



Full wwPDB NMR Structure Validation Report ⓘ

Apr 26, 2016 – 08:52 PM BST

PDB ID : 2J8J
Title : SOLUTION STRUCTURE OF THE A4 DOMAIN OF BLOOD COAGULATION FACTOR XI
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Deposited on : 2006-10-25

This is a Full wwPDB NMR Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/NMRValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

Cyrange : Kirchner and Güntert (2011)
NmrClust : Kelley et al. (1996)
MolProbity : 4.02b-467
Mogul : unknown
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
ShiftChecker : rb-20027457
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20027457

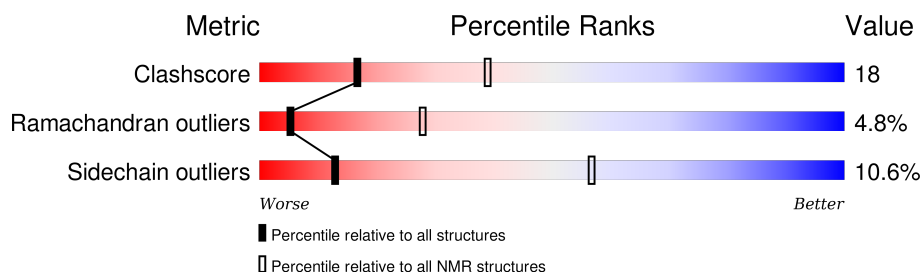
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment was not calculated.

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



Metric	Whole archive (#Entries)	NMR archive (#Entries)
Clashscore	114402	11133
Ramachandran outliers	111179	9975
Sidechain outliers	111093	9958

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

Mol	Chain	Length	Quality of chain
1	A	90	 61% 37% ..
1	B	90	 61% 39%

2 Ensemble composition and analysis ⓘ

This entry contains 14 models. Model 1 is the overall representative, medoid model (most similar to other models).

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:273-A:361, B:272-B:361 (179)	0.91	1

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 1 clusters. No single-model clusters were found.

Cluster number	Models
1	1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14

3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 2484 atoms, of which 1098 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called COAGULATION FACTOR XI.

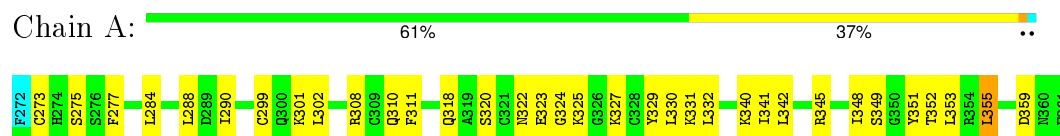
Mol	Chain	Residues	Atoms						Trace
1	A	90	Total	C	H	N	O	S	0
			1242	431	549	121	133	8	
1	B	90	Total	C	H	N	O	S	0
			1242	431	549	121	133	8	

4 Residue-property plots [i](#)

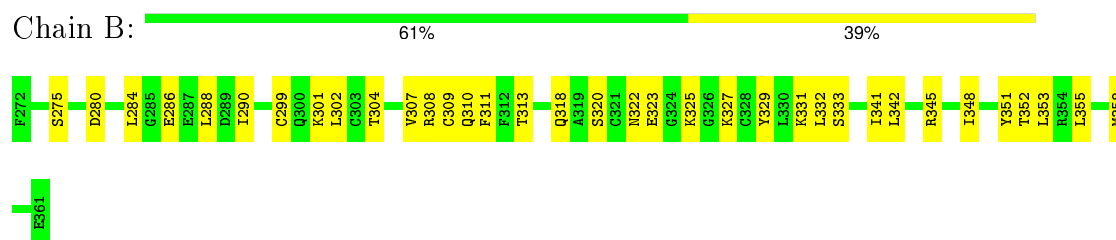
4.1 Average score per residue in the NMR ensemble

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: COAGULATION FACTOR XI



- Molecule 1: COAGULATION FACTOR XI

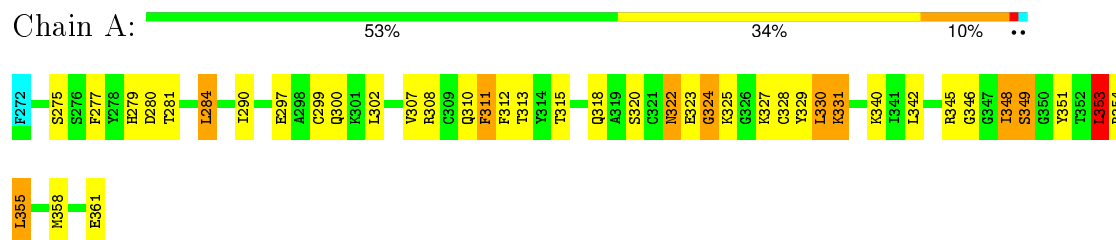


4.2 Scores per residue for each member of the ensemble

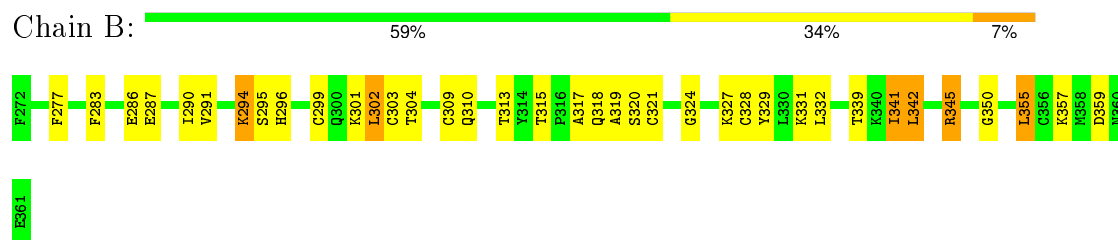
Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1 (medoid)

