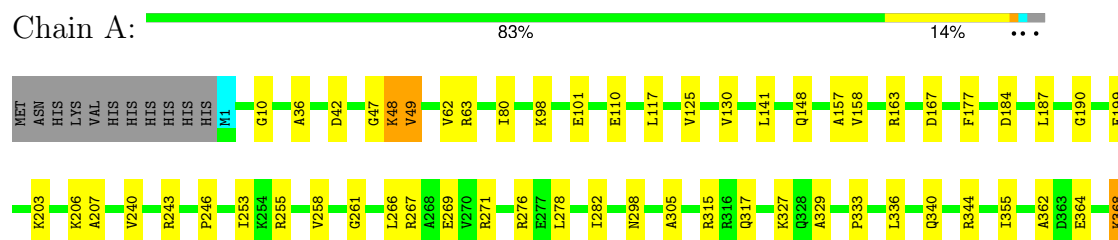


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

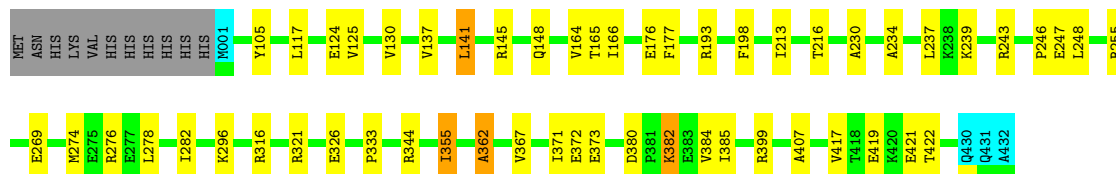
- Molecule 1: Trigger factor





- Molecule 1: Trigger factor

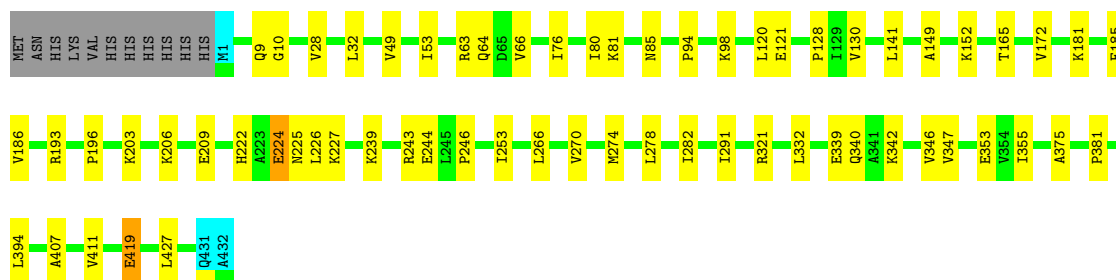
Chain B: 84% 11% ...



4.2.2 Score per residue for model 2

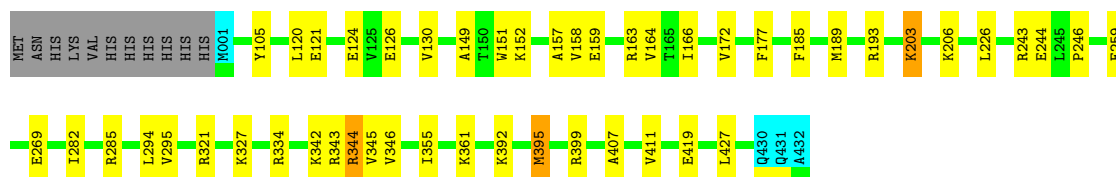
- Molecule 1: Trigger factor

Chain A: 82% 14% ..



- Molecule 1: Trigger factor

Chain B: 86% 10% ...



4.2.3 Score per residue for model 3

- Molecule 1: Trigger factor

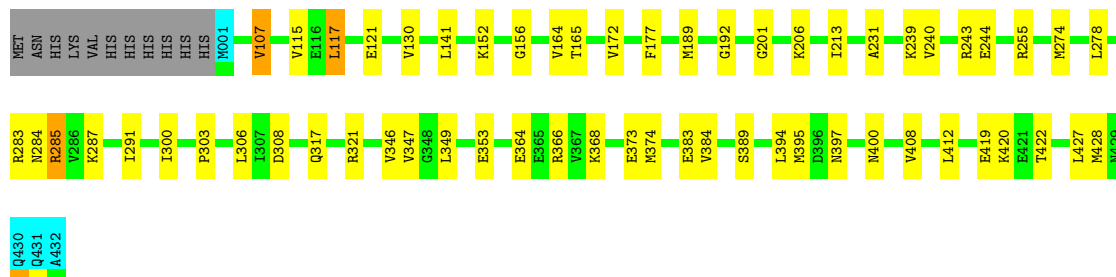
Chain A: 85% 11% ..





• Molecule 1: Trigger factor

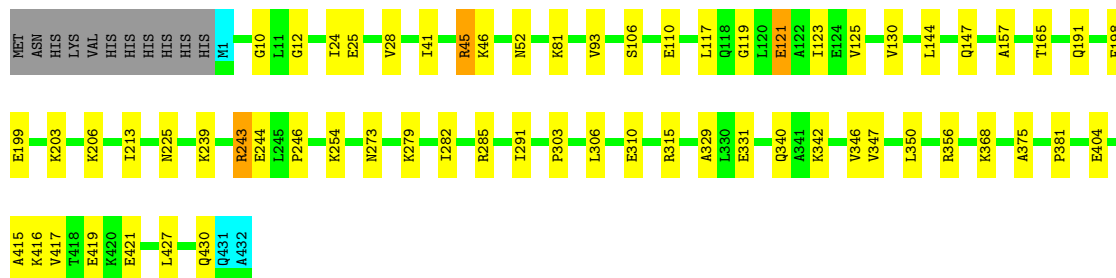
Chain B: 83% 13% ..



4.2.4 Score per residue for model 4

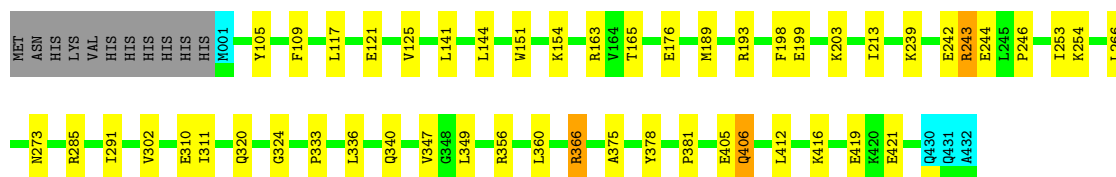
• Molecule 1: Trigger factor

Chain A: 83% 14% ..



• Molecule 1: Trigger factor

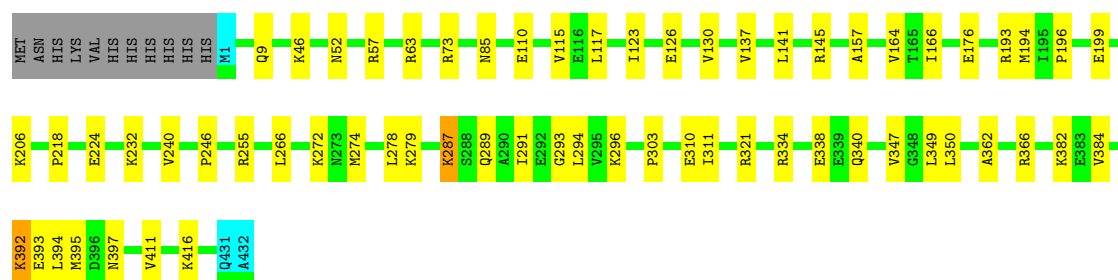
Chain B: 85% 11% ..



4.2.5 Score per residue for model 5 (medoid)

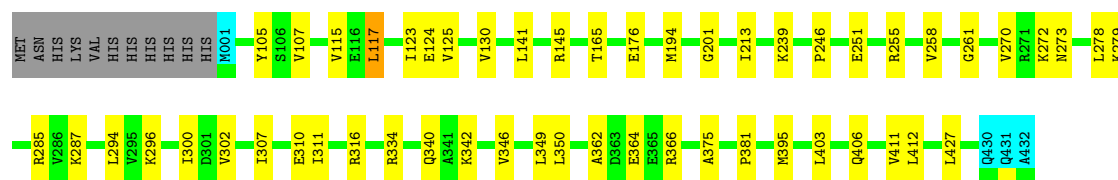
• Molecule 1: Trigger factor

Chain A: 83% 14% ..



- Molecule 1: Trigger factor

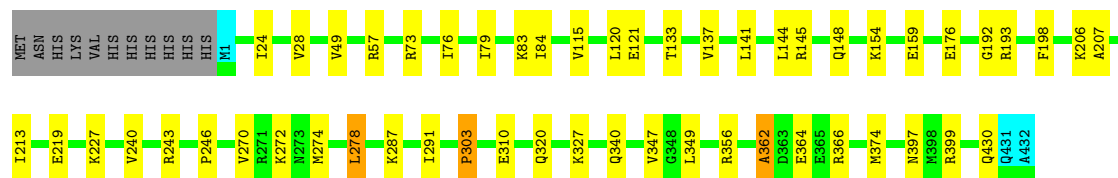
Chain B: 85% 12% ..



4.2.6 Score per residue for model 6

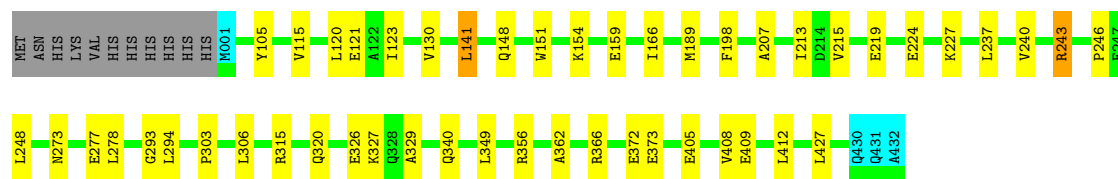
- Molecule 1: Trigger factor

Chain A: 85% 11% ...