- Molecule 1: COAGULATION FACTOR XI

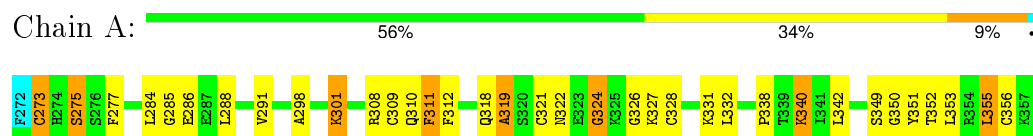


- Molecule 1: COAGULATION FACTOR XI

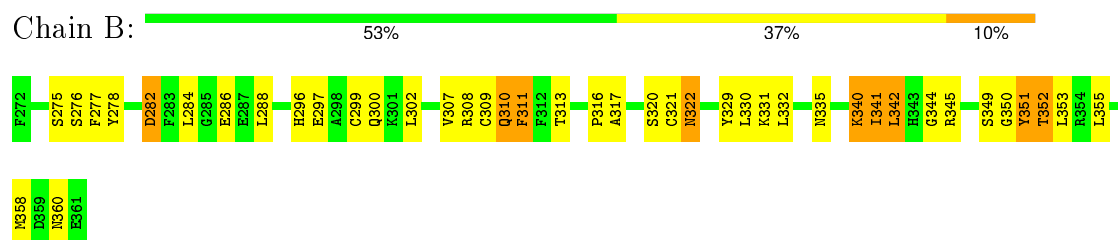


4.2.2 Score per residue for model 2

- Molecule 1: COAGULATION FACTOR XI

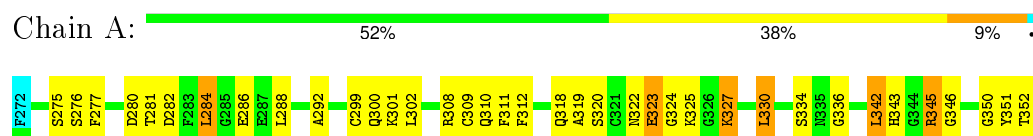


- Molecule 1: COAGULATION FACTOR XI

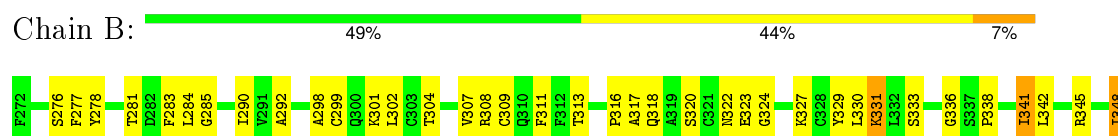


4.2.3 Score per residue for model 3

- Molecule 1: COAGULATION FACTOR XI

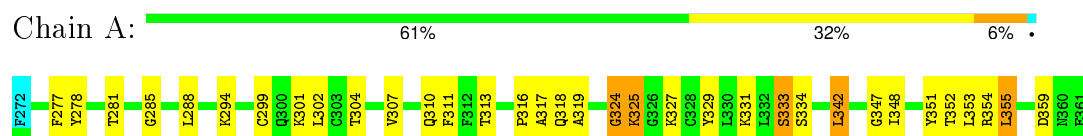


- Molecule 1: COAGULATION FACTOR XI

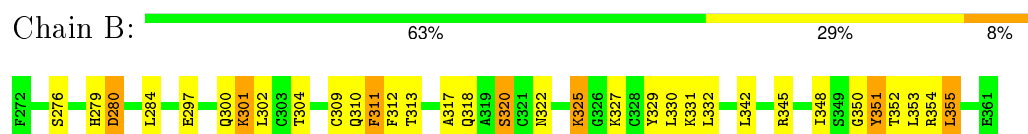


4.2.4 Score per residue for model 4

- Molecule 1: COAGULATION FACTOR XI

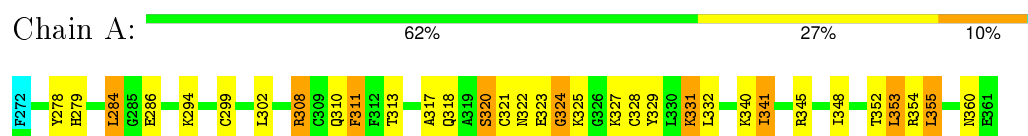


- Molecule 1: COAGULATION FACTOR XI

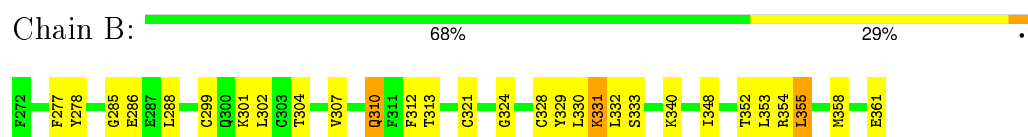


4.2.5 Score per residue for model 5

- Molecule 1: COAGULATION FACTOR XI

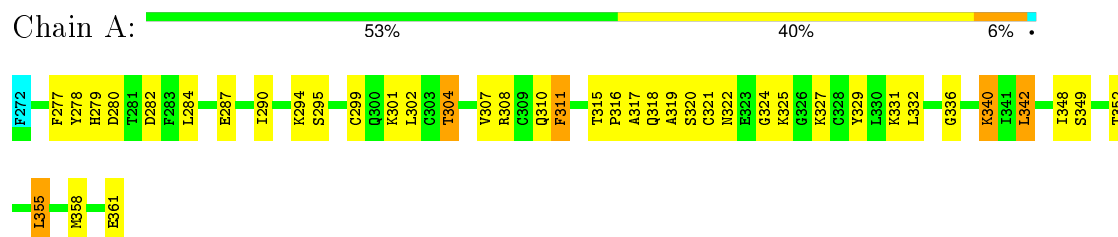


- Molecule 1: COAGULATION FACTOR XI



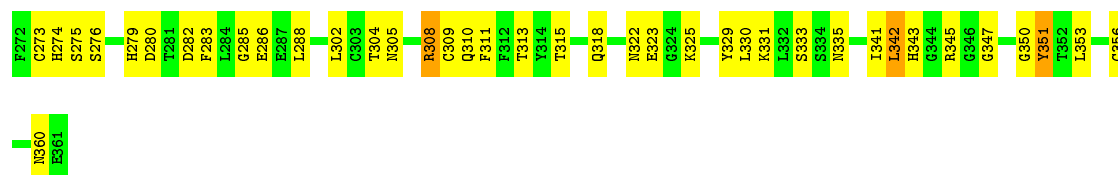
4.2.6 Score per residue for model 6

- Molecule 1: COAGULATION FACTOR XI



- Molecule 1: COAGULATION FACTOR XI

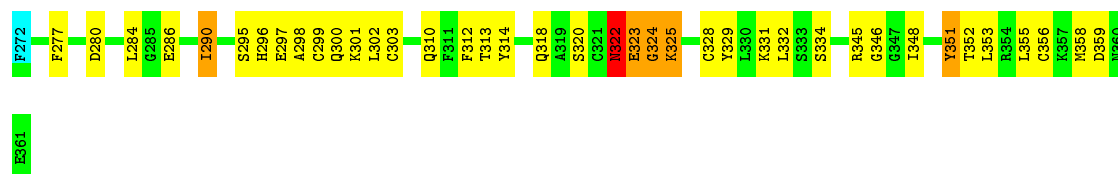




4.2.7 Score per residue for model 7

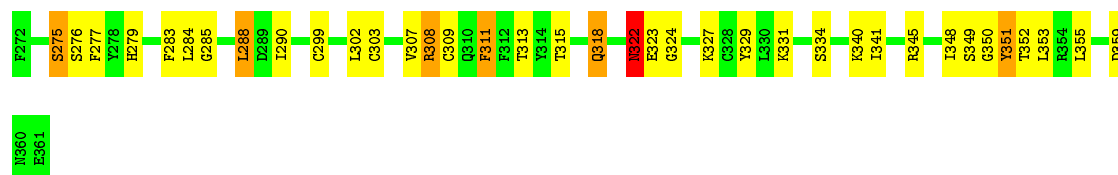
- Molecule 1: COAGULATION FACTOR XI

Chain A: 56% 37% 6% ..



- Molecule 1: COAGULATION FACTOR XI

Chain B: 59% 33% 7% .



4.2.8 Score per residue for model 8

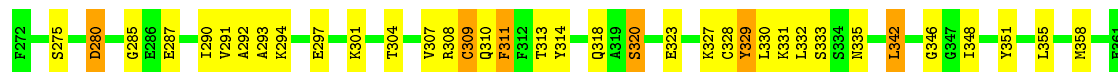
- Molecule 1: COAGULATION FACTOR XI

Chain A: 62% 31% 6% .