- Molecule 1: Trigger factor

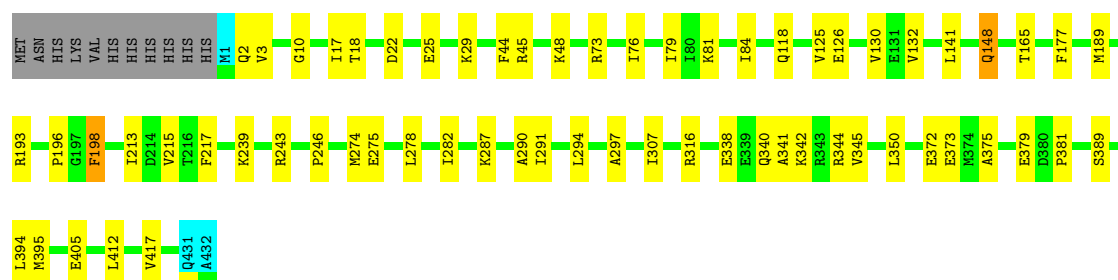
Chain B: 86% 11% ..



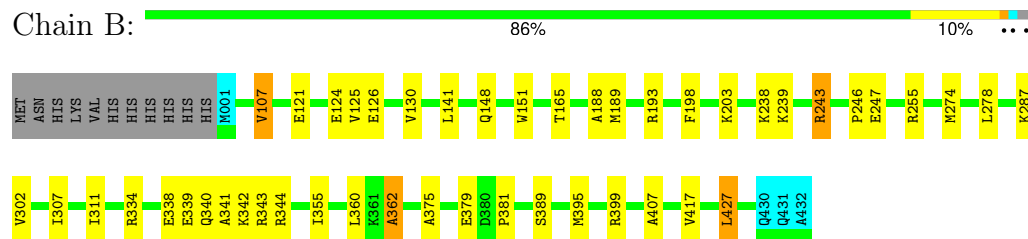
4.2.7 Score per residue for model 7

- Molecule 1: Trigger factor

Chain A: 82% 14% ..

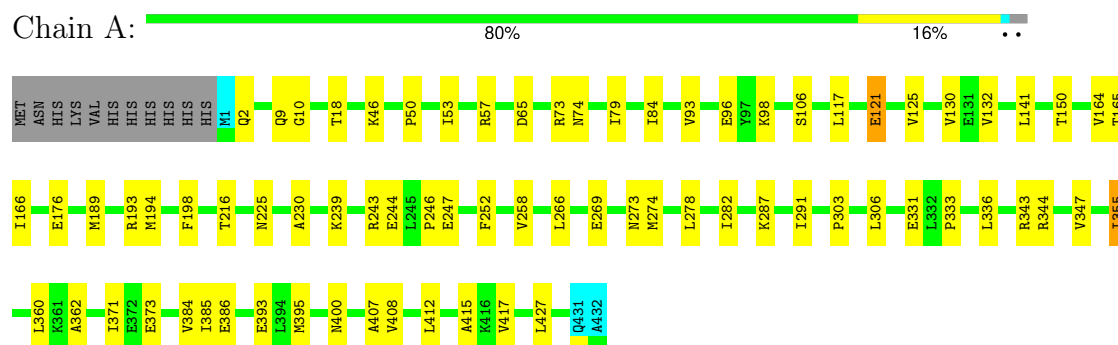


- Molecule 1: Trigger factor

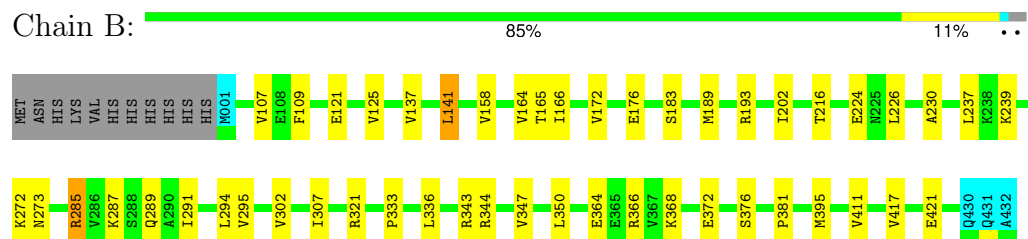


4.2.8 Score per residue for model 8

- Molecule 1: Trigger factor

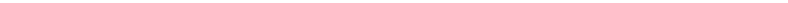


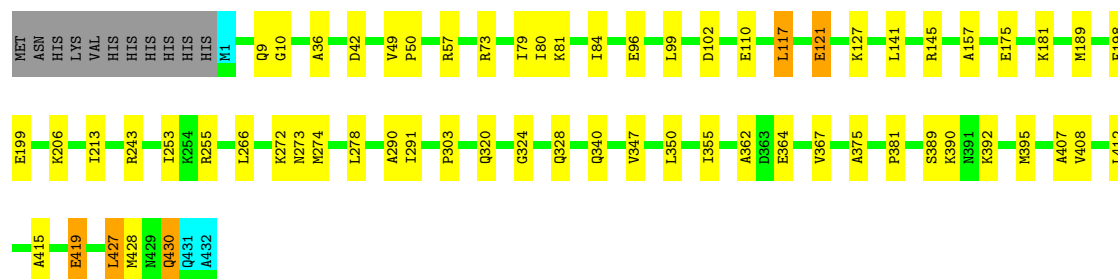
- Molecule 1: Trigger factor




4.2.9 Score per residue for model 9

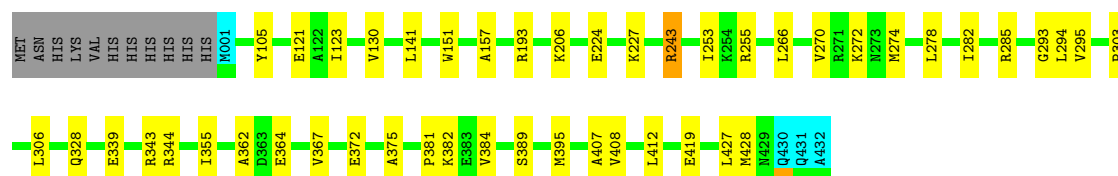
- Molecule 1: Trigger factor

Chain A:  82% 13% ...




- Molecule 1: Trigger factor

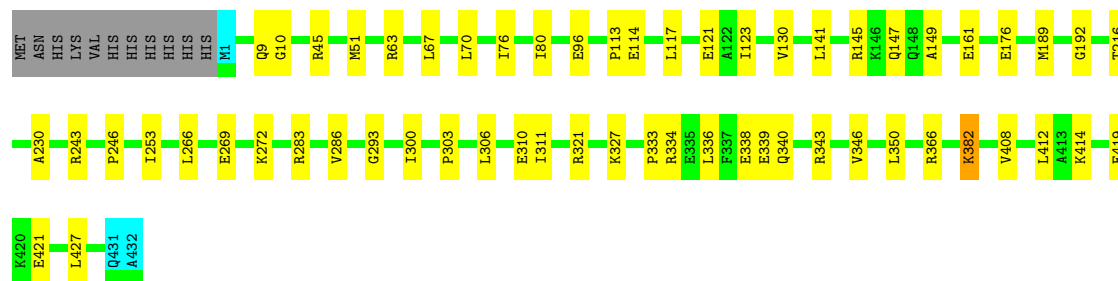
Chain B:  86% 10% ..



4.2.10 Score per residue for model 10

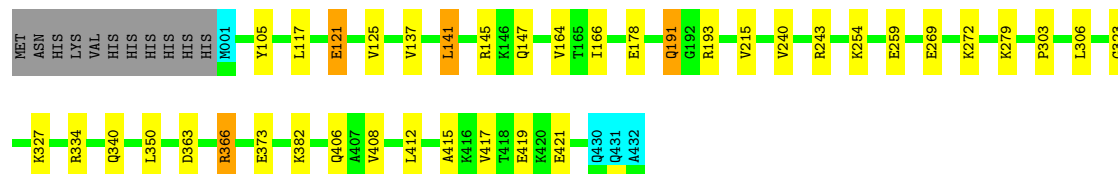
- Molecule 1: Trigger factor

Chain A:  84% 13% 3%



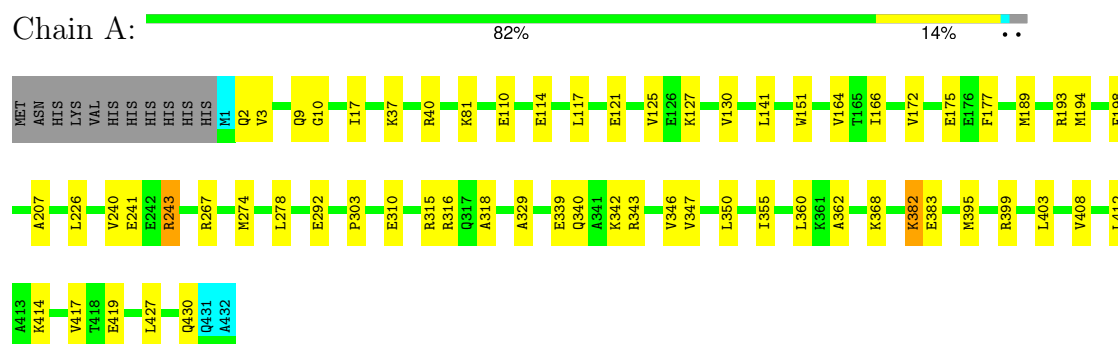
- Molecule 1: Trigger factor

Chain B: 88% 8% ..

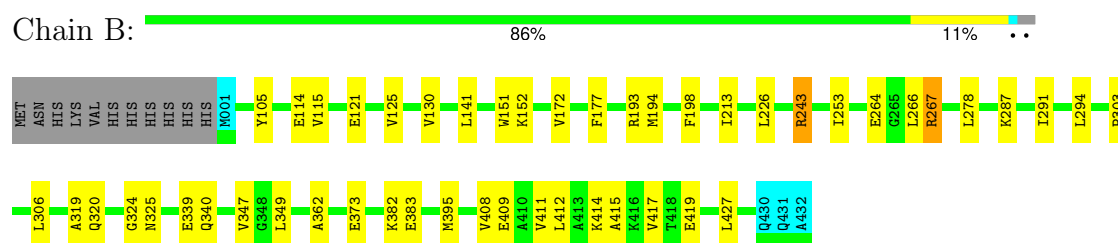


4.2.11 Score per residue for model 11

- Molecule 1: Trigger factor

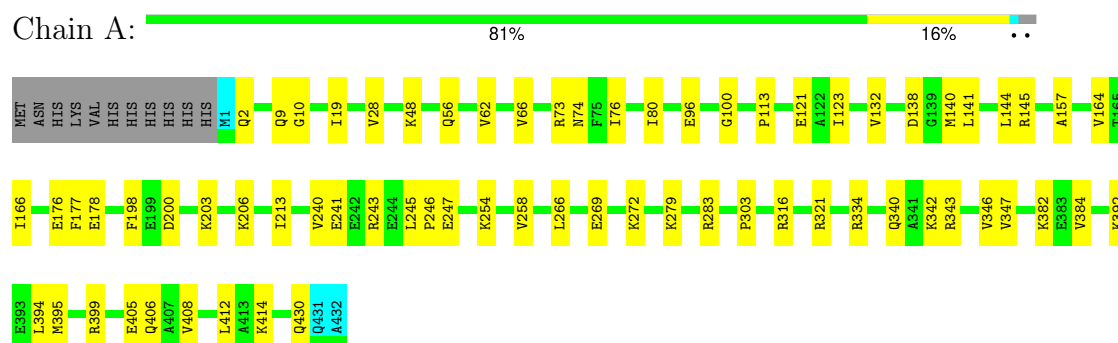


- Molecule 1: Trigger factor

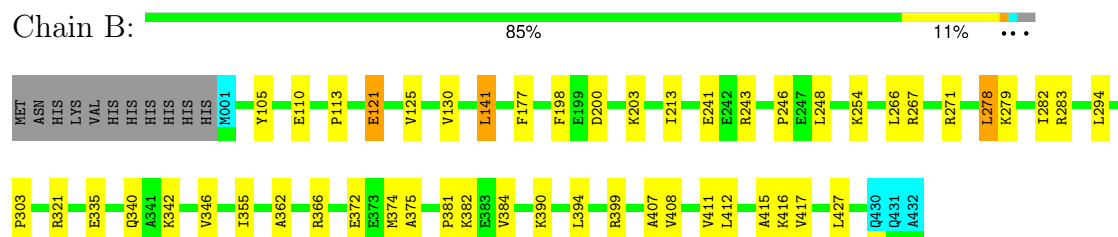


4.2.12 Score per residue for model 12

- Molecule 1: Trigger factor

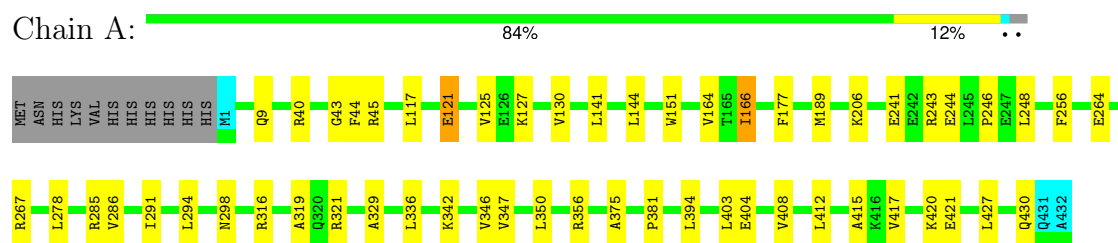


- Molecule 1: Trigger factor

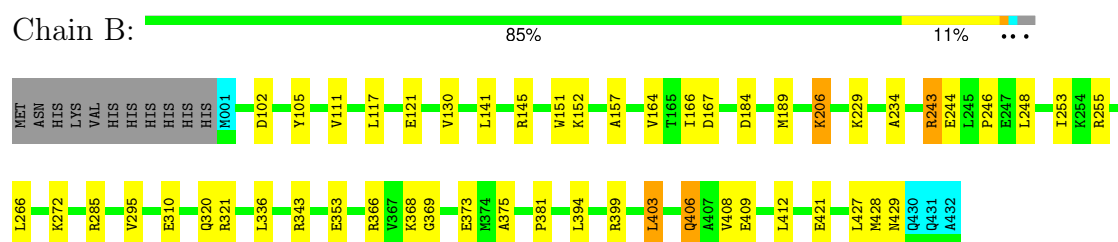


4.2.13 Score per residue for model 13

- Molecule 1: Trigger factor

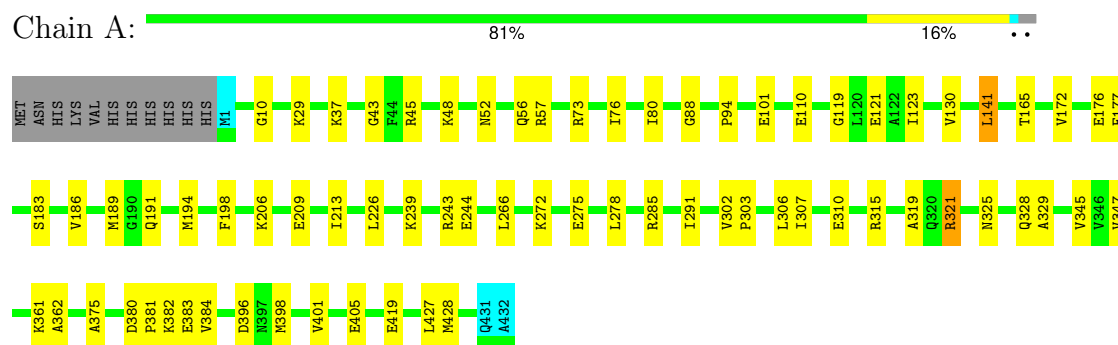


- Molecule 1: Trigger factor

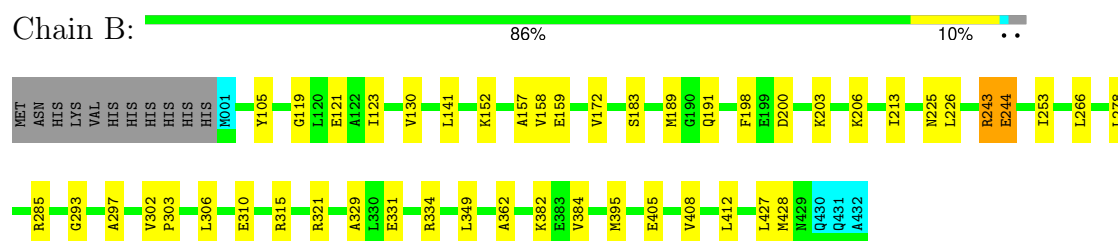


4.2.14 Score per residue for model 14

- Molecule 1: Trigger factor

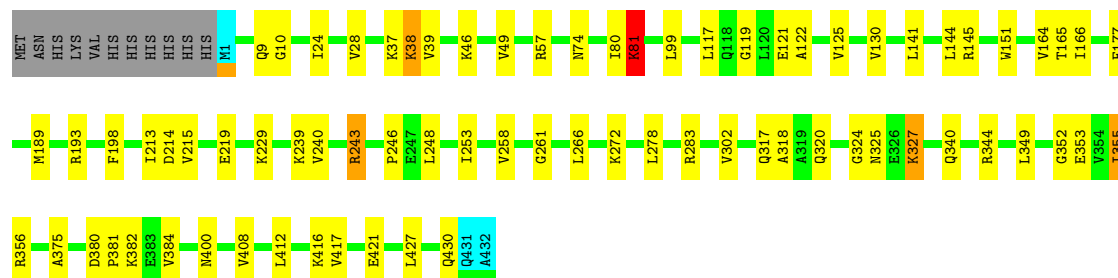



- Molecule 1: Trigger factor

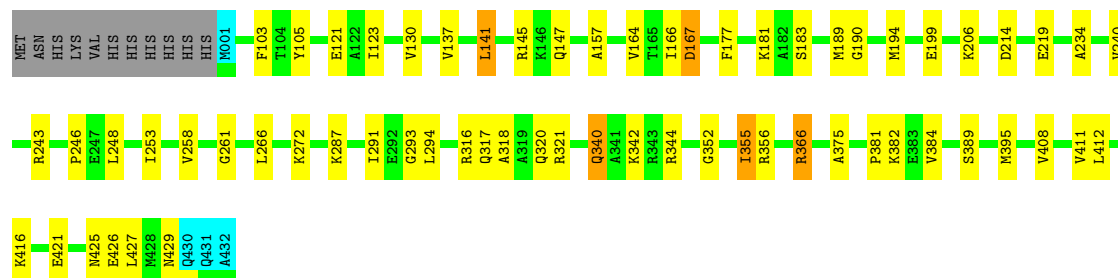


4.2.15 Score per residue for model 15

- Molecule 1: Trigger factor

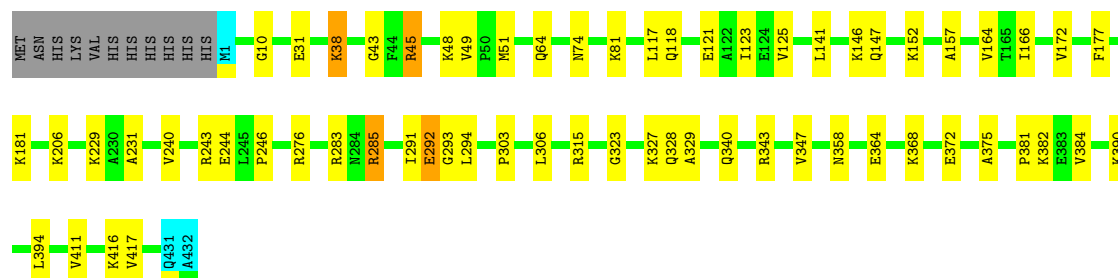

Chain A: 

- Molecule 1: Trigger factor


Chain B: 

4.2.16 Score per residue for model 16

- Molecule 1: Trigger factor

Chain A: 

- Molecule 1: Trigger factor

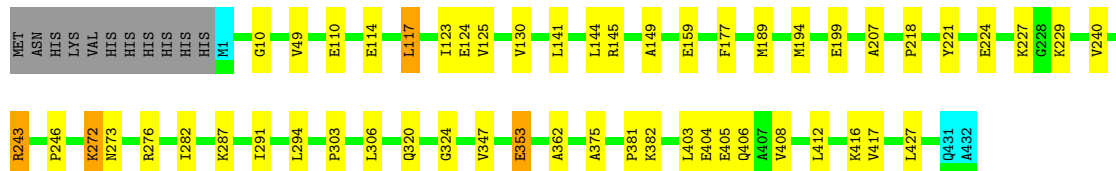
Chain B: 



4.2.17 Score per residue for model 17

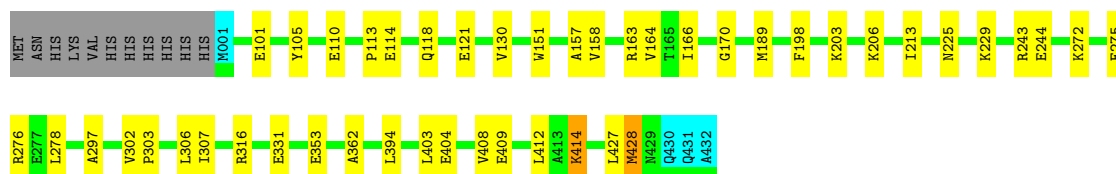
- Molecule 1: Trigger factor

Chain A: 85% 11% ..