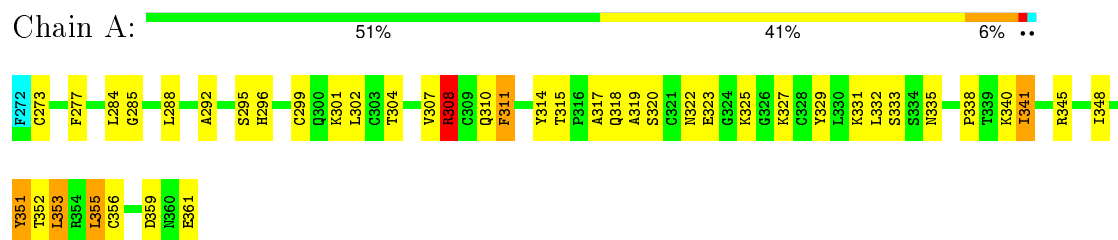
- Molecule 1: COAGULATION FACTOR XI

Chain B: 60% 33% 7%

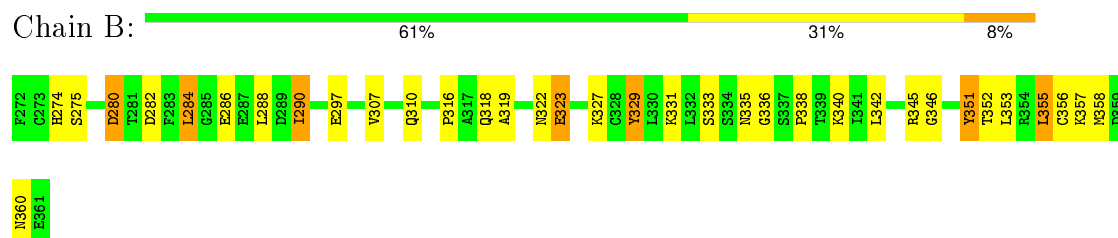


4.2.9 Score per residue for model 9

- Molecule 1: COAGULATION FACTOR XI

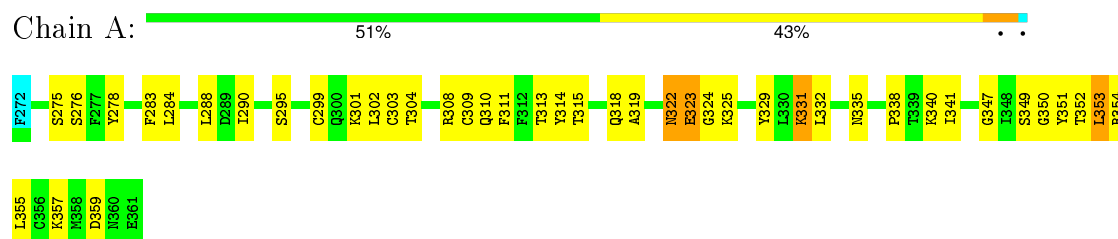


• Molecule 1: COAGULATION FACTOR XI

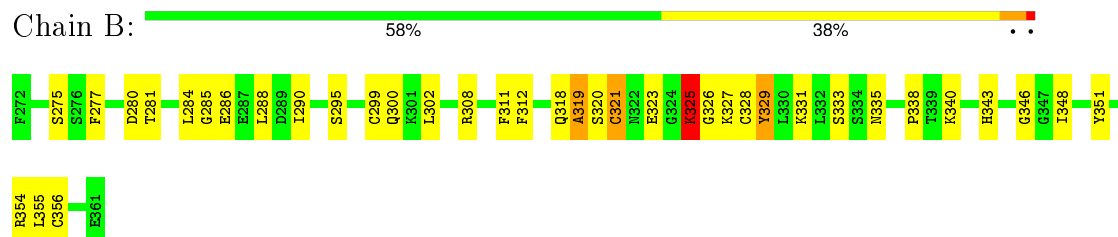


4.2.10 Score per residue for model 10

• Molecule 1: COAGULATION FACTOR XI

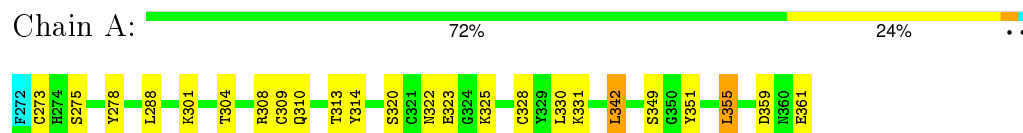


• Molecule 1: COAGULATION FACTOR XI

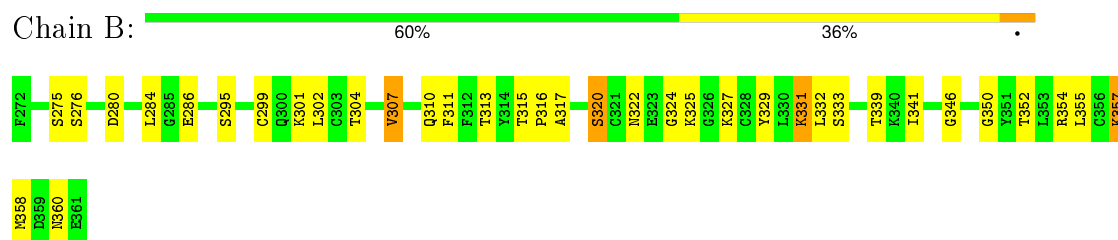


4.2.11 Score per residue for model 11

• Molecule 1: COAGULATION FACTOR XI

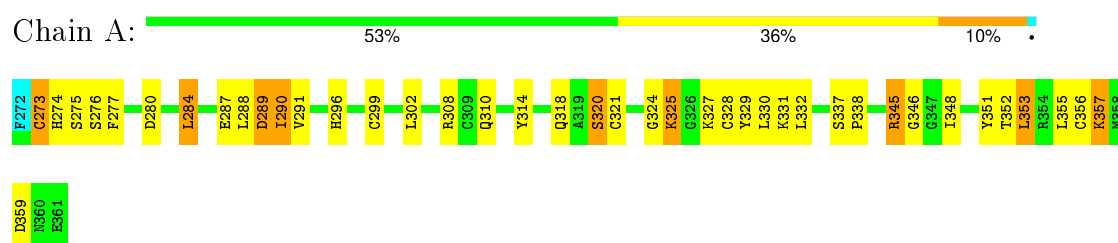


- Molecule 1: COAGULATION FACTOR XI

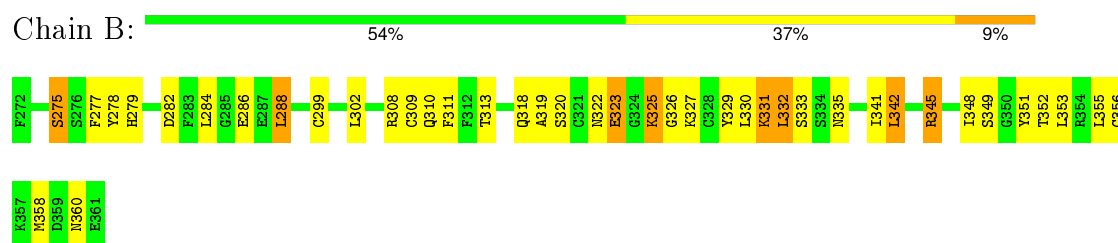


4.2.12 Score per residue for model 12

- Molecule 1: COAGULATION FACTOR XI

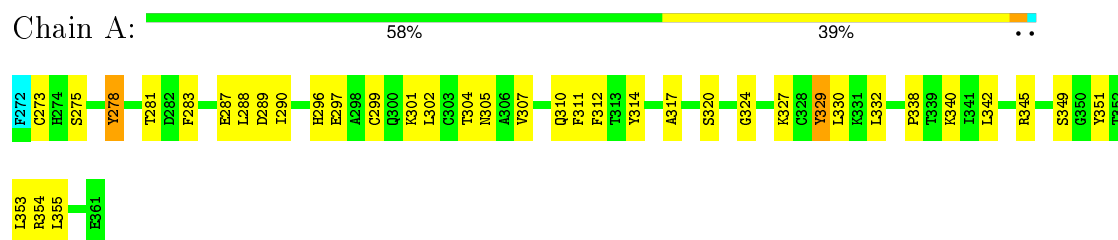


- Molecule 1: COAGULATION FACTOR XI



4.2.13 Score per residue for model 13

- Molecule 1: COAGULATION FACTOR XI



- Molecule 1: COAGULATION FACTOR XI

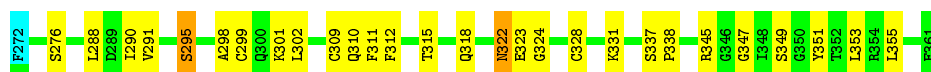




4.2.14 Score per residue for model 14

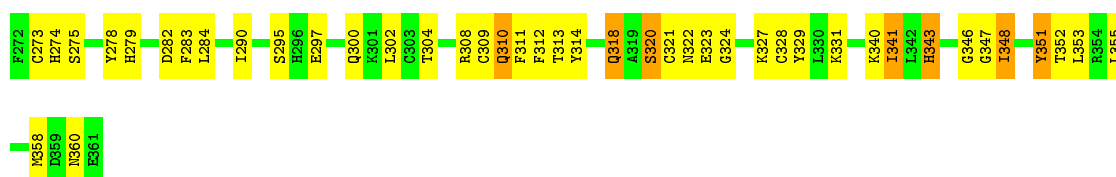
- Molecule 1: COAGULATION FACTOR XI

Chain A: 68% 29% ..



- Molecule 1: COAGULATION FACTOR XI

Chain B: 52% 40% 8%



5 Refinement protocol and experimental data overview

The models were refined using the following method: *CNS*.

Of the 100 calculated structures, 14 were deposited, based on the following criterion: *NO RESTRAINT VIOLATION AND LOWEST ENERGY*.

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

Software name	Classification	Version
CNS	refinement	
CNS	structure solution	

No chemical shift data was provided. No validations of the models with respect to experimental NMR restraints is performed at this time.

6 Model quality ⓘ

6.1 Standard geometry ⓘ

There are no covalent bond-length or bond-angle outliers.

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no planarity outliers.

6.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	682	538	650	28±7
1	B	693	549	658	25±5
All	All	19250	15218	18312	686