- Molecule 1: Trigger factor

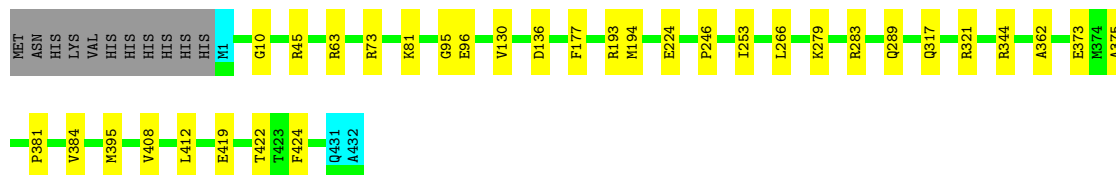
Chain B: 86% 10% ..



4.2.18 Score per residue for model 18

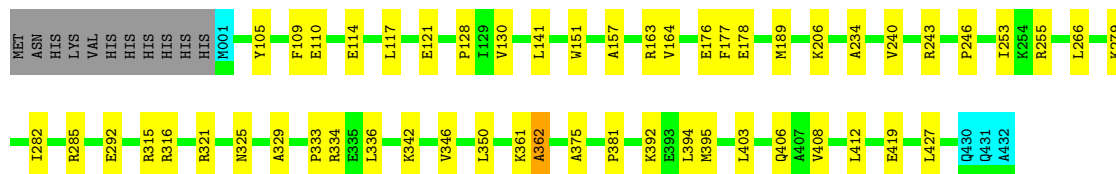
- Molecule 1: Trigger factor

Chain A: 89% 7% ..




- Molecule 1: Trigger factor

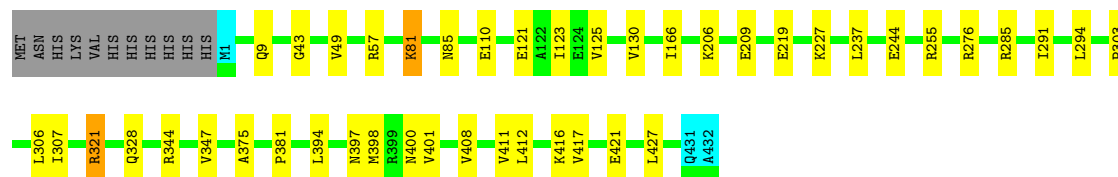
Chain B: 85% 12% ..




4.2.19 Score per residue for model 19

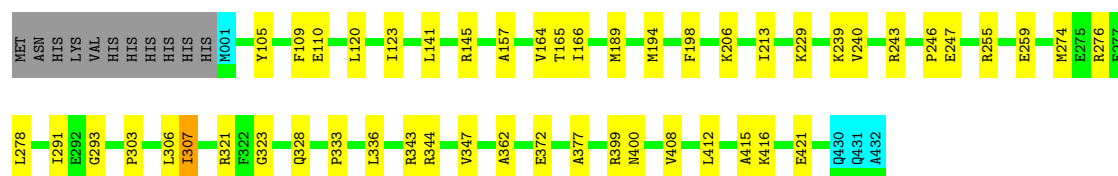
- Molecule 1: Trigger factor

Chain A:  87% 9% ..




- Molecule 1: Trigger factor

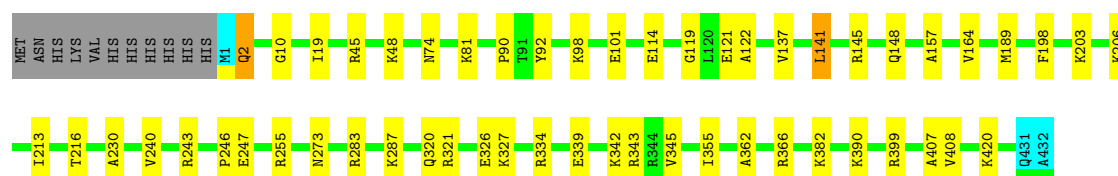
Chain B:  85% 11% ..




4.2.20 Score per residue for model 20

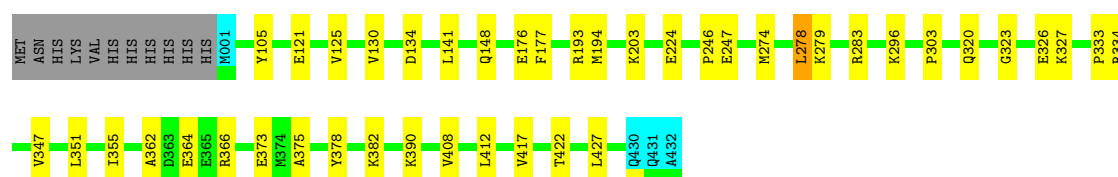
- Molecule 1: Trigger factor

Chain A:  85% 12% ..



- Molecule 1: Trigger factor

Chain B:  87% 9% ..



5 Refinement protocol and experimental data overview

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

Of the 800 calculated structures, 20 were deposited, based on the following criterion: *target function*.

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

Software name	Classification	Version
CNS	refinement	
CYANA	structure calculation	

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)	working_cs.cif
Number of chemical shift lists	1
Total number of shifts	1674
Number of shifts mapped to atoms	1674
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	14%

6 Model quality [i](#)

6.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#Z>5	RMSZ	#Z>5
1	A	0.88±0.01	0±0/3404 (0.0± 0.0%)	0.63±0.01	0±0/4579 (0.0± 0.0%)
1	B	0.88±0.01	0±0/2637 (0.0± 0.0%)	0.64±0.01	0±0/3543 (0.0± 0.0%)
All	All	0.88	0/120820 (0.0%)	0.64	1/162440 (0.0%)

There are no bond-length outliers.

All unique angle outliers are listed below.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	B	321	ARG	NE-CZ-NH1	5.48	123.04	120.30	18	1

There are no chirality outliers.

There are no planarity outliers.

6.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in each chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes averaged over the ensemble.

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	3363	3381	3379	21±5
1	B	3354	3373	2581	18±4
All	All	134340	135080	119200	761

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:194:MET:SD	1:A:199:GLU:HB2	0.66	2.30	5	1
1:A:132:VAL:HG11	1:A:274:MET:SD	0.64	2.33	8	3
1:A:79:ILE:HB	1:A:84:ILE:HB	0.62	1.70	9	4
1:B:189:MET:SD	1:B:243:ARG:HG3	0.61	2.36	13	12
1:A:110:GLU:HB2	1:A:303:PRO:HB3	0.61	1.70	19	6
1:A:389:SER:HA	1:A:395:MET:SD	0.61	2.35	9	2
1:B:130:VAL:HG21	1:B:427:LEU:HD22	0.60	1.73	15	11
1:A:80:ILE:HD13	1:B:384:VAL:HG22	0.59	1.73	3	3
1:A:291:ILE:HG23	1:A:347:VAL:HG21	0.59	1.74	19	10
1:B:158:VAL:HB	1:B:203:LYS:HA	0.59	1.74	2	3
1:A:117:LEU:HB3	1:A:350:LEU:HD22	0.58	1.75	5	6
1:A:224:GLU:HA	1:A:227:LYS:HG2	0.58	1.73	17	2
1:B:320:GLN:HA	1:B:324:GLY:HA2	0.58	1.74	4	2
1:B:125:VAL:HB	1:B:417:VAL:HA	0.58	1.75	10	8
1:A:189:MET:SD	1:A:243:ARG:HG3	0.58	2.39	8	7
1:A:207:ALA:HB2	1:A:240:VAL:HG23	0.58	1.75	6	4
1:A:165:THR:HB	1:A:239:LYS:HB2	0.57	1.74	8	6
1:B:389:SER:HA	1:B:395:MET:SD	0.57	2.39	9	4
1:B:253:ILE:HG23	1:B:266:LEU:HB2	0.57	1.75	15	7
1:A:287:LYS:HE3	1:A:408:VAL:HG21	0.57	1.76	20	1
1:B:117:LEU:HB3	1:B:350:LEU:HD22	0.57	1.75	5	4
1:B:303:PRO:HB2	1:B:306:LEU:HD13	0.57	1.76	9	8
1:A:375:ALA:HB1	1:A:381:PRO:HA	0.56	1.76	17	11
1:B:409:GLU:HA	1:B:412:LEU:HB2	0.56	1.76	16	1
1:A:125:VAL:HB	1:A:417:VAL:HA	0.56	1.77	7	11
1:A:303:PRO:HB2	1:A:306:LEU:HD13	0.56	1.78	10	7
1:B:291:ILE:HG23	1:B:347:VAL:HG21	0.56	1.76	4	3
1:A:258:VAL:HG22	1:A:269:GLU:HG3	0.56	1.76	8	1
1:A:198:PHE:HA	1:A:213:ILE:HD12	0.56	1.76	14	8
1:B:302:VAL:HG12	1:B:349:LEU:HD12	0.55	1.77	14	2
1:A:130:VAL:HG21	1:A:427:LEU:HD22	0.55	1.79	17	8
1:A:164:VAL:HG23	1:A:240:VAL:HG22	0.55	1.79	12	5
1:A:36:ALA:HB1	1:A:42:ASP:HA	0.55	1.78	9	2
1:A:253:ILE:HG23	1:A:266:LEU:HB2	0.55	1.79	15	6
1:B:130:VAL:HG21	1:B:427:LEU:HD12	0.55	1.78	7	1
1:B:167:ASP:HB3	1:B:183:SER:HA	0.54	1.79	15	1
1:A:302:VAL:HG23	1:A:307:ILE:HD11	0.54	1.77	14	1
1:A:130:VAL:HG22	1:A:282:ILE:HD11	0.54	1.78	1	6
1:B:157:ALA:HA	1:B:206:LYS:HA	0.54	1.79	13	9
1:B:172:VAL:HA	1:B:231:ALA:HA	0.54	1.78	3	2
1:A:81:LYS:HD2	1:B:383:GLU:HG3	0.53	1.80	11	1
1:A:302:VAL:HB	1:A:307:ILE:HD11	0.53	1.80	3	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:50:PRO:HD2	1:A:53:ILE:HD12	0.53	1.80	8	1
1:A:121:GLU:HA	1:A:415:ALA:HA	0.53	1.81	4	4
1:B:141:LEU:HD11	1:B:248:LEU:HD22	0.53	1.81	6	2
1:B:219:GLU:HA	1:B:227:LYS:HD2	0.53	1.81	6	1
1:A:189:MET:SD	1:A:243:ARG:NE	0.52	2.82	7	2
1:B:166:ILE:HG21	1:B:237:LEU:HD23	0.52	1.81	8	1
1:B:115:VAL:HG11	1:B:349:LEU:HB3	0.52	1.81	3	4
1:A:355:ILE:HG22	1:A:360:LEU:HD23	0.52	1.81	11	1
1:B:426:GLU:HA	1:B:429:ASN:HB3	0.52	1.81	15	1
1:A:127:LYS:HB3	1:A:419:GLU:HA	0.52	1.82	9	1
1:A:98:LYS:HD2	1:A:101:GLU:HB2	0.52	1.80	20	2
1:A:157:ALA:HA	1:A:206:LYS:HA	0.52	1.80	4	7
1:B:172:VAL:HG11	1:B:226:LEU:HA	0.52	1.81	2	2
1:A:126:GLU:HB3	1:A:289:GLN:HG3	0.52	1.82	5	1
1:B:121:GLU:HA	1:B:415:ALA:HA	0.52	1.82	10	3
1:B:164:VAL:HG23	1:B:240:VAL:HG22	0.52	1.81	16	6
1:A:76:ILE:HD12	1:A:79:ILE:HD11	0.51	1.82	7	2
1:B:355:ILE:HG23	1:B:407:ALA:HB2	0.51	1.81	9	5
1:A:214:ASP:HB3	1:A:232:LYS:HG2	0.51	1.82	3	1
1:B:165:THR:HB	1:B:239:LYS:HB2	0.51	1.82	1	7
1:B:124:GLU:HG3	1:B:289:GLN:NE2	0.51	2.21	7	1
1:A:172:VAL:HA	1:A:231:ALA:HA	0.51	1.82	16	1
1:B:130:VAL:HG22	1:B:282:ILE:HD11	0.51	1.82	18	4
1:B:382:LYS:HA	1:B:385:ILE:HD12	0.51	1.82	1	1
1:B:198:PHE:HA	1:B:213:ILE:HD12	0.50	1.83	12	8
1:A:22:ASP:HA	1:A:25:GLU:HB3	0.50	1.82	7	1
1:A:80:ILE:HD13	1:B:384:VAL:HA	0.50	1.82	12	2
1:B:164:VAL:HG22	1:B:166:ILE:HG23	0.50	1.81	1	9
1:A:164:VAL:HG22	1:A:166:ILE:HG23	0.50	1.83	5	7
1:A:3:VAL:HG12	1:A:17:ILE:HG23	0.50	1.84	11	2
1:B:338:GLU:HA	1:B:341:ALA:HB3	0.50	1.82	7	1
1:B:375:ALA:HB1	1:B:381:PRO:HA	0.50	1.82	4	9
1:B:315:ARG:HB3	1:B:329:ALA:HB1	0.50	1.84	18	2
1:B:362:ALA:HB2	1:B:399:ARG:HG3	0.50	1.82	7	2
1:B:284:ASN:HB3	1:B:285:ARG:HH21	0.50	1.66	3	1
1:A:225:ASN:HB2	1:A:331:GLU:HG2	0.50	1.84	8	2
1:A:2:GLN:HB2	1:A:18:THR:HB	0.50	1.84	8	2
1:A:41:ILE:HG21	1:B:336:LEU:HD13	0.49	1.84	4	1
1:B:224:GLU:HA	1:B:227:LYS:HG2	0.49	1.83	6	2
1:A:161:GLU:HA	1:A:189:MET:SD	0.49	2.47	10	1
1:B:294:LEU:HD21	1:B:411:VAL:HG11	0.49	1.83	15	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:140:MET:SD	1:A:144:LEU:HD23	0.49	2.47	12	1
1:A:398:MET:HA	1:A:401:VAL:HG22	0.49	1.84	14	2
1:B:295:VAL:HG11	1:B:343:ARG:HG2	0.49	1.83	2	2
1:A:151:TRP:HB3	1:A:241:GLU:HB3	0.49	1.85	11	2
1:B:364:GLU:HA	1:B:367:VAL:HG12	0.49	1.85	9	1
1:B:128:PRO:HG2	1:B:285:ARG:HG2	0.49	1.83	18	1
1:A:117:LEU:H	1:A:117:LEU:HD23	0.49	1.67	3	2
1:A:352:GLY:O	1:A:355:ILE:HG12	0.49	2.08	15	1
1:A:355:ILE:HG23	1:A:407:ALA:HB2	0.49	1.85	1	5
1:B:189:MET:SD	1:B:243:ARG:NE	0.49	2.86	3	1
1:B:151:TRP:CZ3	1:B:243:ARG:HG2	0.49	2.43	4	6
1:A:37:LYS:O	1:A:40:ARG:HD2	0.49	2.07	11	1
1:A:144:LEU:HD21	1:A:256:PHE:HZ	0.49	1.67	13	1
1:B:145:ARG:HB3	1:B:248:LEU:HD13	0.48	1.85	1	1
1:B:364:GLU:HG2	1:B:368:LYS:HE3	0.48	1.84	8	1
1:A:115:VAL:HG11	1:A:349:LEU:HB3	0.48	1.85	3	3
1:A:29:LYS:HE3	1:A:52:ASN:HB2	0.48	1.83	14	1
1:A:123:ILE:HG23	1:A:293:GLY:HA3	0.48	1.83	16	3
1:A:364:GLU:O	1:A:368:LYS:HB3	0.48	2.09	16	1
1:A:218:PRO:HG2	1:A:221:TYR:HB2	0.48	1.86	17	1
1:A:315:ARG:HB3	1:A:329:ALA:HB1	0.48	1.84	16	4
1:A:125:VAL:HG22	1:A:412:LEU:HD12	0.48	1.86	7	1
1:A:320:GLN:HA	1:A:324:GLY:HA2	0.48	1.86	9	3
1:A:154:LYS:HE2	1:A:159:GLU:HG2	0.48	1.85	6	1
1:B:151:TRP:CZ3	1:B:163:ARG:HB2	0.48	2.44	2	4
1:B:159:GLU:HA	1:B:203:LYS:HZ3	0.48	1.68	2	1
1:B:408:VAL:O	1:B:412:LEU:HG	0.47	2.09	18	11
1:A:130:VAL:HG11	1:A:427:LEU:HB2	0.47	1.85	11	3
1:A:53:ILE:HD12	1:B:185:PHE:HA	0.47	1.86	2	1
1:A:172:VAL:HG21	1:A:226:LEU:HD22	0.47	1.86	11	3
1:A:338:GLU:HA	1:A:341:ALA:HB3	0.47	1.86	7	1
1:A:283:ARG:HH21	1:A:286:VAL:HG13	0.47	1.68	10	1
1:A:200:ASP:HA	1:A:203:LYS:HE2	0.47	1.86	12	1
1:A:62:VAL:HG23	1:B:321:ARG:NH2	0.47	2.24	1	2
1:A:194:MET:SD	1:A:198:PHE:CD2	0.47	3.08	8	3
1:B:352:GLY:O	1:B:355:ILE:HG12	0.47	2.09	15	1
1:B:110:GLU:HB2	1:B:303:PRO:HB3	0.47	1.86	17	2
1:B:216:THR:HA	1:B:230:ALA:HA	0.47	1.85	8	2
1:A:25:GLU:HG3	1:A:29:LYS:NZ	0.47	2.24	7	1
1:A:216:THR:HA	1:A:230:ALA:HA	0.47	1.86	10	3
1:A:172:VAL:HG11	1:A:226:LEU:HA	0.47	1.87	11	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:371:ILE:HG22	1:A:385:ILE:HG12	0.47	1.86	8	1
1:A:253:ILE:HD12	1:A:266:LEU:HG	0.47	1.85	9	1
1:A:364:GLU:HA	1:A:367:VAL:HG12	0.47	1.86	9	1
1:B:274:MET:O	1:B:278:LEU:HB2	0.47	2.09	3	6
1:A:76:ILE:O	1:A:80:ILE:HG13	0.47	2.10	12	3
1:B:291:ILE:HD12	1:B:347:VAL:HG11	0.47	1.85	3	1
1:A:302:VAL:HG21	1:A:345:VAL:HG23	0.47	1.86	14	1
1:A:123:ILE:HD13	1:A:294:LEU:HD22	0.47	1.84	17	2
1:A:311:ILE:HD11	1:A:338:GLU:HA	0.47	1.86	10	1
1:B:270:VAL:HG12	1:B:274:MET:SD	0.47	2.49	9	1
1:B:408:VAL:O	1:B:412:LEU:HB2	0.47	2.10	20	2
1:A:117:LEU:HD21	1:A:353:GLU:HB3	0.47	1.86	17	1
1:B:294:LEU:HD21	1:B:411:VAL:HG21	0.46	1.86	11	1
1:A:38:LYS:HA	1:B:340:GLN:HG3	0.46	1.86	15	1
1:A:408:VAL:O	1:A:412:LEU:HG	0.46	2.09	13	10
1:B:130:VAL:HG11	1:B:427:LEU:HB2	0.46	1.85	15	4
1:B:364:GLU:O	1:B:368:LYS:HB2	0.46	2.11	3	1
1:B:117:LEU:H	1:B:117:LEU:HD23	0.46	1.70	3	2
1:A:159:GLU:HG3	1:A:161:GLU:H	0.46	1.70	3	1
1:A:291:ILE:HD12	1:A:347:VAL:HG11	0.46	1.87	6	2
1:B:194:MET:SD	1:B:198:PHE:CD2	0.46	3.09	11	1
1:A:190:GLY:HA3	1:A:243:ARG:HH22	0.46	1.70	1	1
1:B:321:ARG:HH11	1:B:321:ARG:HB2	0.46	1.71	1	1
1:A:148:GLN:HE21	1:A:148:GLN:HA	0.46	1.71	7	1
1:A:352:GLY:O	1:A:356:ARG:HG2	0.46	2.11	15	1
1:A:194:MET:HB2	1:A:199:GLU:HB2	0.46	1.86	17	1
1:A:362:ALA:HB2	1:A:399:ARG:HG3	0.46	1.88	20	1
1:B:200:ASP:HA	1:B:203:LYS:HE2	0.46	1.88	14	2
1:B:167:ASP:HB3	1:B:184:ASP:H	0.46	1.71	13	1
1:B:366:ARG:HA	1:B:366:ARG:HE	0.46	1.71	15	1
1:B:360:LEU:HB3	1:B:406:GLN:HE22	0.45	1.71	4	1
1:A:294:LEU:HB3	1:A:350:LEU:HD13	0.45	1.86	7	1
1:B:343:ARG:O	1:B:347:VAL:HG23	0.45	2.11	8	1
1:B:123:ILE:HG23	1:B:293:GLY:HA3	0.45	1.89	9	5
1:A:28:VAL:HA	1:A:66:VAL:HG21	0.45	1.88	12	1
1:A:302:VAL:HG12	1:A:349:LEU:HD12	0.45	1.87	15	1
1:B:276:ARG:HH11	1:B:377:ALA:HB2	0.45	1.71	19	1
1:B:375:ALA:HA	1:B:378:TYR:HD2	0.45	1.70	20	2
1:B:321:ARG:HB2	1:B:321:ARG:NH1	0.45	2.26	1	1
1:A:149:ALA:HB1	1:A:246:PRO:HD2	0.45	1.88	2	3
1:A:274:MET:O	1:A:278:LEU:HB2	0.45	2.11	2	6