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 18.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:320:SER:HA	1:B:329:TYR:HB2	1.03	1.30	11	1
1:A:334:SER:HB2	1:A:359:ASP:HA	0.95	1.35	4	1
1:B:313:THR:HB	1:B:329:TYR:HB3	0.94	1.39	11	8
1:B:284:LEU:HB3	1:B:331:LYS:HD2	0.89	1.44	9	1
1:A:313:THR:HB	1:A:329:TYR:HB3	0.88	1.44	7	4
1:A:358:MET:HA	1:A:361:GLU:HB2	0.85	1.48	1	1
1:A:288:LEU:HB2	1:B:342:LEU:HD13	0.85	1.47	8	1
1:B:320:SER:HB3	1:B:327:LYS:HB2	0.83	1.51	4	2
1:A:343:HIS:HA	1:A:345:ARG:HD2	0.82	1.49	3	1
1:B:285:GLY:HA3	1:B:333:SER:HB3	0.81	1.52	5	2
1:A:311:PHE:HB2	1:A:331:LYS:HE3	0.79	1.55	1	1
1:B:352:THR:HG23	1:B:353:LEU:HD22	0.78	1.56	9	1
1:A:351:TYR:HB2	1:A:355:LEU:HD11	0.77	1.55	14	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:280:ASP:HA	1:A:346:GLY:HA2	0.77	1.54	1	4
1:A:323:GLU:HB2	1:B:323:GLU:HB3	0.77	1.52	14	1
1:A:307:VAL:HA	1:A:355:LEU:HD12	0.77	1.55	6	1
1:A:324:GLY:HA3	1:B:322:ASN:ND2	0.77	1.95	4	1
1:A:284:LEU:HB3	1:A:340:LYS:HB2	0.76	1.55	8	2
1:B:280:ASP:HA	1:B:346:GLY:HA2	0.76	1.57	8	4
1:B:277:PHE:HB3	1:B:348:ILE:HD11	0.75	1.58	5	3
1:A:355:LEU:H	1:A:355:LEU:HD13	0.75	1.42	1	2
1:B:335:ASN:HB2	1:B:360:ASN:HA	0.75	1.57	2	1
1:A:319:ALA:N	1:A:324:GLY:HA2	0.73	1.97	6	1
1:B:312:PHE:HE2	1:B:328:CYS:HB2	0.73	1.43	14	2
1:A:307:VAL:HG13	1:A:355:LEU:HB3	0.73	1.59	1	1
1:A:310:GLN:HA	1:A:355:LEU:HD21	0.72	1.59	8	1
1:A:284:LEU:HB3	1:A:340:LYS:HG2	0.72	1.60	2	1
1:B:332:LEU:HD11	1:B:358:MET:HG3	0.72	1.62	8	1
1:A:299:CYS:O	1:A:302:LEU:HG	0.71	1.85	4	9
1:A:288:LEU:HG	1:B:284:LEU:HD22	0.71	1.60	3	1
1:B:318:GLN:HB3	1:B:324:GLY:H	0.71	1.44	14	1
1:A:320:SER:HB2	1:A:327:LYS:HB2	0.71	1.63	13	2
1:A:290:ILE:HB	1:A:328:CYS:O	0.70	1.86	12	1
1:A:289:ASP:HA	1:A:330:LEU:O	0.70	1.86	12	1
1:A:324:GLY:HA2	1:B:323:GLU:HB3	0.70	1.62	3	1
1:A:318:GLN:HB3	1:A:323:GLU:HA	0.69	1.64	3	2
1:A:299:CYS:O	1:A:302:LEU:HB3	0.69	1.87	3	2
1:A:303:CYS:HB3	1:A:352:THR:HG21	0.69	1.63	10	2
1:A:352:THR:HG22	1:A:355:LEU:HG	0.69	1.62	10	1
1:B:312:PHE:CE2	1:B:328:CYS:HB2	0.69	2.22	14	2
1:A:310:GLN:HB2	1:A:332:LEU:HD12	0.68	1.63	9	2
1:A:287:GLU:HB3	1:A:332:LEU:HB3	0.68	1.66	12	3
1:B:299:CYS:O	1:B:302:LEU:HG	0.68	1.88	10	5
1:B:342:LEU:H	1:B:342:LEU:HD13	0.67	1.48	1	2
1:A:275:SER:HA	1:A:352:THR:HB	0.67	1.66	3	1
1:B:285:GLY:HA3	1:B:333:SER:OG	0.67	1.88	8	3
1:B:308:ARG:HA	1:B:308:ARG:HE	0.67	1.48	7	1
1:B:284:LEU:HA	1:B:331:LYS:HD2	0.67	1.65	4	1
1:B:355:LEU:HD13	1:B:355:LEU:H	0.67	1.50	1	2
1:A:345:ARG:HG2	1:B:290:ILE:HB	0.67	1.66	1	1
1:A:315:THR:OG1	1:A:322:ASN:HA	0.67	1.89	9	2
1:A:287:GLU:CB	1:A:332:LEU:HB3	0.67	2.20	12	1
1:A:334:SER:CB	1:A:359:ASP:HA	0.67	2.15	4	1
1:B:320:SER:OG	1:B:324:GLY:HA3	0.66	1.91	14	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:323:GLU:HB2	1:B:323:GLU:HB2	0.66	1.66	9	1
1:B:314:TYR:HA	1:B:320:SER:H	0.66	1.51	8	1
1:B:354:ARG:H	1:B:354:ARG:HD3	0.65	1.51	3	1
1:B:290:ILE:HD13	1:B:329:TYR:HB3	0.65	1.68	10	2
1:B:310:GLN:HA	1:B:355:LEU:HB2	0.65	1.69	5	1
1:B:355:LEU:O	1:B:358:MET:HG3	0.65	1.92	3	2
1:A:300:GLN:HA	1:A:351:TYR:HE1	0.65	1.51	3	1
1:A:355:LEU:HD13	1:A:355:LEU:H	0.65	1.51	3	1
1:B:300:GLN:HA	1:B:351:TYR:CE1	0.65	2.26	2	1
1:A:289:ASP:HA	1:A:330:LEU:N	0.64	2.07	12	1
1:A:314:TYR:HA	1:A:320:SER:HA	0.64	1.68	11	2
1:B:318:GLN:HB2	1:B:323:GLU:HA	0.64	1.70	13	3
1:B:312:PHE:HE1	1:B:328:CYS:HB2	0.64	1.53	10	1
1:A:352:THR:HG22	1:A:353:LEU:HG	0.64	1.70	2	1
1:B:311:PHE:HA	1:B:351:TYR:HB2	0.64	1.70	7	4
1:B:310:GLN:HB2	1:B:332:LEU:HD12	0.64	1.69	4	2
1:A:318:GLN:HB3	1:A:324:GLY:H	0.63	1.52	5	1
1:A:289:ASP:HA	1:A:330:LEU:H	0.63	1.53	12	1
1:A:286:GLU:HA	1:B:340:LYS:HE3	0.62	1.71	7	1
1:A:320:SER:HB3	1:A:327:LYS:HB2	0.62	1.69	12	2
1:A:356:CYS:HA	1:A:359:ASP:OD1	0.62	1.93	9	1
1:A:313:THR:HB	1:A:329:TYR:CB	0.62	2.23	7	1
1:A:314:TYR:HA	1:A:319:ALA:O	0.62	1.94	10	1
1:A:310:GLN:CB	1:A:332:LEU:HA	0.62	2.24	9	1
1:B:332:LEU:HD11	1:B:358:MET:SD	0.62	2.35	11	1
1:B:288:LEU:HB3	1:B:331:LYS:HB3	0.62	1.71	12	1
1:A:318:GLN:HB3	1:A:325:LYS:H	0.61	1.55	1	3
1:A:288:LEU:HB2	1:B:342:LEU:HB3	0.61	1.71	2	1
1:B:315:THR:HA	1:B:347:GLY:HA3	0.61	1.70	13	1
1:A:288:LEU:H	1:B:341:ILE:HD11	0.61	1.55	14	1
1:A:285:GLY:HA3	1:A:333:SER:CB	0.61	2.24	4	1
1:A:290:ILE:HG13	1:A:329:TYR:CA	0.61	2.25	12	1
1:A:352:THR:HG22	1:A:355:LEU:CG	0.61	2.25	10	1
1:A:304:THR:HA	1:A:353:LEU:HD11	0.61	1.70	13	1
1:A:310:GLN:HB2	1:A:332:LEU:HA	0.61	1.71	12	2
1:A:319:ALA:HB1	1:A:327:LYS:HG3	0.61	1.73	6	1
1:B:283:PHE:CD1	1:B:341:ILE:HB	0.61	2.31	1	1
1:A:310:GLN:HE22	1:A:356:CYS:HA	0.61	1.54	3	1
1:A:287:GLU:O	1:A:331:LYS:HA	0.60	1.96	6	1
1:A:310:GLN:HG2	1:A:332:LEU:CD1	0.60	2.26	10	1
1:A:310:GLN:O	1:A:351:TYR:HB2	0.60	1.95	3	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:279:HIS:HB3	1:B:348:ILE:HB	0.60	1.73	7	1
1:A:324:GLY:HA3	1:A:327:LYS:NZ	0.60	2.11	12	1
1:A:332:LEU:HD11	1:A:358:MET:SD	0.60	2.36	2	1
1:B:292:ALA:HA	1:B:327:LYS:HD3	0.60	1.73	3	1
1:B:298:ALA:O	1:B:301:LYS:HG2	0.60	1.96	3	1
1:A:318:GLN:HB2	1:A:323:GLU:HA	0.60	1.73	14	1
1:B:284:LEU:HG	1:B:288:LEU:HD21	0.59	1.72	9	1
1:A:310:GLN:HA	1:A:355:LEU:HB2	0.59	1.74	9	1
1:A:313:THR:O	1:A:320:SER:HB3	0.59	1.97	11	1
1:B:302:LEU:HD21	1:B:330:LEU:HD21	0.59	1.73	2	1
1:A:310:GLN:HA	1:A:355:LEU:HD13	0.59	1.73	2	3
1:B:282:ASP:HB2	1:B:343:HIS:CG	0.59	2.33	6	1
1:B:284:LEU:CB	1:B:331:LYS:HD2	0.59	2.26	9	1
1:A:312:PHE:HB3	1:A:351:TYR:CE2	0.59	2.33	3	1
1:B:352:THR:HG23	1:B:353:LEU:HG	0.59	1.73	7	1
1:A:340:LYS:HE2	1:B:288:LEU:HB3	0.59	1.74	6	1
1:A:353:LEU:HD12	1:A:354:ARG:H	0.58	1.58	1	1
1:A:342:LEU:HD13	1:A:342:LEU:H	0.58	1.58	11	1
1:A:340:LYS:HD3	1:B:286:GLU:O	0.58	1.98	1	1
1:A:298:ALA:O	1:A:301:LYS:HG2	0.58	1.98	7	1
1:A:320:SER:H	1:A:324:GLY:HA3	0.58	1.58	6	1
1:B:311:PHE:CE2	1:B:331:LYS:HG3	0.58	2.34	6	1
1:A:311:PHE:CD1	1:A:331:LYS:HG2	0.58	2.34	10	1
1:B:309:CYS:SG	1:B:355:LEU:HD12	0.58	2.39	3	1
1:B:311:PHE:CE2	1:B:331:LYS:HE3	0.58	2.33	14	1
1:A:323:GLU:HG2	1:B:324:GLY:HA2	0.58	1.75	11	2
1:A:301:LYS:O	1:A:304:THR:HG22	0.57	1.99	10	5
1:A:309:CYS:O	1:A:355:LEU:HD22	0.57	1.99	10	1
1:B:310:GLN:HA	1:B:355:LEU:HD13	0.57	1.74	8	2
1:A:313:THR:HB	1:A:329:TYR:HD1	0.57	1.59	4	1
1:A:280:ASP:HA	1:A:346:GLY:CA	0.57	2.29	1	2
1:B:284:LEU:HD23	1:B:341:ILE:CG1	0.57	2.29	14	1
1:B:279:HIS:HA	1:B:347:GLY:O	0.57	2.00	14	1
1:B:320:SER:CB	1:B:327:LYS:HB2	0.57	2.28	4	1
1:B:352:THR:O	1:B:355:LEU:HG	0.57	2.00	11	1
1:A:289:ASP:CA	1:A:330:LEU:O	0.57	2.53	12	1
1:B:313:THR:HB	1:B:329:TYR:CB	0.56	2.25	11	1
1:B:299:CYS:O	1:B:302:LEU:HB3	0.56	2.00	3	3
1:B:318:GLN:HG3	1:B:325:LYS:HA	0.56	1.77	4	1
1:A:322:ASN:HB3	1:B:327:LYS:NZ	0.56	2.14	9	1
1:B:282:ASP:O	1:B:341:ILE:HA	0.56	2.01	6	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:288:LEU:H	1:A:288:LEU:HD23	0.56	1.60	13	2
1:A:310:GLN:HB3	1:A:332:LEU:HA	0.56	1.77	9	1
1:A:324:GLY:HA3	1:A:327:LYS:HZ3	0.56	1.61	12	1
1:A:310:GLN:HG2	1:A:332:LEU:HD13	0.56	1.77	10	1
1:A:319:ALA:HB1	1:A:327:LYS:O	0.56	2.01	3	2
1:B:291:VAL:HB	1:B:328:CYS:SG	0.55	2.40	1	1
1:B:283:PHE:CA	1:B:341:ILE:HG22	0.55	2.32	14	1
1:A:283:PHE:HB3	1:A:341:ILE:HG22	0.55	1.78	10	1
1:A:345:ARG:CZ	1:A:345:ARG:HA	0.55	2.31	12	1
1:A:277:PHE:HB3	1:A:348:ILE:HD11	0.55	1.78	1	4
1:B:301:LYS:O	1:B:304:THR:HG22	0.55	2.02	11	4
1:A:340:LYS:CE	1:B:288:LEU:HB3	0.55	2.32	6	1
1:B:288:LEU:HB3	1:B:329:TYR:HE2	0.55	1.62	9	1
1:A:284:LEU:HD22	1:B:288:LEU:HB2	0.55	1.79	7	1
1:A:290:ILE:HD13	1:A:290:ILE:H	0.55	1.59	7	1
1:A:333:SER:HB3	1:A:337:SER:OG	0.55	2.01	8	1
1:B:352:THR:O	1:B:355:LEU:HD22	0.55	2.02	12	3
1:A:298:ALA:O	1:A:301:LYS:HG3	0.55	2.02	2	1
1:A:336:GLY:N	1:A:361:GLU:O	0.55	2.39	6	1
1:B:322:ASN:HB2	1:B:345:ARG:NH1	0.54	2.17	12	1
1:A:315:THR:HG22	1:A:347:GLY:HA3	0.54	1.79	10	1
1:A:336:GLY:HA3	1:A:361:GLU:HA	0.54	1.78	3	1
1:A:311:PHE:CD2	1:A:331:LYS:HD3	0.54	2.37	5	2
1:B:278:TYR:O	1:B:348:ILE:HA	0.54	2.03	13	4
1:A:276:SER:HB2	1:A:351:TYR:CE2	0.54	2.37	14	1
1:A:275:SER:HA	1:A:351:TYR:O	0.54	2.01	2	6
1:A:279:HIS:HA	1:A:348:ILE:HB	0.54	1.79	1	1
1:A:288:LEU:N	1:B:341:ILE:HD11	0.54	2.16	14	1
1:B:313:THR:HA	1:B:349:SER:HB3	0.54	1.80	7	1
1:B:322:ASN:HB2	1:B:345:ARG:HH11	0.54	1.62	12	1
1:B:279:HIS:HA	1:B:348:ILE:HG22	0.54	1.79	12	1
1:B:321:CYS:HA	1:B:329:TYR:CZ	0.54	2.37	10	1
1:B:284:LEU:HG	1:B:340:LYS:O	0.54	2.03	14	1
1:A:289:ASP:CA	1:A:330:LEU:H	0.54	2.16	12	1
1:A:322:ASN:HB3	1:B:327:LYS:HZ2	0.54	1.63	9	1
1:B:317:ALA:HB3	1:B:322:ASN:HD21	0.53	1.63	13	1
1:B:352:THR:HG22	1:B:353:LEU:HD22	0.53	1.80	5	2
1:A:355:LEU:O	1:A:358:MET:HG3	0.53	2.02	1	1
1:A:285:GLY:HA3	1:A:333:SER:OG	0.53	2.03	4	1
1:B:276:SER:O	1:B:350:GLY:HA2	0.53	2.03	4	6
1:B:310:GLN:OE1	1:B:356:CYS:HA	0.53	2.03	6	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:303:CYS:HB3	1:B:355:LEU:HD21	0.53	1.79	7	1
1:B:313:THR:HB	1:B:329:TYR:CE2	0.53	2.38	14	2
1:A:290:ILE:HG13	1:A:330:LEU:N	0.53	2.19	12	1
1:A:352:THR:O	1:A:355:LEU:HG	0.53	2.03	12	1