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:333:PRO:O	1:B:336:LEU:HG	0.45	2.12	8	4
1:B:302:VAL:HG23	1:B:307:ILE:HD11	0.45	1.87	8	4
1:A:48:LYS:HB2	1:B:194:MET:HB2	0.45	1.89	20	1
1:A:219:GLU:HA	1:A:227:LYS:HD2	0.45	1.88	19	2
1:A:372:GLU:HA	1:A:375:ALA:HB3	0.45	1.88	7	1
1:A:342:LYS:HA	1:A:345:VAL:HG22	0.45	1.89	20	1
1:A:294:LEU:HD21	1:A:411:VAL:HG11	0.45	1.87	5	3
1:B:361:LYS:HD3	1:B:362:ALA:N	0.45	2.26	18	1
1:A:392:LYS:HD2	1:A:392:LYS:H	0.45	1.72	5	1
1:A:315:ARG:HG2	1:A:329:ALA:HB1	0.45	1.88	3	2
1:B:300:ILE:HD11	1:B:346:VAL:HA	0.45	1.88	5	2
1:B:317:GLN:O	1:B:321:ARG:HD3	0.45	2.12	3	1
1:A:317:GLN:NE2	1:A:321:ARG:HH12	0.45	2.09	18	1
1:A:110:GLU:HG3	1:A:305:ALA:H	0.45	1.70	1	1
1:A:172:VAL:HG12	1:A:229:LYS:HB3	0.45	1.88	16	1
1:A:342:LYS:O	1:A:346:VAL:HG23	0.44	2.12	12	5
1:A:93:VAL:HB	1:A:106:SER:HB3	0.44	1.89	4	2
1:B:145:ARG:NH1	1:B:247:GLU:HA	0.44	2.27	19	1
1:A:76:ILE:HD11	1:B:394:LEU:HD11	0.44	1.88	3	1
1:B:201:GLY:HA3	1:B:213:ILE:HG21	0.44	1.90	5	2
1:B:125:VAL:HG11	1:B:412:LEU:HD11	0.44	1.88	5	2
1:A:119:GLY:O	1:A:123:ILE:HG13	0.44	2.13	14	2
1:B:158:VAL:HG11	1:B:202:ILE:HG22	0.44	1.88	8	1
1:B:152:LYS:HE3	1:B:244:GLU:HG3	0.44	1.87	14	1
1:B:307:ILE:HD11	1:B:345:VAL:HG21	0.44	1.89	16	1
1:B:224:GLU:H	1:B:333:PRO:HD3	0.44	1.72	20	1
1:A:333:PRO:O	1:A:336:LEU:HG	0.44	2.12	1	3
1:A:325:ASN:ND2	1:A:327:LYS:HD2	0.44	2.28	15	1
1:B:344:ARG:HH21	1:B:345:VAL:HG12	0.44	1.73	2	1
1:B:406:GLN:HA	1:B:409:GLU:HB3	0.44	1.90	13	1
1:B:189:MET:SD	1:B:243:ARG:CZ	0.44	3.06	18	1
1:A:130:VAL:HG23	1:A:278:LEU:HD11	0.44	1.90	5	1
1:A:137:VAL:HG22	1:A:274:MET:SD	0.44	2.53	5	1
1:B:311:ILE:HD11	1:B:338:GLU:HA	0.44	1.89	16	1
1:B:342:LYS:O	1:B:346:VAL:HG23	0.44	2.12	5	4
1:A:24:ILE:O	1:A:28:VAL:HG23	0.44	2.11	6	3
1:A:141:LEU:HD21	1:A:266:LEU:HD11	0.44	1.88	5	2
1:A:311:ILE:HG12	1:A:334:ARG:HG3	0.44	1.87	5	1
1:B:355:ILE:HA	1:B:360:LEU:HB2	0.44	1.89	7	1
1:A:81:LYS:HA	1:A:81:LYS:NZ	0.44	2.28	15	1
1:B:294:LEU:HD11	1:B:411:VAL:HG21	0.43	1.90	5	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:339:GLU:O	1:A:343:ARG:HG2	0.43	2.13	20	2
1:A:83:LYS:HA	1:A:83:LYS:HE2	0.43	1.88	6	1
1:B:339:GLU:O	1:B:343:ARG:HD3	0.43	2.13	7	1
1:A:56:GLN:HE22	1:A:100:GLY:HA3	0.43	1.73	12	1
1:A:319:ALA:HB2	1:A:329:ALA:HB2	0.43	1.90	13	1
1:A:28:VAL:HG22	1:A:66:VAL:HG21	0.43	1.91	2	1
1:B:258:VAL:HG12	1:B:261:GLY:H	0.43	1.73	5	2
1:B:154:LYS:HE2	1:B:159:GLU:HG2	0.43	1.90	6	1
1:A:428:MET:N	1:A:428:MET:SD	0.43	2.91	9	1
1:A:57:ARG:HD2	1:B:183:SER:O	0.43	2.12	14	1
1:B:178:GLU:HB2	1:B:323:GLY:HA2	0.43	1.89	10	1
1:A:272:LYS:HA	1:A:272:LYS:HE3	0.43	1.91	17	1
1:A:12:GLY:HA2	1:A:110:GLU:HG2	0.43	1.91	4	1
1:B:149:ALA:HB1	1:B:246:PRO:HD2	0.43	1.91	2	1
1:B:172:VAL:HG21	1:B:226:LEU:HD22	0.43	1.90	14	2
1:A:141:LEU:HD22	1:A:144:LEU:HD11	0.43	1.91	12	1
1:B:179:GLY:HA3	1:B:323:GLY:HA2	0.43	1.89	16	1
1:B:347:VAL:HG13	1:B:351:LEU:HD12	0.43	1.90	20	1
1:A:147:GLN:HA	1:A:243:ARG:NH2	0.43	2.29	4	1
1:B:141:LEU:HD23	1:B:270:VAL:HG21	0.43	1.91	5	1
1:A:145:ARG:NH1	1:A:247:GLU:HA	0.43	2.28	12	1
1:A:62:VAL:HG23	1:B:321:ARG:HH21	0.43	1.74	1	1
1:B:294:LEU:HB3	1:B:350:LEU:HD13	0.43	1.91	8	3
1:B:319:ALA:HB1	1:B:325:ASN:O	0.43	2.14	11	1
1:A:163:ARG:HA	1:A:187:LEU:O	0.43	2.14	1	1
1:B:207:ALA:HB2	1:B:240:VAL:HG23	0.43	1.89	6	1
1:A:321:ARG:CZ	1:A:321:ARG:HA	0.43	2.44	14	1
1:A:51:MET:SD	1:A:51:MET:N	0.43	2.91	16	1
1:A:285:ARG:NE	1:A:285:ARG:HA	0.43	2.29	16	1
1:B:363:ASP:HB2	1:B:366:ARG:HB2	0.42	1.91	10	1
1:A:382:LYS:HD3	1:A:382:LYS:H	0.42	1.73	11	1
1:B:113:PRO:HG2	1:B:303:PRO:HD3	0.42	1.90	12	1
1:A:380:ASP:O	1:A:384:VAL:HG23	0.42	2.14	15	2
1:A:172:VAL:HG23	1:A:177:PHE:CD1	0.42	2.49	16	1
1:A:287:LYS:O	1:A:291:ILE:HG12	0.42	2.15	5	4
1:B:311:ILE:HG12	1:B:334:ARG:HB2	0.42	1.91	7	1
1:A:427:LEU:HB3	1:A:428:MET:SD	0.42	2.54	9	1
1:B:428:MET:N	1:B:428:MET:SD	0.42	2.92	17	2
1:B:119:GLY:HA3	1:B:297:ALA:HB1	0.42	1.92	14	1
1:A:151:TRP:CZ3	1:A:243:ARG:HG2	0.42	2.49	15	1
1:A:130:VAL:HG12	1:A:422:THR:HB	0.42	1.91	18	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:206:LYS:O	1:A:209:GLU:HG2	0.42	2.14	14	3
1:B:287:LYS:O	1:B:291:ILE:HG12	0.42	2.14	7	4
1:A:137:VAL:HG13	1:A:270:VAL:HG11	0.42	1.90	6	1
1:A:67:LEU:HD23	1:A:70:LEU:HD12	0.42	1.90	10	1
1:A:40:ARG:HD3	1:B:340:GLN:HB2	0.42	1.90	11	1
1:A:343:ARG:O	1:A:347:VAL:HG23	0.42	2.15	12	2
1:B:273:ASN:O	1:B:277:GLU:HG2	0.42	2.14	6	1
1:A:243:ARG:HD2	1:A:245:LEU:HD21	0.42	1.92	12	1
1:A:127:LYS:HE3	1:A:286:VAL:HG21	0.42	1.90	13	1
1:B:225:ASN:HB2	1:B:331:GLU:HB3	0.42	1.92	17	2
1:A:292:GLU:HG3	1:A:343:ARG:HH12	0.42	1.74	16	1
1:A:48:LYS:HD3	1:A:49:VAL:H	0.42	1.75	1	1
1:B:372:GLU:HG2	1:B:385:ILE:HD13	0.42	1.92	1	1
1:A:198:PHE:H	1:A:215:VAL:HG11	0.42	1.75	7	1
1:A:362:ALA:HB3	1:A:399:ARG:HH11	0.42	1.73	6	1
1:A:290:ALA:HB2	1:A:412:LEU:HD21	0.42	1.92	9	1
1:A:300:ILE:HD11	1:A:346:VAL:HA	0.42	1.91	10	1
1:A:80:ILE:HD12	1:B:384:VAL:HA	0.42	1.92	14	1
1:A:319:ALA:HB1	1:A:325:ASN:O	0.42	2.14	14	1
1:B:118:GLN:O	1:B:297:ALA:HB1	0.42	2.15	17	1
1:B:317:GLN:O	1:B:321:ARG:HG2	0.42	2.14	15	1
1:A:290:ALA:HB2	1:A:412:LEU:HD13	0.42	1.90	7	1
1:B:376:SER:HA	1:B:381:PRO:HG3	0.42	1.92	8	1
1:B:369:GLY:O	1:B:373:GLU:HG3	0.42	2.14	13	1
1:A:137:VAL:O	1:A:141:LEU:HB2	0.42	2.14	20	1
1:A:32:LEU:HD23	1:B:321:ARG:HH21	0.42	1.75	2	1
1:A:382:LYS:HE3	1:A:382:LYS:HA	0.42	1.91	10	1
1:A:90:PRO:HG2	1:A:92:TYR:CZ	0.42	2.50	20	1
1:B:320:GLN:HE21	1:B:321:ARG:NH1	0.42	2.13	13	1
1:A:76:ILE:O	1:A:80:ILE:HG12	0.42	2.15	14	1
1:A:166:ILE:HG22	1:A:237:LEU:HA	0.42	1.92	19	1
1:A:258:VAL:HG12	1:A:261:GLY:H	0.41	1.74	1	2
1:B:320:GLN:HG2	1:B:321:ARG:NH2	0.41	2.30	15	1
1:B:315:ARG:NH2	1:B:334:ARG:HB3	0.41	2.30	18	1
1:B:194:MET:SD	1:B:198:PHE:CE1	0.41	3.13	19	1
1:B:147:GLN:HE21	1:B:190:GLY:HA3	0.41	1.75	15	1
1:B:137:VAL:O	1:B:141:LEU:HB2	0.41	2.15	15	4
1:A:120:LEU:HD22	1:A:411:VAL:HG23	0.41	1.92	2	1
1:A:141:LEU:HD21	1:A:270:VAL:HG11	0.41	1.92	2	1
1:B:123:ILE:HD13	1:B:294:LEU:HD22	0.41	1.92	6	2
1:A:362:ALA:HB3	1:A:399:ARG:HG2	0.41	1.92	11	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:364:GLU:O	1:B:368:LYS:HB3	0.41	2.15	16	1
1:B:120:LEU:O	1:B:415:ALA:HA	0.41	2.16	19	1
1:B:403:LEU:HD23	1:B:406:GLN:NE2	0.41	2.30	5	1
1:A:113:PRO:HG2	1:A:303:PRO:HD3	0.41	1.91	12	1
1:A:110:GLU:HG3	1:A:305:ALA:N	0.41	2.31	1	1
1:B:115:VAL:HG13	1:B:353:GLU:HG3	0.41	1.93	3	1
1:A:355:ILE:HA	1:A:360:LEU:HB2	0.41	1.92	8	1
1:A:88:GLY:HA3	1:A:306:LEU:HD11	0.41	1.91	14	1
1:B:154:LYS:HB2	1:B:242:GLU:HB2	0.41	1.93	4	1
1:A:167:ASP:HB3	1:A:184:ASP:H	0.41	1.76	1	1
1:B:366:ARG:HE	1:B:405:GLU:HB3	0.41	1.75	4	1
1:A:150:THR:HG23	1:A:252:PHE:HB2	0.41	1.93	8	1
1:B:191:GLN:HE21	1:B:191:GLN:HA	0.41	1.75	10	1
1:B:194:MET:HB3	1:B:199:GLU:HB2	0.41	1.93	15	1
1:A:177:PHE:HE2	1:A:181:LYS:HB3	0.41	1.75	16	1
1:A:267:ARG:O	1:A:271:ARG:HG2	0.41	2.16	1	1
1:B:367:VAL:O	1:B:371:ILE:HG13	0.41	2.15	1	1
1:A:128:PRO:HD2	1:A:282:ILE:HG23	0.41	1.93	2	1
1:A:317:GLN:O	1:A:321:ARG:HD3	0.41	2.16	3	1
1:A:328:GLN:O	1:A:331:GLU:HB3	0.41	2.16	3	1
1:B:375:ALA:HA	1:B:378:TYR:CD2	0.41	2.51	4	1
1:B:403:LEU:HD23	1:B:406:GLN:HE21	0.41	1.76	5	1
1:B:405:GLU:O	1:B:409:GLU:HG2	0.41	2.15	6	1
1:A:48:LYS:HE2	1:B:188:ALA:HB3	0.41	1.92	7	1
1:A:307:ILE:HD11	1:A:345:VAL:HG21	0.41	1.93	7	1
1:A:51:MET:N	1:A:51:MET:SD	0.41	2.94	10	1
1:A:408:VAL:O	1:A:412:LEU:HB2	0.41	2.15	10	1
1:A:258:VAL:HG21	1:A:266:LEU:HA	0.41	1.91	12	1
1:B:267:ARG:O	1:B:271:ARG:HG2	0.41	2.16	12	1
1:A:119:GLY:HA2	1:A:122:ALA:HB3	0.41	1.92	20	2
1:B:352:GLY:O	1:B:356:ARG:HG2	0.41	2.16	15	1
1:A:38:LYS:HA	1:A:38:LYS:HE2	0.41	1.92	16	1
1:A:136:ASP:HB3	1:A:424:PHE:HB3	0.41	1.93	18	1
1:B:307:ILE:H	1:B:307:ILE:HD13	0.41	1.76	19	1
1:A:158:VAL:HB	1:A:203:LYS:HA	0.41	1.92	1	1
1:B:166:ILE:HG22	1:B:237:LEU:HA	0.41	1.93	6	1
1:B:264:GLU:HA	1:B:267:ARG:HE	0.41	1.76	11	1
1:A:19:ILE:HG12	1:A:74:ASN:HD22	0.41	1.76	12	1
1:B:121:GLU:HG2	1:B:414:LYS:HB3	0.41	1.91	17	1
1:A:222:HIS:O	1:A:332:LEU:HG	0.40	2.16	2	1
1:B:395:MET:O	1:B:399:ARG:HG3	0.40	2.16	2	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:311:ILE:HG12	1:B:334:ARG:HE	0.40	1.76	5	1
1:A:118:GLN:O	1:A:297:ALA:HB1	0.40	2.15	7	1
1:B:254:LYS:HD3	1:B:259:GLU:HA	0.40	1.92	10	1
1:A:364:GLU:O	1:A:368:LYS:HB2	0.40	2.16	1	1
1:B:380:ASP:O	1:B:384:VAL:HG23	0.40	2.17	1	1
1:A:64:GLN:HE21	1:A:64:GLN:HA	0.40	1.76	3	1
1:A:80:ILE:HG23	1:B:383:GLU:HB2	0.40	1.92	3	1
1:A:130:VAL:HG21	1:A:278:LEU:HD21	0.40	1.91	5	1
1:A:196:PRO:HD2	1:A:218:PRO:HD3	0.40	1.93	5	1
1:A:325:ASN:HB2	1:A:328:GLN:HG2	0.40	1.92	14	1
1:A:126:GLU:H	1:A:289:GLN:HG2	0.40	1.76	3	1
1:B:315:ARG:HG2	1:B:329:ALA:HB1	0.40	1.91	6	1
1:B:399:ARG:O	1:B:403:LEU:HB2	0.40	2.16	13	1
1:A:127:LYS:HB2	1:A:419:GLU:HA	0.40	1.93	11	1
1:A:40:ARG:HH11	1:B:336:LEU:HA	0.40	1.77	13	1
1:B:295:VAL:HG21	1:B:343:ARG:HD2	0.40	1.93	13	1
1:A:39:VAL:HG11	1:B:318:ALA:HB2	0.40	1.94	15	1
1:A:19:ILE:HG12	1:A:74:ASN:ND2	0.40	2.31	20	1
1:A:57:ARG:HD3	1:B:183:SER:O	0.40	2.17	8	1
1:B:291:ILE:O	1:B:295:VAL:HG23	0.40	2.16	8	1
1:B:278:LEU:O	1:B:282:ILE:HG12	0.40	2.16	12	1
1:A:124:GLU:HG2	1:A:416:LYS:HD2	0.40	1.93	17	1

6.3 Torsion angles ⓘ

6.3.1 Protein backbone ⓘ

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	429/443 (97%)	384±6 (89±1%)	40±6 (9±1%)	5±2 (1±0%)	17	64
1	B	330/443 (74%)	302±4 (92±1%)	26±4 (8±1%)	2±1 (1±0%)	26	73
All	All	15180/17720 (86%)	13711 (90%)	1321 (9%)	148 (1%)	20	68

All 55 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	10	GLY	15
1	B	246	PRO	13
1	A	246	PRO	12
1	B	362	ALA	12
1	A	49	VAL	9
1	A	362	ALA	9
1	A	430	GLN	7
1	B	234	ALA	4
1	A	81	LYS	4
1	A	45	ARG	4
1	A	43	GLY	4
1	A	48	LYS	3
1	A	94	PRO	2
1	A	196	PRO	2
1	A	46	LYS	2
1	A	192	GLY	2
1	A	44	PHE	2
1	A	2	GLN	2
1	A	248	LEU	2
1	B	248	LEU	2
1	B	323	GLY	2
1	A	47	GLY	1
1	B	237	LEU	1
1	B	333	PRO	1
1	A	419	GLU	1
1	A	156	GLY	1
1	A	193	ARG	1
1	A	386	GLU	1
1	B	156	GLY	1
1	B	192	GLY	1
1	B	123	ILE	1
1	A	303	PRO	1
1	A	198	PHE	1
1	B	198	PHE	1
1	B	379	GLU	1
1	A	247	GLU	1
1	B	285	ARG	1
1	A	50	PRO	1
1	A	99	LEU	1
1	A	102	ASP	1
1	B	193	ARG	1
1	A	96	GLU	1
1	A	113	PRO	1