1:B:318:GLN:HG3	1:B:323:GLU:OE1	0.53	2.04	3	1
1:B:283:PHE:HA	1:B:341:ILE:HG22	0.53	1.81	14	1
1:A:312:PHE:CE1	1:A:328:CYS:HB2	0.52	2.39	2	1
1:B:330:LEU:HD23	1:B:330:LEU:H	0.52	1.64	6	1
1:A:310:GLN:NE2	1:A:359:ASP:HA	0.52	2.19	11	1
1:A:288:LEU:HG	1:B:342:LEU:HA	0.52	1.81	12	1
1:A:332:LEU:HG	1:A:333:SER:N	0.52	2.18	8	2
1:A:311:PHE:HB2	1:A:331:LYS:HB2	0.52	1.82	14	1
1:B:287:GLU:HB2	1:B:332:LEU:CD2	0.52	2.35	1	1
1:A:336:GLY:CA	1:A:361:GLU:HA	0.52	2.33	3	1
1:A:313:THR:HB	1:A:329:TYR:CD1	0.52	2.40	4	1
1:B:311:PHE:HB2	1:B:331:LYS:HE2	0.52	1.81	11	1
1:B:284:LEU:HD23	1:B:285:GLY:N	0.52	2.20	7	1
1:A:335:ASN:CB	1:A:361:GLU:HA	0.52	2.35	9	1
1:A:278:TYR:CZ	1:A:349:SER:HB2	0.52	2.39	6	1
1:B:310:GLN:HA	1:B:355:LEU:HB3	0.52	1.82	13	1
1:A:352:THR:O	1:A:353:LEU:HB2	0.52	2.05	3	1
1:B:310:GLN:O	1:B:351:TYR:HB2	0.52	2.04	2	2
1:A:343:HIS:CA	1:A:345:ARG:HD2	0.52	2.29	3	1
1:B:300:GLN:HA	1:B:351:TYR:HE1	0.52	1.62	2	1
1:B:280:ASP:HA	1:B:346:GLY:CA	0.52	2.35	9	1
1:A:302:LEU:HD13	1:A:303:CYS:N	0.52	2.19	8	1
1:A:319:ALA:HB3	1:A:324:GLY:O	0.52	2.05	2	1
1:B:351:TYR:HB3	1:B:355:LEU:HD11	0.51	1.82	3	1
1:A:309:CYS:CB	1:A:330:LEU:HD11	0.51	2.35	8	1
1:A:284:LEU:HD13	1:B:284:LEU:HD21	0.51	1.82	10	1
1:A:314:TYR:CD1	1:A:319:ALA:HA	0.51	2.40	9	1
1:A:352:THR:HG23	1:A:353:LEU:HD22	0.51	1.80	3	1
1:B:297:GLU:HB3	1:B:301:LYS:HE3	0.51	1.81	8	1
1:B:324:GLY:HA3	1:B:327:LYS:HD3	0.51	1.80	7	1
1:B:282:ASP:O	1:B:341:ILE:HG22	0.51	2.05	14	1
1:A:324:GLY:HA3	1:B:322:ASN:HD21	0.51	1.62	4	1
1:B:299:CYS:HB3	1:B:312:PHE:CZ	0.51	2.40	5	1
1:B:354:ARG:O	1:B:357:LYS:HG3	0.51	2.06	11	1
1:A:299:CYS:O	1:A:302:LEU:HD12	0.51	2.05	8	1
1:B:284:LEU:HD23	1:B:341:ILE:HG13	0.51	1.81	14	1
1:B:311:PHE:CD1	1:B:331:LYS:HG3	0.51	2.41	8	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:340:LYS:HD3	1:B:286:GLU:HA	0.51	1.83	10	1
1:B:288:LEU:HD22	1:B:331:LYS:HD2	0.51	1.83	13	1
1:B:313:THR:CB	1:B:329:TYR:HB3	0.51	2.36	12	2
1:A:342:LEU:HG	1:B:288:LEU:HB2	0.51	1.83	2	1
1:A:345:ARG:N	1:A:345:ARG:HD2	0.51	2.21	9	1
1:A:307:VAL:O	1:A:308:ARG:HB3	0.51	2.06	9	1
1:B:320:SER:HB2	1:B:323:GLU:O	0.51	2.06	3	1
1:B:335:ASN:ND2	1:B:360:ASN:HA	0.51	2.21	9	1
1:B:299:CYS:HA	1:B:302:LEU:HG	0.50	1.81	13	1
1:A:281:THR:HA	1:A:345:ARG:HG2	0.50	1.82	3	1
1:B:320:SER:O	1:B:329:TYR:HB2	0.50	2.06	2	1
1:A:315:THR:HG21	1:A:322:ASN:HA	0.50	1.83	1	1
1:A:278:TYR:O	1:A:348:ILE:HA	0.50	2.06	5	3
1:A:340:LYS:HE2	1:B:286:GLU:HB3	0.50	1.83	9	1
1:B:318:GLN:NE2	1:B:323:GLU:HB3	0.50	2.22	6	1
1:A:309:CYS:O	1:A:355:LEU:HG	0.50	2.06	11	1
1:A:352:THR:CG2	1:A:355:LEU:HB2	0.50	2.36	8	1
1:A:327:LYS:HD2	1:B:322:ASN:OD1	0.50	2.06	4	1
1:B:311:PHE:CE1	1:B:331:LYS:HB2	0.50	2.41	2	1
1:B:340:LYS:HA	1:B:340:LYS:HE3	0.50	1.82	2	1
1:B:332:LEU:HD11	1:B:358:MET:HG2	0.50	1.84	2	1
1:A:292:ALA:CB	1:A:327:LYS:HA	0.50	2.37	3	1
1:B:320:SER:HB3	1:B:327:LYS:O	0.50	2.06	8	1
1:A:345:ARG:NE	1:A:345:ARG:HA	0.50	2.22	5	3
1:B:311:PHE:HA	1:B:351:TYR:CD2	0.50	2.41	7	1
1:B:308:ARG:HD3	1:B:358:MET:HB2	0.50	1.83	2	1
1:A:288:LEU:HD23	1:A:331:LYS:HG2	0.50	1.84	9	1
1:A:277:PHE:CD1	1:A:350:GLY:HA3	0.50	2.42	3	1
1:A:281:THR:HA	1:A:342:LEU:O	0.50	2.07	1	3
1:B:308:ARG:NH1	1:B:361:GLU:O	0.50	2.45	3	1
1:B:318:GLN:HB2	1:B:322:ASN:O	0.50	2.06	7	1
1:B:309:CYS:O	1:B:355:LEU:HB2	0.49	2.07	8	1
1:A:316:PRO:HD3	1:A:347:GLY:HA3	0.49	1.84	4	1
1:A:337:SER:HB3	1:A:338:PRO:HD2	0.49	1.84	12	2
1:A:282:ASP:HB3	1:A:342:LEU:HD21	0.49	1.83	6	1
1:A:322:ASN:N	1:A:322:ASN:HD22	0.49	2.05	7	1
1:B:352:THR:HB	1:B:353:LEU:HD22	0.49	1.83	2	1
1:A:310:GLN:OE1	1:A:355:LEU:HD23	0.49	2.08	9	1
1:B:310:GLN:HB2	1:B:332:LEU:HA	0.49	1.85	1	2
1:B:307:VAL:O	1:B:308:ARG:HG2	0.49	2.08	2	1
1:B:275:SER:HB3	1:B:277:PHE:HE2	0.49	1.68	2	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:288:LEU:HD13	1:B:284:LEU:HD22	0.49	1.85	10	1
1:B:297:GLU:O	1:B:300:GLN:HG2	0.49	2.07	4	3
1:A:329:TYR:CD1	1:A:331:LYS:HD2	0.49	2.43	9	1
1:B:304:THR:OG1	1:B:353:LEU:HD11	0.49	2.07	6	1
1:B:275:SER:HA	1:B:351:TYR:O	0.49	2.07	10	4
1:A:289:ASP:O	1:A:330:LEU:HG	0.49	2.08	13	1
1:B:280:ASP:CA	1:B:346:GLY:HA2	0.48	2.37	10	1
1:B:308:ARG:NE	1:B:308:ARG:HA	0.48	2.22	7	1
1:B:355:LEU:O	1:B:358:MET:HG2	0.48	2.08	14	1
1:A:311:PHE:HB3	1:A:351:TYR:HD1	0.48	1.67	4	1
1:A:298:ALA:HA	1:A:301:LYS:HE3	0.48	1.84	14	1
1:A:285:GLY:O	1:B:340:LYS:HE2	0.48	2.07	9	1
1:A:310:GLN:HA	1:A:352:THR:CG2	0.48	2.39	6	1
1:A:282:ASP:O	1:A:342:LEU:HD13	0.48	2.07	3	1
1:A:320:SER:HB2	1:A:328:CYS:HA	0.48	1.85	11	1
1:B:286:GLU:HB3	1:B:333:SER:HB3	0.48	1.85	12	1
1:A:277:PHE:HB3	1:A:348:ILE:HG23	0.48	1.84	9	1
1:A:290:ILE:O	1:B:345:ARG:HD3	0.48	2.08	13	1
1:A:353:LEU:CD1	1:A:354:ARG:H	0.48	2.21	1	1
1:A:320:SER:HB3	1:A:324:GLY:HA3	0.48	1.84	1	1
1:B:282:ASP:HB3	1:B:342:LEU:HD23	0.48	1.85	12	1
1:A:296:HIS:HE1	1:A:325:LYS:HB2	0.48	1.67	9	1
1:A:334:SER:HB2	1:A:359:ASP:CA	0.48	2.25	4	1
1:A:352:THR:O	1:A:355:LEU:HD12	0.48	2.08	5	2
1:A:318:GLN:NE2	1:A:323:GLU:HG3	0.48	2.24	10	1
1:B:355:LEU:HD23	1:B:356:CYS:N	0.48	2.24	9	2
1:B:283:PHE:HB2	1:B:311:PHE:CE2	0.48	2.43	6	1
1:A:312:PHE:O	1:A:349:SER:HA	0.48	2.08	14	3
1:A:289:ASP:HB2	1:A:329:TYR:CD2	0.48	2.44	12	1
1:A:301:LYS:HA	1:A:304:THR:HG22	0.48	1.84	13	2
1:A:352:THR:HG23	1:A:355:LEU:HB2	0.48	1.85	8	1
1:A:351:TYR:CZ	1:A:356:CYS:HB2	0.48	2.44	7	1
1:B:277:PHE:HB3	1:B:348:ILE:HB	0.48	1.86	12	1
1:A:310:GLN:HB3	1:A:351:TYR:HE1	0.48	1.68	4	1
1:B:279:HIS:O	1:B:280:ASP:HB3	0.48	2.09	4	2
1:A:312:PHE:HA	1:A:330:LEU:HA	0.47	1.85	13	1
1:A:310:GLN:NE2	1:A:359:ASP:HB3	0.47	2.23	7	2
1:A:318:GLN:NE2	1:A:323:GLU:HB3	0.47	2.24	14	1
1:A:340:LYS:N	1:A:340:LYS:HD2	0.47	2.24	5	2
1:B:325:LYS:HD2	1:B:326:GLY:N	0.47	2.24	12	1
1:A:273:CYS:HB2	1:A:353:LEU:O	0.47	2.10	2	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:320:SER:HB2	1:A:326:GLY:HA3	0.47	1.86	8	1
1:B:284:LEU:N	1:B:284:LEU:HD13	0.47	2.24	9	1
1:B:345:ARG:HA	1:B:345:ARG:NE	0.47	2.25	9	1
1:A:284:LEU:CD1	1:A:342:LEU:HD12	0.47	2.39	3	1
1:B:351:TYR:HB3	1:B:356:CYS:SG	0.47	2.49	12	1
1:B:284:LEU:HG	1:B:331:LYS:HD3	0.47	1.86	4	1
1:A:311:PHE:HD2	1:A:331:LYS:HD3	0.47	1.69	8	2
1:A:281:THR:HA	1:A:345:ARG:CG	0.47	2.40	3	1
1:B:352:THR:O	1:B:353:LEU:HB2	0.47	2.10	5	4
1:A:288:LEU:HD21	1:B:341:ILE:O	0.47	2.10	12	1
1:A:355:LEU:HD22	1:A:356:CYS:N	0.47	2.25	9	1
1:B:299:CYS:O	1:B:302:LEU:HD12	0.47	2.10	1	1
1:B:278:TYR:HB3	1:B:281:THR:HG21	0.47	1.85	3	1
1:B:315:THR:HG22	1:B:347:GLY:HA3	0.47	1.85	6	1
1:A:278:TYR:CE2	1:A:349:SER:HB2	0.47	2.45	10	2
1:B:319:ALA:HB3	1:B:327:LYS:O	0.47	2.10	1	1
1:B:320:SER:O	1:B:321:CYS:SG	0.47	2.73	1	1
1:B:291:VAL:O	1:B:327:LYS:HB3	0.47	2.10	8	1
1:B:290:ILE:HD13	1:B:329:TYR:HB2	0.47	1.86	8	1
1:B:290:ILE:HD13	1:B:329:TYR:CB	0.47	2.40	14	2
1:A:283:PHE:HB2	1:A:311:PHE:CE2	0.46	2.45	13	1
1:B:300:GLN:OE1	1:B:301:LYS:HG3	0.46	2.10	13	1
1:A:320:SER:OG	1:A:327:LYS:HB3	0.46	2.10	3	1
1:A:340:LYS:NZ	1:B:286:GLU:HA	0.46	2.24	2	1
1:A:338:PRO:HG2	1:B:338:PRO:HG2	0.46	1.86	9	1
1:B:318:GLN:HG3	1:B:325:LYS:HB2	0.46	1.86	13	1
1:A:273:CYS:SG	1:A:354:ARG:HA	0.46	2.50	13	1
1:A:287:GLU:CG	1:A:332:LEU:HB3	0.46	2.40	8	1
1:A:279:HIS:CE1	1:A:348:ILE:HD12	0.46	2.46	5	1
1:B:288:LEU:HD13	1:B:331:LYS:HE2	0.46	1.85	5	1
1:A:318:GLN:C	1:A:324:GLY:HA2	0.46	2.31	6	1
1:B:342:LEU:HD22	1:B:342:LEU:O	0.46	2.11	6	1
1:B:279:HIS:CB	1:B:348:ILE:HB	0.46	2.40	7	1
1:B:285:GLY:HA3	1:B:333:SER:CB	0.46	2.41	10	2
1:B:318:GLN:HB3	1:B:325:LYS:N	0.46	2.26	13	1
1:B:357:LYS:HB3	1:B:357:LYS:NZ	0.46	2.25	1	1
1:A:275:SER:HB3	1:A:277:PHE:HE2	0.46	1.69	3	1
1:A:360:ASN:O	1:A:361:GLU:HG2	0.46	2.10	2	1
1:A:277:PHE:HA	1:A:349:SER:O	0.46	2.11	6	1
1:A:276:SER:O	1:A:350:GLY:HA2	0.46	2.11	10	2
1:B:288:LEU:HD13	1:B:331:LYS:HE3	0.46	1.87	10	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:304:THR:HG23	1:B:353:LEU:HG	0.46	1.86	14	1
1:A:315:THR:HG1	1:A:322:ASN:HA	0.46	1.70	9	1
1:A:315:THR:HA	1:A:347:GLY:HA3	0.46	1.88	8	1
1:B:343:HIS:CE1	1:B:346:GLY:HA3	0.46	2.45	14	1
1:A:320:SER:HB2	1:A:323:GLU:O	0.46	2.10	9	1
1:A:284:LEU:H	1:A:284:LEU:HD13	0.46	1.69	5	2
1:A:310:GLN:OE1	1:A:358:MET:HB3	0.46	2.10	7	1
1:B:311:PHE:CZ	1:B:331:LYS:HD2	0.45	2.46	10	1
1:A:291:VAL:O	1:A:327:LYS:HB3	0.45	2.11	8	1
1:A:330:LEU:O	1:A:331:LYS:HG3	0.45	2.11	12	1
1:A:299:CYS:HA	1:A:302:LEU:HD23	0.45	1.88	5	1
1:A:323:GLU:OE1	1:B:324:GLY:HA2	0.45	2.11	5	1
1:B:277:PHE:CD2	1:B:350:GLY:HA3	0.45	2.45	1	3
1:A:284:LEU:HD23	1:A:285:GLY:N	0.45	2.26	2	1
1:A:335:ASN:HB3	1:A:361:GLU:HA	0.45	1.88	9	1
1:A:318:GLN:HE22	1:A:323:GLU:HG3	0.45	1.71	10	1
1:A:345:ARG:H	1:A:345:ARG:HD3	0.45	1.72	3	1
1:A:286:GLU:OE1	1:A:334:SER:HB3	0.45	2.11	3	1
1:B:308:ARG:HE	1:B:308:ARG:HA	0.45	1.72	13	1
1:A:342:LEU:CD1	1:A:342:LEU:H	0.45	2.23	11	1
1:A:345:ARG:HB2	1:B:290:ILE:HG13	0.45	1.87	14	1
1:A:290:ILE:HD13	1:B:322:ASN:HB2	0.45	1.87	14	1
1:B:275:SER:HB3	1:B:277:PHE:CE2	0.45	2.46	2	1
1:B:355:LEU:HD12	1:B:356:CYS:N	0.45	2.27	10	1
1:B:318:GLN:HB2	1:B:323:GLU:CA	0.45	2.41	13	1
1:B:286:GLU:HB3	1:B:333:SER:HA	0.45	1.87	11	1
1:A:355:LEU:N	1:A:355:LEU:HD13	0.45	2.25	6	1
1:A:322:ASN:HB3	1:B:320:SER:OG	0.45	2.11	10	1
1:B:342:LEU:HB3	1:B:345:ARG:HE	0.45	1.72	3	1
1:A:345:ARG:HD2	1:B:290:ILE:HB	0.45	1.88	7	1
1:A:273:CYS:HB3	1:A:353:LEU:O	0.45	2.12	12	1
1:A:311:PHE:O	1:A:331:LYS:HG3	0.45	2.12	6	1
1:A:311:PHE:HB2	1:A:331:LYS:HD3	0.45	1.89	10	1
1:A:311:PHE:CB	1:A:331:LYS:HE3	0.45	2.38	1	1
1:A:353:LEU:HD13	1:A:354:ARG:HD2	0.45	1.89	10	1
1:B:302:LEU:HD13	1:B:303:CYS:N	0.45	2.26	1	1
1:A:275:SER:HB3	1:A:277:PHE:CE2	0.45	2.46	3	1
1:B:293:ALA:H	1:B:327:LYS:HE2	0.45	1.72	8	1
1:A:308:ARG:O	1:A:308:ARG:HD2	0.45	2.12	8	1
1:B:310:GLN:C	1:B:351:TYR:HB2	0.45	2.33	2	1
1:A:355:LEU:H	1:A:355:LEU:HD22	0.45	1.72	6	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:278:TYR:HB3	1:B:281:THR:CG2	0.45	2.42	3	1
1:B:342:LEU:N	1:B:342:LEU:HD13	0.45	2.26	6	2
1:B:278:TYR:CZ	1:B:349:SER:HB2	0.45	2.47	2	1
1:A:313:THR:OG1	1:A:331:LYS:HE2	0.44	2.12	7	2
1:B:315:THR:OG1	1:B:322:ASN:HA	0.44	2.12	7	1
1:B:330:LEU:HD23	1:B:331:LYS:N	0.44	2.27	5	1
1:A:288:LEU:HD12	1:A:329:TYR:HE2	0.44	1.70	13	1
1:A:331:LYS:HD3	1:A:331:LYS:N	0.44	2.27	1	1
1:A:284:LEU:HD22	1:A:284:LEU:O	0.44	2.13	3	1
1:A:320:SER:CB	1:A:328:CYS:HA	0.44	2.43	11	1
1:A:287:GLU:HG2	1:A:332:LEU:HB3	0.44	1.88	8	1
1:A:290:ILE:HG13	1:A:329:TYR:C	0.44	2.32	12	1
1:A:292:ALA:HB3	1:A:327:LYS:HA	0.44	1.89	9	1
1:A:324:GLY:HA2	1:B:323:GLU:HB2	0.44	1.88	7	3
1:A:342:LEU:HD23	1:A:342:LEU:N	0.44	2.27	8	1
1:A:351:TYR:CD1	1:A:355:LEU:HD21	0.44	2.48	9	1
1:B:318:GLN:HB3	1:B:324:GLY:O	0.44	2.12	3	1
1:A:318:GLN:HA	1:A:325:LYS:HA	0.44	1.88	12	1
1:B:278:TYR:CZ	1:B:349:SER:HB3	0.44	2.48	12	1
1:A:318:GLN:HB2	1:A:325:LYS:HA	0.44	1.89	4	1
1:A:291:VAL:HG23	1:A:328:CYS:SG	0.44	2.52	2	1
1:B:314:TYR:O	1:B:348:ILE:HB	0.44	2.12	8	1
1:B:288:LEU:CD2	1:B:331:LYS:HG2	0.44	2.43	7	1
1:A:310:GLN:NE2	1:A:332:LEU:HB2	0.44	2.28	10	1
1:B:322:ASN:O	1:B:323:GLU:HB2	0.44	2.12	13	1
1:B:310:GLN:NE2	1:B:359:ASP:HB2	0.44	2.28	1	1
1:A:278:TYR:HB2	1:A:349:SER:OG	0.44	2.13	11	1
1:B:313:THR:OG1	1:B:331:LYS:HE3	0.44	2.12	4	1
1:A:311:PHE:CD2	1:A:331:LYS:HG3	0.44	2.48	2	1
1:A:284:LEU:HD22	1:A:288:LEU:HD21	0.44	1.88	10	1
1:A:309:CYS:SG	1:A:355:LEU:HD22	0.44	2.53	14	1
1:B:288:LEU:HG	1:B:331:LYS:HB3	0.44	1.88	9	1
1:B:309:CYS:HB2	1:B:330:LEU:HD11	0.44	1.89	12	1
1:A:286:GLU:HG2	1:B:340:LYS:HE2	0.44	1.89	5	1
1:B:320:SER:HB2	1:B:327:LYS:HB2	0.43	1.88	10	1
1:A:307:VAL:HG23	1:A:355:LEU:HB3	0.43	1.90	13	1
1:B:341:ILE:HD13	1:B:341:ILE:H	0.43	1.72	2	1
1:B:282:ASP:HB3	1:B:342:LEU:HD22	0.43	1.89	9	1
1:B:313:THR:HG22	1:B:329:TYR:O	0.43	2.13	8	1
1:A:322:ASN:HD22	1:A:323:GLU:N	0.43	2.11	8	1
1:A:342:LEU:H	1:A:342:LEU:HD23	0.43	1.73	8	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:315:THR:HG22	1:A:347:GLY:CA	0.43	2.43	14	1
1:B:313:THR:HB	1:B:329:TYR:CZ	0.43	2.47	14	1
1:B:332:LEU:HG	1:B:333:SER:N	0.43	2.27	12	1
1:A:277:PHE:HB3	1:A:348:ILE:CD1	0.43	2.43	12	1
1:B:310:GLN:CD	1:B:332:LEU:HB2	0.43	2.34	5	1
1:B:296:HIS:HB2	1:B:319:ALA:CB	0.43	2.44	1	1
1:A:330:LEU:HD13	1:A:330:LEU:N	0.43	2.28	1	1
1:A:284:LEU:HD13	1:A:284:LEU:H	0.43	1.73	1	1
1:B:292:ALA:HA	1:B:327:LYS:HG3	0.43	1.90	8	1
1:A:311:PHE:CE2	1:A:331:LYS:HB2	0.43	2.48	8	1
1:B:310:GLN:HG3	1:B:311:PHE:HD1	0.43	1.72	6	1
1:B:325:LYS:HG2	1:B:326:GLY:N	0.43	2.28	10	1
1:B:288:LEU:HD21	1:B:329:TYR:CE1	0.43	2.48	7	1
1:A:287:GLU:HB3	1:A:332:LEU:CB	0.43	2.41	12	1
1:A:296:HIS:CE1	1:A:314:TYR:HE2	0.43	2.31	13	1
1:B:307:VAL:HB	1:B:355:LEU:HB3	0.43	1.91	11	1
1:B:312:PHE:HB3	1:B:351:TYR:CE2	0.43	2.49	4	1
1:A:312:PHE:HE1	1:A:328:CYS:HB2	0.43	1.71	2	1
1:B:317:ALA:HB3	1:B:322:ASN:ND2	0.43	2.27	13	1
1:A:300:GLN:HA	1:A:351:TYR:CE1	0.43	2.40	3	1
1:B:311:PHE:CE2	1:B:331:LYS:HD2	0.43	2.48	10	1
1:A:288:LEU:HB2	1:B:342:LEU:HD11	0.43	1.91	3	1
1:A:291:VAL:HB	1:A:328:CYS:SG	0.43	2.54	14	1
1:A:308:ARG:O	1:A:332:LEU:HD13	0.43	2.12	5	1
1:A:311:PHE:HD1	1:A:331:LYS:HG2	0.43	1.69	10	1
1:A:329:TYR:CE1	1:A:331:LYS:HD2	0.43	2.49	4	1
1:B:352:THR:HA	1:B:355:LEU:HD23	0.43	1.91	2	1
1:A:318:GLN:HB2	1:A:323:GLU:CA	0.43	2.43	14	1
1:A:342:LEU:N	1:A:342:LEU:HD13	0.43	2.28	6	1
1:B:335:ASN:OD1	1:B:360:ASN:HA	0.42	2.14	12	1
1:A:352:THR:HG22	1:A:353:LEU:HD22	0.42	1.90	9	1
1:B:283:PHE:CE2	1:B:341:ILE:HG13	0.42	2.49	3	1
1:B:303:CYS:SG	1:B:351:TYR:CE2	0.42	3.12	7	1
1:B:311:PHE:HA	1:B:351:TYR:HD2	0.42	1.74	7	1
1:B:283:PHE:CD2	1:B:341:ILE:HG22	0.42	2.49	7	1
1:A:284:LEU:HG	1:B:284:LEU:HD23	0.42	1.92	2	1
1:A:310:GLN:HB3	1:A:355:LEU:HD23	0.42	1.89	5	1
1:B:309:CYS:O	1:B:355:LEU:HG	0.42	2.13	13	1
1:B:320:SER:OG	1:B:327:LYS:HB2	0.42	2.14	12	2
1:B:330:LEU:C	1:B:331:LYS:HD3	0.42	2.35	3	1
1:A:330:LEU:H	1:A:330:LEU:HD23	0.42	1.75	3	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:310:GLN:HE21	1:A:359:ASP:HA	0.42	1.74	8	1
1:A:324:GLY:CA	1:B:323:GLU:HG3	0.42	2.45	14	1
1:B:318:GLN:HB3	1:B:324:GLY:N	0.42	2.22	14	1
1:B:281:THR:HG22	1:B:343:HIS:HA	0.42	1.90	10	1
1:B:317:ALA:O	1:B:318:GLN:HB2	0.42	2.14	1	1
1:A:323:GLU:CG	1:B:324:GLY:HA2	0.42	2.43	11	1
1:A:340:LYS:HG2	1:B:286:GLU:O	0.42	2.15	5	1
1:A:322:ASN:OD1	1:B:327:LYS:HE3	0.42	2.15	3	1
1:B:287:GLU:HG3	1:B:332:LEU:HB3	0.42	1.91	8	1
1:A:341:ILE:HD13	1:A:341:ILE:N	0.42	2.30	5	2
1:B:311:PHE:CD2	1:B:331:LYS:HE3	0.42	2.49	7	1
1:A:284:LEU:HA	1:A:331:LYS:HD2	0.42	1.90	12	1
1:A:335:ASN:HB3	1:A:361:GLU:CA	0.42	2.44	9	1
1:A:345:ARG:HD3	1:B:290:ILE:O	0.42	2.15	9	1
1:A:322:ASN:O	1:A:323:GLU:HB2	0.42	2.15	10	1
1:A:286:GLU:O	1:B:340:LYS:HD3	0.42	2.14	2	1
1:A:326:GLY:O	1:A:327:LYS:HG3	0.42	2.14	2	1
1:A:308:ARG:O	1:A:308:ARG:HG2	0.42	2.14	9	1
1:A:314:TYR:CD2	1:A:319:ALA:HA	0.42	2.49	10	1
1:A:288:LEU:HB2	1:B:341:ILE:CD1	0.42	2.45	14	1
1:A:276:SER:HB3	1:A:351:TYR:CZ	0.42	2.49	12	1
1:B:319:ALA:HB1	1:B:327:LYS:O	0.42	2.15	10	1
1:B:318:GLN:O	1:B:319:ALA:HB2	0.42	2.15	10	1
1:A:312:PHE:HE2	1:A:328:CYS:HB3	0.42	1.74	1	2
1:B:320:SER:HG	1:B:329:TYR:HD1	0.42	1.56	8	1
1:B:309:CYS:HB3	1:B:330:LEU:HD21	0.42	1.92	8	1
1:A:307:VAL:HB	1:A:355:LEU:HB3	0.42	1.89	4	1
1:B:335:ASN:HB2	1:B:360:ASN:CA	0.42	2.36	2	1
1:A:288:LEU:HD21	1:A:329:TYR:HE2	0.42	1.75	4	1
1:A:311:PHE:CE2	1:A:331:LYS:HE2	0.42	2.49	9	1
1:B:286:GLU:CB	1:B:333:SER:HA	0.41	2.45	11	1
1:A:318:GLN:HB3	1:A:324:GLY:N	0.41	2.29	12	1
1:A:277:PHE:CD2	1:A:350:GLY:HA3	0.41	2.50	2	1
1:A:288:LEU:HD23	1:B:341:ILE:HG13	0.41	1.92	14	1
1:B:309:CYS:HB3	1:B:330:LEU:HD11	0.41	1.92	4	1
1:B:344:GLY:C	1:B:345:ARG:HD2	0.41	2.34	2	1
1:B:297:GLU:CD	1:B:297:GLU:H	0.41	2.18	9	1
1:A:291:VAL:HG13	1:B:345:ARG:HG2	0.41	1.92	12	1
1:A:352:THR:HG23	1:A:353:LEU:HD23	0.41	1.91	4	1
1:B:286:GLU:HB2	1:B:337:SER:HB3	0.41	1.91	13	1
1:B:311:PHE:HB3	1:B:351:TYR:HD2	0.41	1.75	13	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:309:CYS:HB3	1:A:330:LEU:HD11	0.41	1.92	11	1
1:A:338:PRO:HB2	1:A:340:LYS:HE3	0.41	1.93	2	1
1:A:323:GLU:CD	1:B:324:GLY:HA2	0.41	2.36	1	1
1:A:290:ILE:HG23	1:B:345:ARG:HB2	0.41	1.93	1	1
1:A:279:HIS:O	1:A:280:ASP:HB3	0.41	2.16	8	1
1:A:320:SER:N	1:A:324:GLY:HA3	0.41	2.29	6	1
1:A:277:PHE:HB3	1:A:348:ILE:CG2	0.41	2.45	7	1
1:A:315:THR:CG2	1:A:322:ASN:HA	0.41	2.45	6	1
1:A:297:GLU:O	1:A:300:GLN:HG2	0.41	2.16	1	1
1:B:314:TYR:CZ	1:B:348:ILE:HG13	0.41	2.51	14	1
1:A:321:CYS:SG	1:B:322:ASN:ND2	0.41	2.94	12	1
1:A:341:ILE:N	1:A:341:ILE:HD13	0.41	2.31	9	1
1:B:312:PHE:CE1	1:B:328:CYS:HB2	0.41	2.43	10	1
1:B:294:LYS:HD2	1:B:294:LYS:N	0.41	2.30	1	1
1:B:282:ASP:O	1:B:341:ILE:C	0.41	2.59	14	1
1:A:356:CYS:HA	1:A:359:ASP:OD2	0.41	2.15	2	1
1:B:335:ASN:CG	1:B:336:GLY:H	0.41	2.17	9	1
1:B:283:PHE:HB2	1:B:311:PHE:CZ	0.41	2.51	3	1
1:B:307:VAL:HG23	1:B:355:LEU:HA	0.41	1.91	3	1
1:A:356:CYS:O	1:A:359:ASP:HB3	0.41	2.16	12	1
1:B:301:LYS:HA	1:B:304:THR:OG1	0.41	2.14	3	1
1:B:315:THR:HB	1:B:316:PRO:HD2	0.41	1.92	11	1
1:A:330:LEU:HD23	1:A:331:LYS:N	0.41	2.30	12	1
1:A:332:LEU:HD21	1:A:358:MET:HE1	0.41	1.92	2	1
1:B:302:LEU:HA	1:B:305:ASN:HD21	0.41	1.75	6	1
1:A:322:ASN:ND2	1:A:323:GLU:H	0.40	2.14	8	1
1:A:312:PHE:CE2	1:A:328:CYS:HB3	0.40	2.51	7	1
1:A:297:GLU:HG3	1:A:300:GLN:OE1	0.40	2.16	7	1
1:A:323:GLU:CB	1:B:323:GLU:HB3	0.40	2.37	14	1
1:B:320:SER:CA	1:B:329:TYR:HB2	0.40	2.23	11	1
1:B:288:LEU:HB3	1:B:329:TYR:CE2	0.40	2.49	9	1
1:B:320:SER:O	1:B:322:ASN:N	0.40	2.54	13	1
1:B:345:ARG:CD	1:B:345:ARG:H	0.40	2.30	13	1
1:A:289:ASP:C	1:A:330:LEU:H	0.40	2.19	12	1
1:A:301:LYS:HD2	1:A:301:LYS:N	0.40	2.32	3	1
1:B:282:ASP:O	1:B:341:ILE:CG2	0.40	2.70	14	1
1:A:357:LYS:O	1:A:357:LYS:HE2	0.40	2.17	12	1
1:A:288:LEU:HD22	1:B:342:LEU:HG	0.40	1.92	4	1
1:B:278:TYR:HE2	1:B:282:ASP:HA	0.40	1.75	2	1
1:A:355:LEU:C	1:A:355:LEU:HD22	0.40	2.37	5	1
1:A:341:ILE:H	1:A:341:ILE:HD13	0.40	1.75	9	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	88/90 (98%)	67±3 (77±4%)	17±3 (19±4%)	4±2 (4±2%)	6	30
1	B	88/90 (98%)	68±2 (77±2%)	16±3 (18±3%)	5±2 (5±2%)	5	25
All	All	2464/2520 (98%)	1893 (77%)	452 (18%)	119 (5%)	5	28

All 41 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	308	ARG	9
1	A	353	LEU	6
1	B	307	VAL	6
1	A	325	LYS	5
1	A	317	ALA	5
1	B	295	SER	5
1	B	317	ALA	5
1	B	318	GLN	5
1	B	322	ASN	5
1	A	324	GLY	5
1	B	319	ALA	4
1	A	295	SER	4
1	B	316	PRO	4
1	B	275	SER	4
1	B	320	SER	4
1	A	322	ASN	4
1	B	321	CYS	3
1	B	308	ARG	3
1	B	325	LYS	3
1	B	353	LEU	2
1	A	273	CYS	2
1	B	360	ASN	2
1	A	320	SER	2
1	B	359	ASP	2
1	A	338	PRO	2
1	A	321	CYS	2

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Mol	Chain	Res	Type	Models (Total)
1	B	338	PRO	2
1	B	309	CYS	1
1	B	274	HIS	1
1	A	319	ALA	1
1	B	333	SER	1
1	A	316	PRO	1
1	B	273	CYS	1
1	A	280	ASP	1
1	A	333	SER	1
1	A	275	SER	1
1	A	290	ILE	1
1	A	323	GLU	1
1	A	318	GLN	1
1	A	289	ASP	1
1	B	336	GLY	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	75/76 (99%)	68±3 (90±4%)	7±3 (10±4%)	15	59
1	B	76/76 (100%)	67±2 (89±3%)	9±2 (11±3%)	11	54
All	All	2114/2128 (99%)	1890 (89%)	224 (11%)	13	57

All 91 unique residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	355	LEU	9
1	B	351	TYR	7
1	B	345	ARG	6
1	A	311	PHE	6
1	B	309	CYS	5
1	B	331	LYS	5
1	A	342	LEU	5
1	A	284	LEU	5
1	B	308	ARG	5

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Mol	Chain	Res	Type	Models (Total)
1	A	331	LYS	5
1	B	341	ILE	5
1	B	355	LEU	5
1	B	342	LEU	5
1	B	311	PHE	5
1	A	322	ASN	5
1	A	353	LEU	4
1	B	354	ARG	4
1	B	325	LYS	3
1	A	341	ILE	3
1	B	274	HIS	3
1	B	310	GLN	3
1	B	329	TYR	3
1	B	348	ILE	3
1	A	345	ARG	3
1	B	322	ASN	3
1	B	280	ASP	3
1	B	284	LEU	3
1	A	351	TYR	3
1	A	340	LYS	3
1	B	335	ASN	3
1	A	294	LYS	3
1	B	302	LEU	3
1	B	323	GLU	3
1	A	290	ILE	3
1	A	323	GLU	3
1	B	360	ASN	2
1	B	321	CYS	2
1	A	273	CYS	2
1	A	330	LEU	2
1	A	296	HIS	2
1	A	325	LYS	2
1	B	294	LYS	2
1	A	309	CYS	2
1	B	275	SER	2
1	A	354	ARG	2
1	B	358	MET	2
1	A	359	ASP	2
1	A	321	CYS	2
1	A	295	SER	2
1	B	352	THR	2
1	A	357	LYS	2

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Mol	Chain	Res	Type	Models (Total)
1	B	288	LEU	2
1	B	357	LYS	2
1	B	339	THR	2
1	B	340	LYS	2
1	B	300	GLN	2
1	A	329	TYR	2
1	B	290	ILE	2
1	A	335	ASN	1
1	A	279	HIS	1
1	B	332	LEU	1
1	A	301	LYS	1
1	B	304	THR	1
1	A	328	CYS	1
1	A	308	ARG	1
1	A	327	LYS	1
1	A	360	ASN	1
1	A	334	SER	1
1	B	286	GLU	1
1	B	296	HIS	1
1	A	302	LEU	1
1	A	274	HIS	1
1	A	358	MET	1
1	B	301	LYS	1
1	A	361	GLU	1
1	B	328	CYS	1
1	B	282	ASP	1
1	A	278	TYR	1
1	A	314	TYR	1
1	A	305	ASN	1
1	B	273	CYS	1
1	A	348	ILE	1
1	B	343	HIS	1
1	B	334	SER	1
1	A	304	THR	1
1	A	310	GLN	1
1	A	349	SER	1
1	A	297	GLU	1
1	B	315	THR	1
1	B	361	GLU	1
1	B	327	LYS	1

6.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

6.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.6 Ligand geometry [i](#)

There are no ligands in this entry.

6.7 Other polymers [i](#)

There are no such molecules in this entry.

6.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

7 Chemical shift validation

No chemical shift data were provided