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Mol	Chain	Res	Type	Models (Total)
1	A	123	ILE	1
1	A	132	VAL	1
1	A	178	GLU	1
1	A	166	ILE	1
1	B	102	ASP	1
1	A	323	GLY	1
1	A	117	LEU	1
1	B	113	PRO	1
1	B	170	GLY	1
1	A	95	GLY	1
1	B	178	GLU	1
1	B	303	PRO	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	357/370 (96%)	335±4 (94±1%)	22±4 (6±1%)	22	71
1	B	275/370 (74%)	256±3 (93±1%)	19±3 (7±1%)	19	68
All	All	12640/14800 (85%)	11826 (94%)	814 (6%)	21	70

All 247 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	B	141	LEU	16
1	B	105	TYR	15
1	A	121	GLU	15
1	A	141	LEU	14
1	B	121	GLU	14
1	B	243	ARG	11
1	A	177	PHE	10
1	A	340	GLN	10
1	A	9	GLN	10
1	B	366	ARG	10
1	B	177	PHE	9
1	B	382	LYS	9

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Mol	Chain	Res	Type	Models (Total)
1	A	81	LYS	9
1	A	382	LYS	9
1	B	193	ARG	8
1	B	255	ARG	8
1	B	419	GLU	8
1	A	193	ARG	8
1	A	243	ARG	8
1	A	244	GLU	8
1	B	285	ARG	8
1	A	73	ARG	8
1	A	272	LYS	8
1	A	344	ARG	7
1	B	344	ARG	7
1	B	421	GLU	7
1	A	394	LEU	7
1	B	244	GLU	7
1	B	395	MET	7
1	B	340	GLN	7
1	A	145	ARG	7
1	B	272	LYS	7
1	B	278	LEU	7
1	A	255	ARG	6
1	A	327	LYS	6
1	B	176	GLU	6
1	B	316	ARG	6
1	B	373	GLU	6
1	A	419	GLU	6
1	A	283	ARG	6
1	A	45	ARG	6
1	A	310	GLU	6
1	A	176	GLU	6
1	A	63	ARG	5
1	A	278	LEU	5
1	B	117	LEU	5
1	B	152	LYS	5
1	A	279	LYS	5
1	A	316	ARG	5
1	A	366	ARG	5
1	A	273	ASN	5
1	A	285	ARG	5
1	A	416	LYS	5
1	A	421	GLU	5

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Mol	Chain	Res	Type	Models (Total)
1	B	310	GLU	5
1	B	406	GLN	5
1	B	416	LYS	5
1	A	57	ARG	5
1	A	395	MET	5
1	B	279	LYS	5
1	B	372	GLU	5
1	A	321	ARG	5
1	B	394	LEU	5
1	A	117	LEU	4
1	A	148	GLN	4
1	A	276	ARG	4
1	A	397	ASN	4
1	B	124	GLU	4
1	B	148	GLN	4
1	B	203	LYS	4
1	B	327	LYS	4
1	B	334	ARG	4
1	A	373	GLU	4
1	B	283	ARG	4
1	B	428	MET	4
1	A	144	LEU	4
1	B	145	ARG	4
1	A	405	GLU	4
1	A	96	GLU	4
1	B	321	ARG	4
1	A	114	GLU	4
1	A	199	GLU	3
1	A	269	GLU	3
1	A	368	LYS	3
1	A	430	GLN	3
1	B	247	GLU	3
1	B	269	GLU	3
1	B	276	ARG	3
1	B	296	LYS	3
1	B	326	GLU	3
1	B	355	ILE	3
1	B	422	THR	3
1	A	64	GLN	3
1	A	85	ASN	3
1	A	203	LYS	3
1	A	224	GLU	3

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Mol	Chain	Res	Type	Models (Total)
1	A	353	GLU	3
1	A	37	LYS	3
1	A	206	LYS	3
1	B	107	VAL	3
1	A	356	ARG	3
1	A	404	GLU	3
1	B	273	ASN	3
1	A	392	LYS	3
1	A	400	ASN	3
1	A	328	GLN	3
1	A	390	LYS	3
1	A	334	ARG	3
1	A	414	LYS	3
1	A	403	LEU	3
1	B	114	GLU	3
1	B	229	LYS	3
1	B	403	LEU	3
1	A	298	ASN	2
1	A	98	LYS	2
1	A	152	LYS	2
1	A	181	LYS	2
1	B	120	LEU	2
1	B	126	GLU	2
1	B	259	GLU	2
1	B	392	LYS	2
1	A	342	LYS	2
1	A	374	MET	2
1	A	428	MET	2
1	B	206	LYS	2
1	B	374	MET	2
1	B	400	ASN	2
1	A	52	ASN	2
1	A	191	GLN	2
1	A	254	LYS	2
1	B	254	LYS	2
1	B	356	ARG	2
1	A	46	LYS	2
1	A	287	LYS	2
1	A	393	GLU	2
1	B	287	LYS	2
1	B	364	GLU	2
1	A	320	GLN	2

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Mol	Chain	Res	Type	Models (Total)
1	B	215	VAL	2
1	B	320	GLN	2
1	A	275	GLU	2
1	B	342	LYS	2
1	A	74	ASN	2
1	A	355	ILE	2
1	A	175	GLU	2
1	B	328	GLN	2
1	B	339	GLU	2
1	A	147	GLN	2
1	B	147	GLN	2
1	B	191	GLN	2
1	A	267	ARG	2
1	A	292	GLU	2
1	B	409	GLU	2
1	B	414	LYS	2
1	A	406	GLN	2
1	B	390	LYS	2
1	B	399	ARG	2
1	A	420	LYS	2
1	B	353	GLU	2
1	A	38	LYS	2
1	A	229	LYS	2
1	B	292	GLU	2
1	A	48	LYS	1
1	A	422	THR	1
1	A	225	ASN	1
1	B	189	MET	1
1	B	361	LYS	1
1	A	308	ASP	1
1	B	308	ASP	1
1	B	397	ASN	1
1	B	420	LYS	1
1	A	25	GLU	1
1	B	144	LEU	1
1	B	199	GLU	1
1	B	311	ILE	1
1	A	232	LYS	1
1	A	296	LYS	1
1	A	338	GLU	1
1	B	194	MET	1
1	B	251	GLU	1

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Mol	Chain	Res	Type	Models (Total)
1	A	120	LEU	1
1	A	133	THR	1
1	A	303	PRO	1
1	A	364	GLU	1
1	A	126	GLU	1
1	A	217	PHE	1
1	A	379	GLU	1
1	B	238	LYS	1
1	B	427	LEU	1
1	A	65	ASP	1
1	A	266	LEU	1
1	A	343	ARG	1
1	A	386	GLU	1
1	B	224	GLU	1
1	B	289	GLN	1
1	A	427	LEU	1
1	A	2	GLN	1
1	A	339	GLU	1
1	B	267	ARG	1
1	A	138	ASP	1
1	A	241	GLU	1
1	A	399	ARG	1
1	B	241	GLU	1
1	B	266	LEU	1
1	B	335	GLU	1
1	A	264	GLU	1
1	A	294	LEU	1
1	B	368	LYS	1
1	B	429	ASN	1
1	A	56	GLN	1
1	A	101	GLU	1
1	A	186	VAL	1
1	A	361	LYS	1
1	A	383	GLU	1
1	A	396	ASP	1
1	B	159	GLU	1
1	B	405	GLU	1
1	A	99	LEU	1
1	A	214	ASP	1
1	A	215	VAL	1
1	A	219	GLU	1
1	A	317	GLN	1

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Mol	Chain	Res	Type	Models (Total)
1	B	167	ASP	1
1	B	181	LYS	1
1	B	214	ASP	1
1	B	219	GLU	1
1	B	425	ASN	1
1	A	31	GLU	1
1	A	118	GLN	1
1	A	146	LYS	1
1	A	358	ASN	1
1	A	372	GLU	1
1	B	101	GLU	1
1	B	128	PRO	1
1	B	146	LYS	1
1	B	225	ASN	1
1	A	159	GLU	1
1	B	275	GLU	1
1	B	404	GLU	1
1	A	289	GLN	1
1	B	325	ASN	1
1	A	307	ILE	1
1	B	307	ILE	1
1	B	343	ARG	1
1	A	247	GLU	1
1	A	326	GLU	1
1	B	134	ASP	1

6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

6.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

6.6 Ligand geometry

There are no ligands in this entry.

6.7 Other polymers

There are no such molecules in this entry.

6.8 Polymer linkage issues

There are no chain breaks in this entry.

7 Chemical shift validation [i](#)

The completeness of assignment taking into account all chemical shift lists is 14% for the well-defined parts and 14% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *starch-3let.str*

7.1.1 Bookkeeping [i](#)

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	1674
Number of shifts mapped to atoms	1674
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	1

7.1.2 Chemical shift referencing [i](#)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	0	—	None (insufficient data)
$^{13}\text{C}_\beta$	41	0.00 ± 0.00	None needed (< 0.5 ppm)
$^{13}\text{C}'$	0	—	None (insufficient data)
^{15}N	331	-0.42 ± 0.21	None needed (< 0.5 ppm)

7.1.3 Completeness of resonance assignments [i](#)

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 14%, i.e. 1662 atoms were assigned a chemical shift out of a possible 11739. 0 out of 146 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	658/4301 (15%)	329/1754 (19%)	0/1714 (0%)	329/833 (39%)
Sidechain	880/6898 (13%)	660/4446 (15%)	220/2165 (10%)	0/287 (0%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	124/540 (23%)	62/262 (24%)	62/268 (23%)	0/10 (0%)
Overall	1662/11739 (14%)	1051/6462 (16%)	282/4147 (7%)	329/1130 (29%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 14%, i.e. 1674 atoms were assigned a chemical shift out of a possible 11832. 0 out of 146 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	662/4336 (15%)	331/1768 (19%)	0/1728 (0%)	331/840 (39%)
Sidechain	888/6956 (13%)	666/4484 (15%)	222/2182 (10%)	0/290 (0%)
Aromatic	124/540 (23%)	62/262 (24%)	62/268 (23%)	0/10 (0%)
Overall	1674/11832 (14%)	1059/6514 (16%)	284/4178 (7%)	331/1140 (29%)

7.1.4 Statistically unusual chemical shifts [i](#)

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.

List Id	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	109	PHE	CE2	137.12	124.80 – 136.72	5.3

7.1.5 Random Coil Index (RCI) plots [i](#)

The image below reports *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. If well-defined core and ill-defined regions are not identified then it is shown as gray bars.

Random coil index (RCI) for chain A:

