



Full wwPDB NMR Structure Validation Report ⓘ

Mar 9, 2026 – 12:59 PM UTC

PDB ID : 2A0T / pdb_00002a0t
Title : NMR structure of the FHA1 domain of Rad53 in complex with a biological relevant phosphopeptide derived from Madt1
Authors : Mahajan, A.; Yuan, C.; Pike, B.L.; Heierhorst, J.; Chang, C.-F.; Tsai, M.-D.
Deposited on : 2005-06-16

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

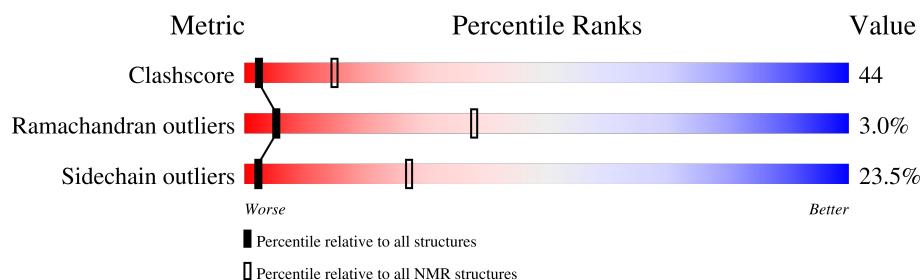
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment was not calculated.

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



Metric	Whole archive (#Entries)	NMR archive (#Entries)
Clashscore	229148	14424
Ramachandran outliers	224038	12848
Sidechain outliers	223484	12823

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

Mol	Chain	Length	Quality of chain
1	A	151	
2	B	10	

2 Ensemble composition and analysis

This entry contains 20 models. Model 4 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *closest to the average, 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:30-A:51, A:64-A:93, A:99-A:151 (105)	0.36	4

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

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

The models can be grouped into 4 clusters and 3 single-model clusters were found.

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

3 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 2581 atoms, of which 1295 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Serine/threonine-protein kinase RAD53.

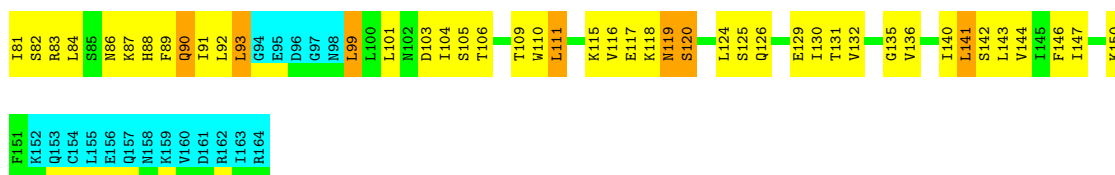
Mol	Chain	Residues	Atoms						Trace
1	A	151	Total	C	H	N	O	S	0
			2424	751	1224	215	230	4	

- Molecule 2 is a protein called Hypothetical 73.8 kDa protein in SAS3-SEC17 intergenic region, residues 301-310.

Mol	Chain	Residues	Atoms						Trace
2	B	10	Total	C	H	N	O	P	0
			157	50	71	11	24	1	

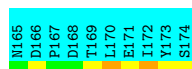
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	169	TPO	THR	modified residue	UNP P34217



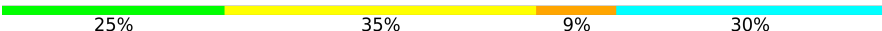
- Molecule 2: Hypothetical 73.8 kDa protein in SAS3-SEC17 intergenic region, residues 301-310

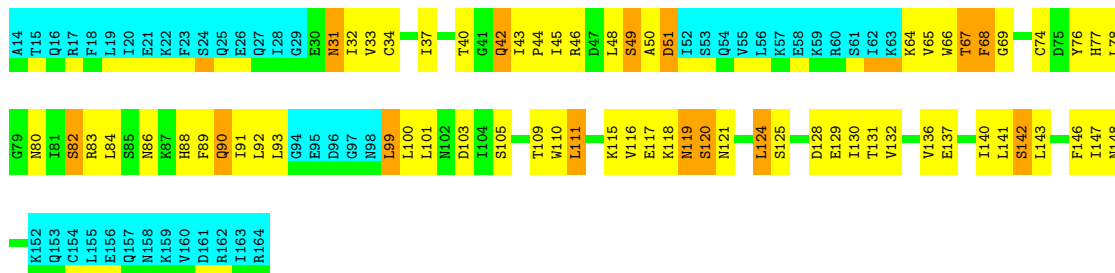
Chain B:  100%



4.2.2 Score per residue for model 2

- Molecule 1: Serine/threonine-protein kinase RAD53

Chain A:  25% 35% 9% 30%



- Molecule 2: Hypothetical 73.8 kDa protein in SAS3-SEC17 intergenic region, residues 301-310

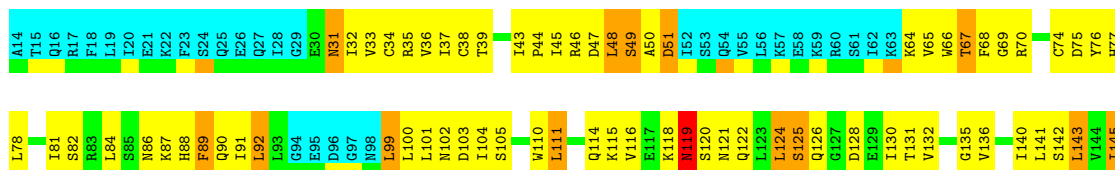
Chain B:  100%



4.2.3 Score per residue for model 3

- Molecule 1: Serine/threonine-protein kinase RAD53

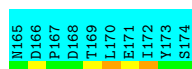
Chain A:  21% 40% 9% 30%





- Molecule 2: Hypothetical 73.8 kDa protein in SAS3-SEC17 intergenic region, residues 301-310

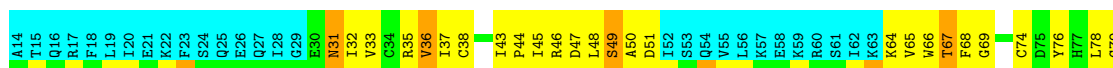
Chain B:  100%



4.2.4 Score per residue for model 4 (medoid)

- Molecule 1: Serine/threonine-protein kinase RAD53

Chain A:  23% 38% 8% 30%



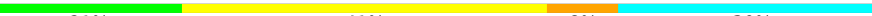
- Molecule 2: Hypothetical 73.8 kDa protein in SAS3-SEC17 intergenic region, residues 301-310

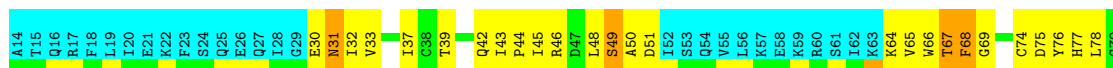
Chain B:  100%

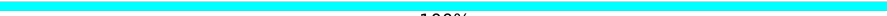


4.2.5 Score per residue for model 5

- Molecule 1: Serine/threonine-protein kinase RAD53

Chain A:  21% 41% 8% 30%

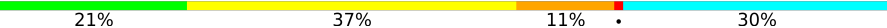


Chain B:  100%



4.2.8 Score per residue for model 8

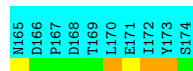
- Molecule 1: Serine/threonine-protein kinase RAD53

Chain A:  21% 37% 11% 30%



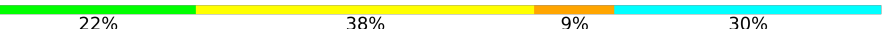
- Molecule 2: Hypothetical 73.8 kDa protein in SAS3-SEC17 intergenic region, residues 301-310

Chain B:  100%



4.2.9 Score per residue for model 9

- Molecule 1: Serine/threonine-protein kinase RAD53

Chain A:  22% 38% 9% 30%



- Molecule 2: Hypothetical 73.8 kDa protein in SAS3-SEC17 intergenic region, residues 301-310

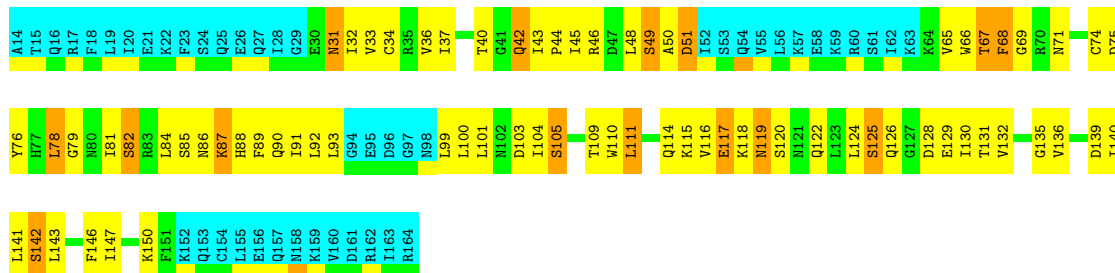
Chain B:  100%



4.2.10 Score per residue for model 10

- Molecule 1: Serine/threonine-protein kinase RAD53

Chain A: 21% 39% 10% 30%



- Molecule 2: Hypothetical 73.8 kDa protein in SAS3-SEC17 intergenic region, residues 301-310

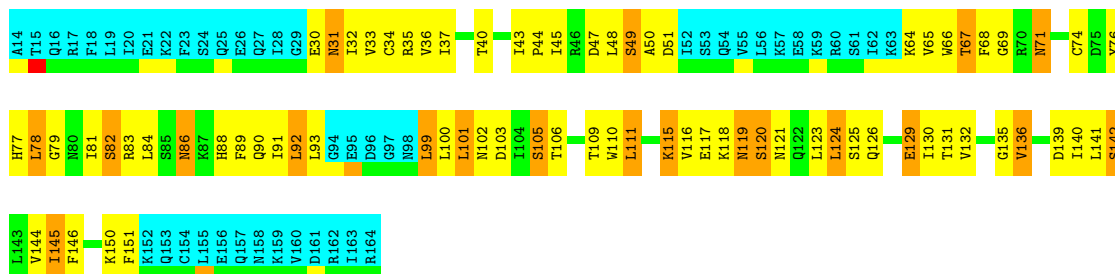
Chain B: 100%



4.2.11 Score per residue for model 11

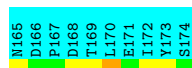
- Molecule 1: Serine/threonine-protein kinase RAD53

Chain A: 19% 37% 13% 30%



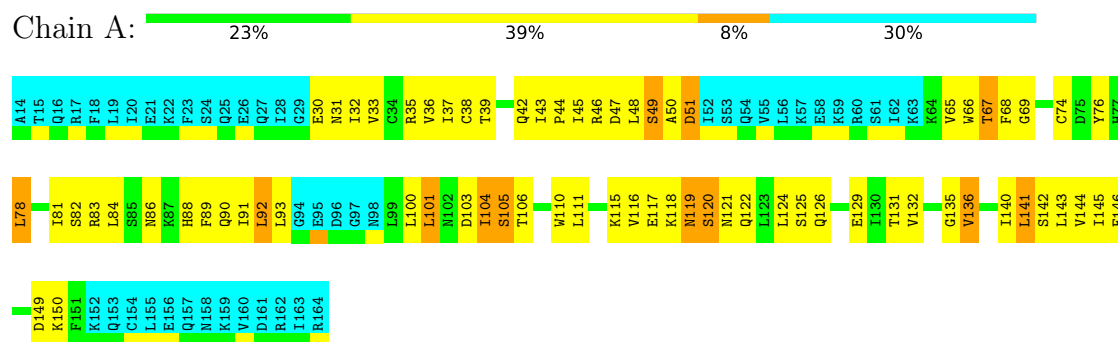
- Molecule 2: Hypothetical 73.8 kDa protein in SAS3-SEC17 intergenic region, residues 301-310

Chain B: 100%

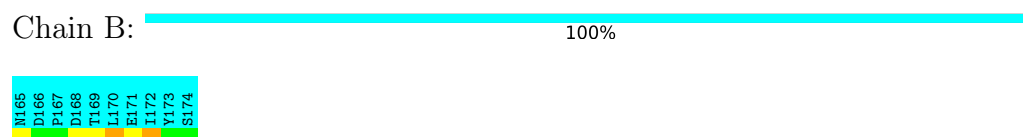


4.2.12 Score per residue for model 12

- Molecule 1: Serine/threonine-protein kinase RAD53

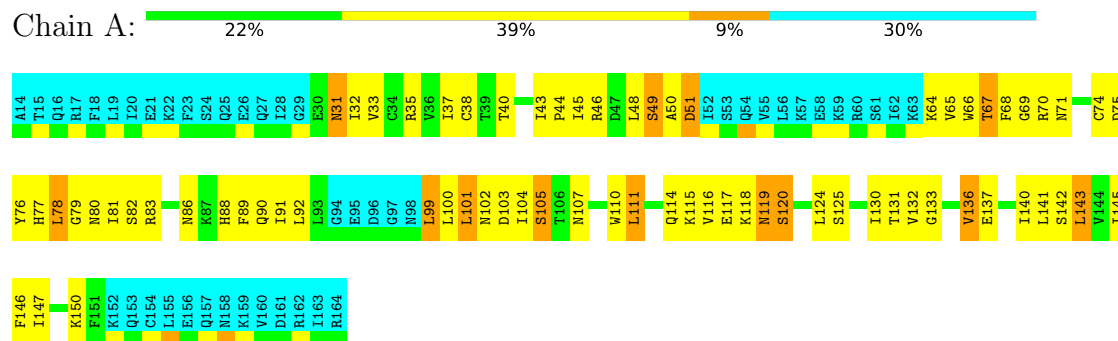


- Molecule 2: Hypothetical 73.8 kDa protein in SAS3-SEC17 intergenic region, residues 301-310

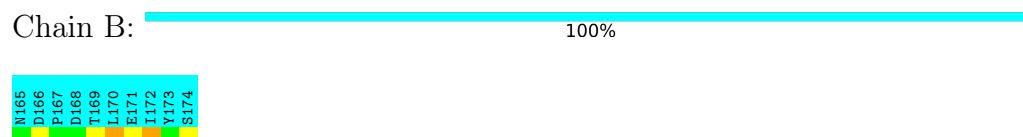


4.2.13 Score per residue for model 13

- Molecule 1: Serine/threonine-protein kinase RAD53

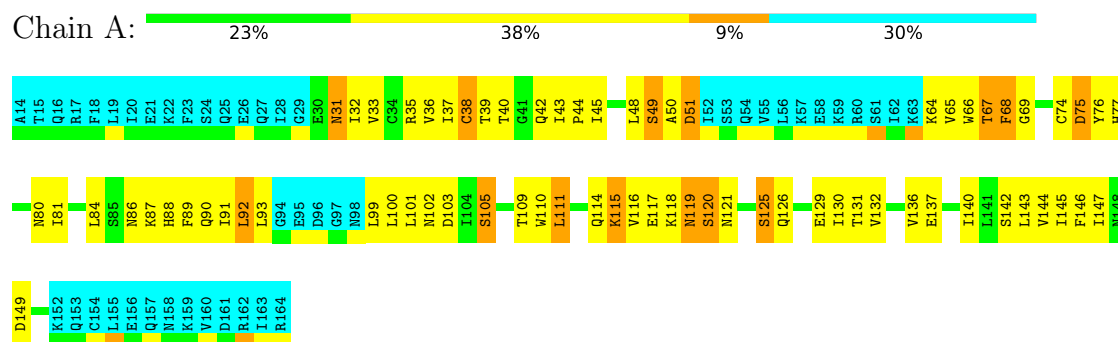


- Molecule 2: Hypothetical 73.8 kDa protein in SAS3-SEC17 intergenic region, residues 301-310

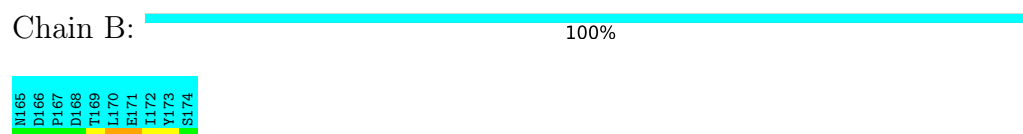


4.2.14 Score per residue for model 14

- Molecule 1: Serine/threonine-protein kinase RAD53

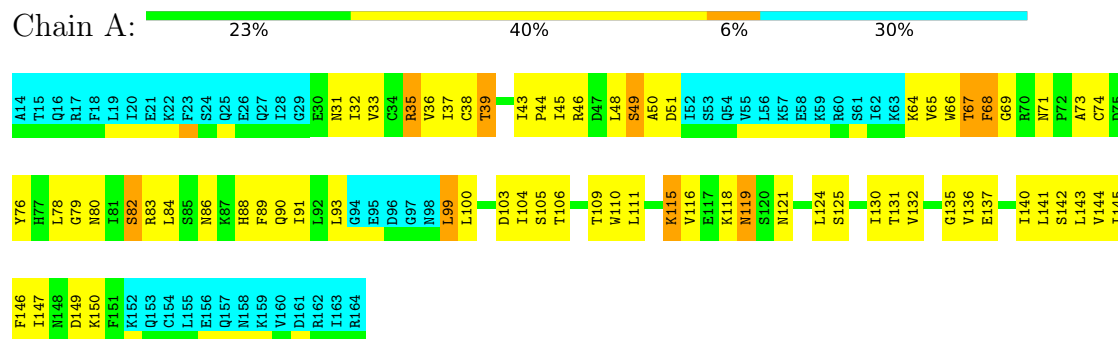


- Molecule 2: Hypothetical 73.8 kDa protein in SAS3-SEC17 intergenic region, residues 301-310

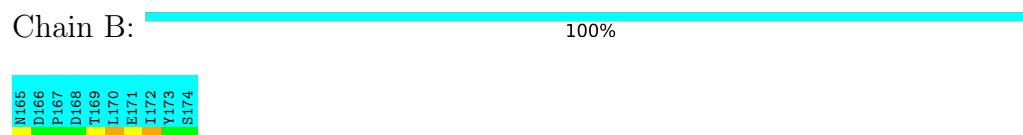


4.2.15 Score per residue for model 15

- Molecule 1: Serine/threonine-protein kinase RAD53

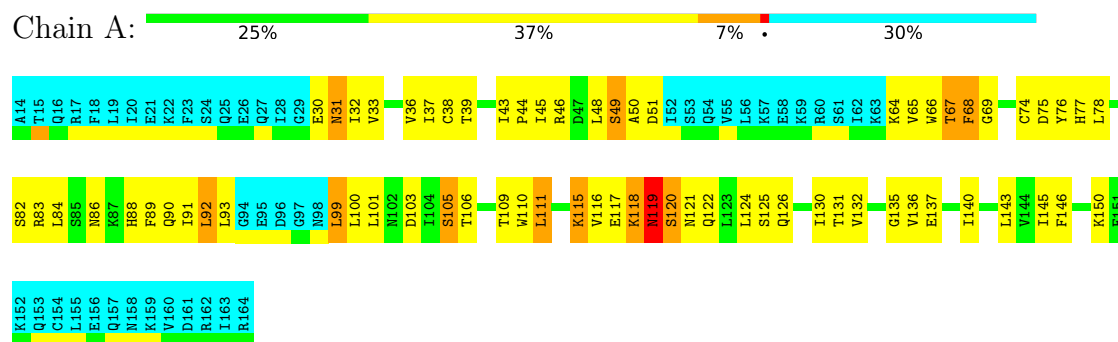


- Molecule 2: Hypothetical 73.8 kDa protein in SAS3-SEC17 intergenic region, residues 301-310

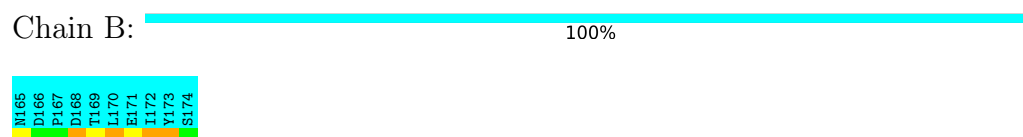


4.2.16 Score per residue for model 16

- Molecule 1: Serine/threonine-protein kinase RAD53

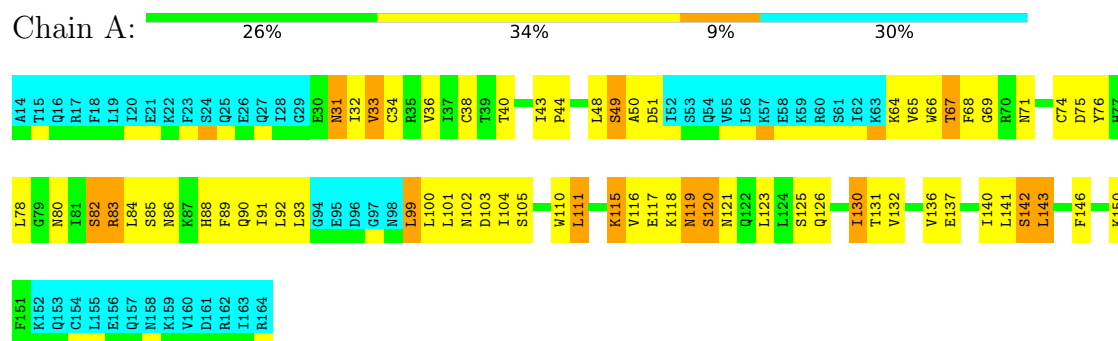


- Molecule 2: Hypothetical 73.8 kDa protein in SAS3-SEC17 intergenic region, residues 301-310

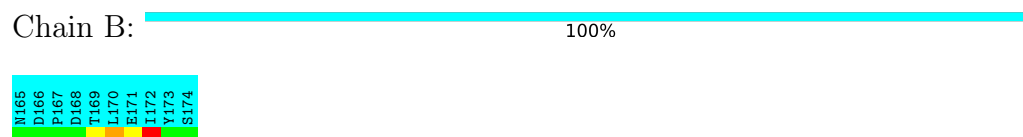


4.2.17 Score per residue for model 17

- Molecule 1: Serine/threonine-protein kinase RAD53

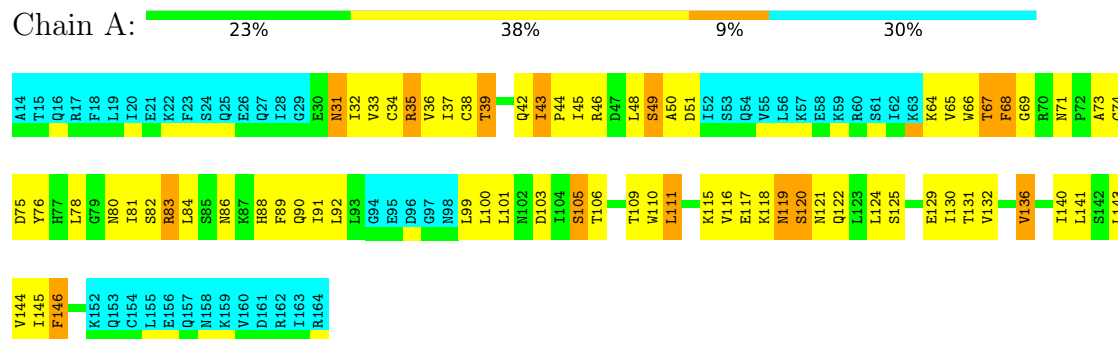


- Molecule 2: Hypothetical 73.8 kDa protein in SAS3-SEC17 intergenic region, residues 301-310

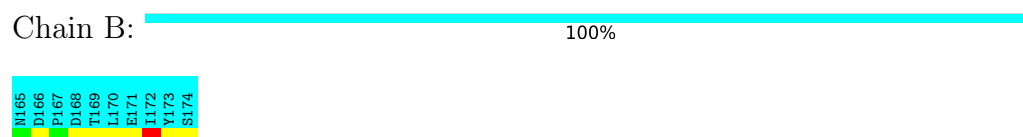


4.2.18 Score per residue for model 18

- Molecule 1: Serine/threonine-protein kinase RAD53

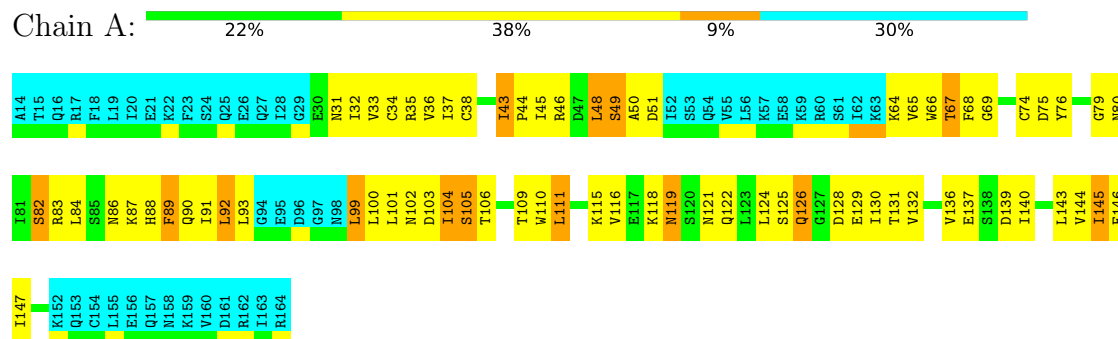


- Molecule 2: Hypothetical 73.8 kDa protein in SAS3-SEC17 intergenic region, residues 301-310

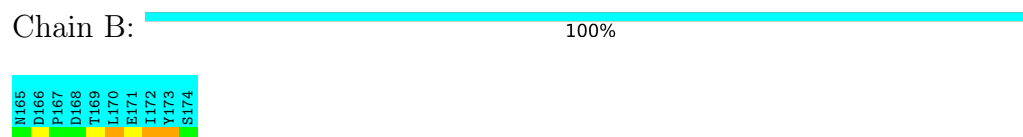


4.2.19 Score per residue for model 19

- Molecule 1: Serine/threonine-protein kinase RAD53

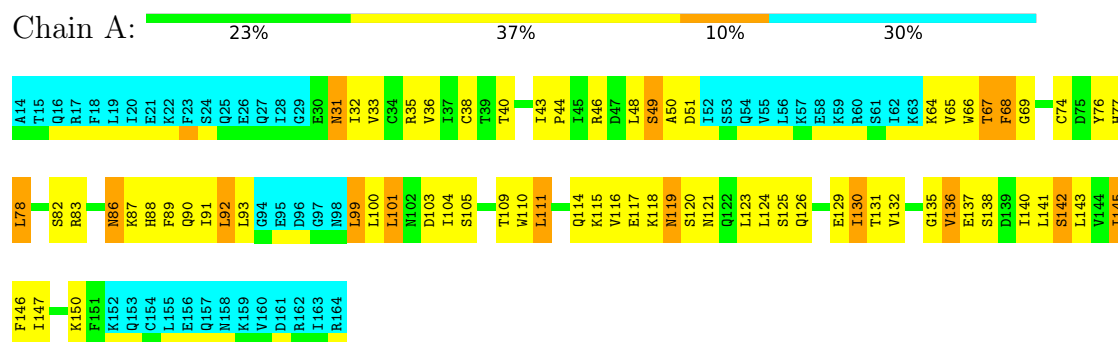


- Molecule 2: Hypothetical 73.8 kDa protein in SAS3-SEC17 intergenic region, residues 301-310

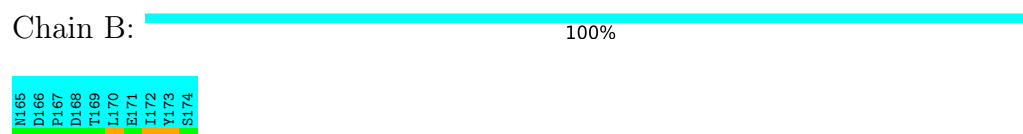


4.2.20 Score per residue for model 20

- Molecule 1: Serine/threonine-protein kinase RAD53



- Molecule 2: Hypothetical 73.8 kDa protein in SAS3-SEC17 intergenic region, residues 301-310



5 Refinement protocol and experimental data overview

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

Of the 50 calculated structures, 20 were deposited, based on the following criterion: *structures with acceptable covalent geometry, structures with the least restraint violations, structures with the lowest energy*.

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

Software name	Classification	Version
CNS	structure solution	1.1
CNS	refinement	1.1

No chemical shift data was provided.

6 Model quality

6.1 Standard geometry

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

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	822	831	829	73±6
2	B	0	0	0	0±0
All	All	16440	16620	16580	1457

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 44.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:130:ILE:HD11	1:A:145:ILE:HD11	1.00	1.33	9	6
1:A:81:ILE:HD13	1:A:84:LEU:HD12	0.97	1.36	18	6
1:A:33:VAL:HG12	1:A:99:LEU:HD11	0.89	1.45	15	7
1:A:93:LEU:HD12	1:A:99:LEU:HD11	0.89	1.44	10	1
1:A:33:VAL:HG23	1:A:49:SER:HA	0.87	1.46	3	19
1:A:33:VAL:HG12	1:A:99:LEU:HD21	0.86	1.44	9	3
1:A:67:THR:HG23	1:A:90:GLN:HG3	0.85	1.48	1	15
1:A:129:GLU:CG	1:A:144:VAL:HG22	0.81	2.05	19	10
1:A:84:LEU:HD21	1:A:132:VAL:HG21	0.81	1.53	10	2
1:A:78:LEU:HD23	1:A:84:LEU:HD13	0.81	1.50	17	2
1:A:78:LEU:HD13	1:A:84:LEU:HD13	0.79	1.55	3	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:111:LEU:HD12	1:A:116:VAL:HG11	0.78	1.54	20	2
1:A:110:TRP:CE2	1:A:115:LYS:HB2	0.77	2.15	5	20
1:A:35:ARG:NE	1:A:45:ILE:HG21	0.77	1.95	15	1
1:A:68:PHE:CE1	1:A:91:ILE:HD13	0.76	2.16	11	1
1:A:103:ASP:OD2	1:A:116:VAL:HG23	0.76	1.81	10	20
1:A:48:LEU:HD23	1:A:66:TRP:CD2	0.75	2.17	1	9
1:A:33:VAL:HG11	1:A:93:LEU:HD22	0.75	1.59	6	10
1:A:81:ILE:HD13	1:A:84:LEU:CD1	0.74	2.13	18	4
1:A:33:VAL:HG23	1:A:49:SER:CA	0.74	2.12	9	19
1:A:67:THR:HG23	1:A:90:GLN:CG	0.74	2.12	2	12
1:A:81:ILE:HB	1:A:84:LEU:HD12	0.73	1.61	5	1
1:A:101:LEU:HD11	1:A:130:ILE:HD11	0.71	1.60	11	3
1:A:141:LEU:HD23	1:A:142:SER:N	0.70	2.01	3	5
1:A:33:VAL:CG1	1:A:93:LEU:HD13	0.70	2.15	12	5
1:A:124:LEU:HD21	1:A:147:ILE:HG12	0.70	1.63	6	6
1:A:33:VAL:CG1	1:A:93:LEU:HD22	0.70	2.16	19	10
1:A:40:THR:HG21	1:A:142:SER:OG	0.70	1.87	10	4
1:A:37:ILE:HD12	1:A:146:PHE:CE1	0.70	2.20	1	1
1:A:34:CYS:SG	1:A:48:LEU:HD12	0.70	2.26	17	8
1:A:100:LEU:HD22	1:A:121:ASN:HB3	0.69	1.63	4	4
1:A:43:ILE:HD13	1:A:78:LEU:HD22	0.69	1.64	6	2
1:A:37:ILE:HG23	1:A:45:ILE:HG12	0.69	1.63	11	18
1:A:68:PHE:CE1	1:A:91:ILE:HD12	0.69	2.22	7	2
1:A:124:LEU:HD11	1:A:145:ILE:HG21	0.69	1.65	19	3
1:A:142:SER:C	1:A:143:LEU:HD12	0.69	2.13	10	1
1:A:129:GLU:HG2	1:A:144:VAL:HG22	0.69	1.63	19	9
1:A:125:SER:O	1:A:147:ILE:HD11	0.69	1.88	3	4
1:A:33:VAL:HG12	1:A:99:LEU:CD2	0.69	2.17	7	2
1:A:99:LEU:HB2	1:A:124:LEU:HD13	0.68	1.63	5	3
1:A:92:LEU:HD21	1:A:121:ASN:OD1	0.68	1.89	6	2
1:A:38:CYS:HA	1:A:143:LEU:HD23	0.68	1.63	18	5
1:A:111:LEU:HD23	1:A:114:GLN:O	0.68	1.89	14	2
1:A:92:LEU:HD11	1:A:121:ASN:ND2	0.67	2.04	11	2
1:A:48:LEU:HD22	1:A:66:TRP:CD1	0.67	2.24	17	5
1:A:36:VAL:HG11	1:A:68:PHE:CE2	0.67	2.24	4	6
1:A:42:GLN:OE1	1:A:141:LEU:HD23	0.67	1.89	10	1
1:A:100:LEU:HD23	1:A:121:ASN:HB3	0.67	1.67	8	6
1:A:36:VAL:HG21	1:A:68:PHE:CE2	0.67	2.24	11	7
1:A:43:ILE:HD13	1:A:78:LEU:HB3	0.67	1.67	20	2
1:A:111:LEU:CD1	1:A:116:VAL:HG11	0.66	2.20	20	2
1:A:92:LEU:HD11	1:A:102:ASN:HB2	0.66	1.68	8	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:92:LEU:HD21	1:A:102:ASN:HB2	0.66	1.68	11	1
1:A:92:LEU:HD11	1:A:121:ASN:OD1	0.66	1.91	6	2
1:A:84:LEU:HD21	1:A:132:VAL:CG2	0.66	2.20	10	4
1:A:100:LEU:HD13	1:A:122:GLN:O	0.65	1.91	19	2
1:A:103:ASP:CG	1:A:118:LYS:HA	0.65	2.17	4	20
1:A:78:LEU:HD13	1:A:84:LEU:CD1	0.65	2.22	3	1
1:A:69:GLY:CA	1:A:78:LEU:HD21	0.65	2.22	12	4
1:A:38:CYS:HA	1:A:143:LEU:HD13	0.65	1.69	15	7
1:A:40:THR:HG21	1:A:142:SER:CB	0.65	2.21	10	3
1:A:99:LEU:C	1:A:100:LEU:HD12	0.65	2.15	8	2
1:A:69:GLY:HA2	1:A:78:LEU:HD12	0.64	1.69	4	3
1:A:37:ILE:HD12	1:A:146:PHE:CD1	0.63	2.28	1	1
1:A:130:ILE:HG13	1:A:145:ILE:HD11	0.63	1.70	4	2
1:A:100:LEU:HD23	1:A:121:ASN:OD1	0.63	1.93	6	1
1:A:83:ARG:NH1	1:A:136:VAL:HG23	0.63	2.08	19	1
1:A:141:LEU:HD22	1:A:143:LEU:CD2	0.63	2.24	20	6
1:A:99:LEU:CB	1:A:124:LEU:HD22	0.63	2.23	16	1
1:A:130:ILE:CD1	1:A:145:ILE:HD11	0.62	2.24	18	4
1:A:42:GLN:OE1	1:A:141:LEU:HD12	0.62	1.94	18	1
1:A:99:LEU:HB3	1:A:124:LEU:HD22	0.62	1.71	16	1
1:A:69:GLY:HA3	1:A:86:ASN:O	0.62	1.94	17	20
1:A:101:LEU:HD12	1:A:122:GLN:O	0.62	1.95	7	2
1:A:68:PHE:CD2	1:A:76:TYR:CG	0.62	2.88	11	10
1:A:34:CYS:SG	1:A:48:LEU:HD22	0.62	2.34	9	2
1:A:68:PHE:CD1	1:A:76:TYR:HB2	0.61	2.30	19	2
1:A:101:LEU:HD11	1:A:124:LEU:HD13	0.61	1.71	19	1
1:A:101:LEU:HD11	1:A:124:LEU:HA	0.61	1.71	6	4
1:A:81:ILE:CD1	1:A:84:LEU:HD12	0.61	2.21	18	2
1:A:33:VAL:CG2	1:A:93:LEU:HD22	0.61	2.25	17	1
1:A:99:LEU:HB2	1:A:124:LEU:HD22	0.61	1.73	15	1
1:A:100:LEU:HD23	1:A:122:GLN:O	0.61	1.94	10	5
1:A:99:LEU:HD12	1:A:99:LEU:N	0.61	2.10	7	2
1:A:131:THR:HG22	1:A:140:ILE:CG2	0.60	2.26	1	18
1:A:36:VAL:HG21	1:A:76:TYR:CE1	0.60	2.31	7	1
1:A:142:SER:C	1:A:143:LEU:HD22	0.60	2.22	9	8
1:A:68:PHE:CZ	1:A:91:ILE:HD12	0.60	2.32	16	6
1:A:88:HIS:CE1	1:A:105:SER:OG	0.60	2.55	6	8
1:A:123:LEU:HD23	1:A:124:LEU:O	0.60	1.96	11	4
1:A:33:VAL:HG13	1:A:93:LEU:HD22	0.59	1.74	19	2
1:A:111:LEU:HD22	1:A:116:VAL:CG1	0.59	2.27	8	2
1:A:78:LEU:HD23	1:A:84:LEU:CD1	0.59	2.26	17	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:100:LEU:HD23	1:A:122:GLN:C	0.59	2.22	10	5
1:A:93:LEU:HD13	1:A:99:LEU:HG	0.58	1.75	14	3
1:A:147:ILE:HD12	1:A:147:ILE:N	0.58	2.13	20	4
1:A:67:THR:HG23	1:A:90:GLN:CD	0.58	2.23	12	5
1:A:136:VAL:HG11	1:A:139:ASP:CB	0.58	2.27	5	1
1:A:33:VAL:CG1	1:A:93:LEU:HD12	0.58	2.28	10	1
1:A:40:THR:HG23	1:A:142:SER:HB2	0.58	1.75	13	1
1:A:81:ILE:HB	1:A:84:LEU:HD13	0.58	1.73	6	2
1:A:33:VAL:HG11	1:A:93:LEU:HD12	0.58	1.74	10	1
1:A:93:LEU:CD1	1:A:99:LEU:HD11	0.58	2.25	10	1
1:A:111:LEU:HD12	1:A:116:VAL:CG1	0.58	2.27	20	2
1:A:38:CYS:SG	1:A:43:ILE:HD12	0.58	2.39	7	1
1:A:32:ILE:HA	1:A:49:SER:HB3	0.58	1.75	13	20
1:A:110:TRP:NE1	1:A:115:LYS:HB2	0.58	2.14	8	16
1:A:124:LEU:HD21	1:A:145:ILE:HD13	0.58	1.75	8	1
1:A:91:ILE:HG12	1:A:101:LEU:HD13	0.57	1.75	14	1
1:A:91:ILE:HD11	1:A:145:ILE:HD11	0.57	1.75	19	1
1:A:65:VAL:HG22	1:A:92:LEU:CB	0.57	2.29	7	8
1:A:69:GLY:N	1:A:78:LEU:HD21	0.57	2.14	20	2
1:A:71:ASN:OD1	1:A:73:ALA:HB3	0.57	1.99	18	2
1:A:65:VAL:HG13	1:A:91:ILE:C	0.57	2.24	15	17
1:A:124:LEU:HD12	1:A:147:ILE:HG12	0.57	1.75	5	1
1:A:99:LEU:O	1:A:100:LEU:HD12	0.57	2.00	8	6
1:A:100:LEU:HD13	1:A:121:ASN:HB3	0.57	1.76	16	1
1:A:65:VAL:HG13	1:A:91:ILE:O	0.57	2.00	13	18
1:A:99:LEU:CB	1:A:124:LEU:HD13	0.56	2.30	1	2
1:A:92:LEU:HD23	1:A:92:LEU:N	0.56	2.15	11	2
1:A:67:THR:O	1:A:75:ASP:N	0.56	2.38	13	11
1:A:93:LEU:C	1:A:93:LEU:HD13	0.56	2.25	2	3
1:A:117:GLU:O	1:A:120:SER:HB3	0.56	2.01	6	2
1:A:126:GLN:HA	1:A:147:ILE:HD13	0.56	1.77	14	4
1:A:81:ILE:N	1:A:81:ILE:HD12	0.56	2.15	14	3
1:A:37:ILE:HG23	1:A:45:ILE:CG1	0.56	2.31	15	12
1:A:43:ILE:HD12	1:A:143:LEU:HD21	0.56	1.77	19	3
1:A:33:VAL:CG2	1:A:50:ALA:HB3	0.55	2.31	17	1
1:A:84:LEU:HD21	1:A:132:VAL:HG23	0.55	1.77	15	10
1:A:84:LEU:CD2	1:A:132:VAL:HG21	0.55	2.30	10	2
1:A:124:LEU:C	1:A:124:LEU:HD22	0.55	2.27	9	3
1:A:68:PHE:CD2	1:A:89:PHE:CE2	0.55	2.94	11	7
1:A:48:LEU:HD23	1:A:66:TRP:CE3	0.55	2.36	1	6
1:A:78:LEU:HD12	1:A:78:LEU:O	0.55	2.02	8	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:33:VAL:HG21	1:A:93:LEU:HD22	0.55	1.77	17	1
1:A:67:THR:HG22	1:A:87:LYS:HB3	0.55	1.79	19	2
1:A:78:LEU:HD12	1:A:79:GLY:O	0.54	2.03	11	2
1:A:48:LEU:HD11	1:A:68:PHE:HZ	0.54	1.63	17	1
1:A:36:VAL:HG21	1:A:68:PHE:CZ	0.54	2.37	17	2
1:A:33:VAL:CG1	1:A:99:LEU:HD11	0.54	2.27	15	1
1:A:93:LEU:HD23	1:A:99:LEU:HG	0.54	1.79	15	1
1:A:68:PHE:CG	1:A:89:PHE:CE2	0.53	2.97	8	13
1:A:68:PHE:CD2	1:A:76:TYR:CD2	0.53	2.96	13	3
1:A:65:VAL:HG12	1:A:90:GLN:HG2	0.53	1.78	15	11
1:A:143:LEU:HD12	1:A:143:LEU:N	0.53	2.18	10	1
1:A:66:TRP:HB3	1:A:68:PHE:CE1	0.53	2.38	19	2
1:A:88:HIS:CD2	1:A:105:SER:OG	0.53	2.61	18	12
1:A:42:GLN:CD	1:A:141:LEU:HD11	0.53	2.28	12	1
1:A:88:HIS:CE1	1:A:132:VAL:HB	0.53	2.39	8	18
1:A:100:LEU:C	1:A:101:LEU:HD22	0.53	2.29	2	2
1:A:103:ASP:O	1:A:119:ASN:N	0.53	2.42	14	20
1:A:43:ILE:HG23	1:A:44:PRO:HD2	0.53	1.81	11	9
1:A:99:LEU:HD13	1:A:124:LEU:HD23	0.53	1.80	7	1
1:A:88:HIS:CG	1:A:105:SER:HB2	0.52	2.39	6	8
1:A:65:VAL:HG22	1:A:92:LEU:HB3	0.52	1.79	3	2
1:A:68:PHE:N	1:A:68:PHE:CD1	0.52	2.77	16	12
1:A:87:LYS:CB	1:A:104:ILE:HD12	0.52	2.35	1	3
1:A:48:LEU:HD21	1:A:68:PHE:HZ	0.52	1.65	9	5
1:A:92:LEU:HD12	1:A:100:LEU:HB2	0.52	1.81	14	1
1:A:68:PHE:CE1	1:A:91:ILE:CD1	0.52	2.92	11	1
1:A:101:LEU:HD12	1:A:124:LEU:CD2	0.52	2.34	11	1
1:A:40:THR:CG2	1:A:142:SER:HB2	0.52	2.35	13	6
1:A:129:GLU:CD	1:A:144:VAL:HG22	0.52	2.30	12	2
1:A:39:THR:OG1	1:A:144:VAL:HG23	0.52	2.05	15	2
1:A:68:PHE:CD1	1:A:76:TYR:CB	0.52	2.93	19	1
1:A:111:LEU:HD23	1:A:128:ASP:OD2	0.52	2.05	3	1
1:A:90:GLN:OE1	1:A:104:ILE:HG21	0.52	2.04	17	3
1:A:92:LEU:HD23	1:A:102:ASN:HB2	0.52	1.81	17	2
1:A:88:HIS:CD2	1:A:105:SER:HB2	0.51	2.40	6	8
1:A:43:ILE:CG2	1:A:44:PRO:HD2	0.51	2.35	14	20
1:A:38:CYS:SG	1:A:141:LEU:HD21	0.51	2.44	13	2
1:A:141:LEU:HD22	1:A:143:LEU:HD22	0.51	1.81	17	2
1:A:84:LEU:HD22	1:A:88:HIS:CE1	0.51	2.41	2	2
1:A:110:TRP:O	1:A:130:ILE:HA	0.51	2.05	14	7
1:A:68:PHE:CD2	1:A:89:PHE:CZ	0.51	2.99	7	6

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:84:LEU:HD12	1:A:84:LEU:N	0.51	2.21	1	2
1:A:141:LEU:C	1:A:141:LEU:HD23	0.51	2.30	11	1
1:A:68:PHE:CD2	1:A:76:TYR:CB	0.51	2.94	1	13
1:A:81:ILE:HD11	1:A:141:LEU:HD12	0.51	1.83	11	1
1:A:88:HIS:CE1	1:A:105:SER:HB3	0.50	2.41	8	12
1:A:43:ILE:CG2	1:A:76:TYR:CZ	0.50	2.94	3	5
1:A:36:VAL:HG23	1:A:48:LEU:CD1	0.50	2.36	11	1
1:A:65:VAL:HG23	1:A:91:ILE:O	0.50	2.06	17	1
1:A:33:VAL:CG2	1:A:50:ALA:N	0.50	2.75	8	19
1:A:48:LEU:HD23	1:A:66:TRP:CG	0.50	2.40	15	8
1:A:136:VAL:CG1	1:A:139:ASP:CB	0.50	2.89	5	1
1:A:101:LEU:HD11	1:A:130:ILE:HG12	0.50	1.83	9	1
1:A:42:GLN:HB2	1:A:43:ILE:HD12	0.50	1.83	14	1
1:A:40:THR:CG2	1:A:142:SER:CB	0.50	2.89	17	4
1:A:68:PHE:CD2	1:A:76:TYR:CD1	0.50	3.00	11	1
1:A:36:VAL:CG2	1:A:48:LEU:HD11	0.50	2.37	19	2
1:A:131:THR:HG23	1:A:140:ILE:CG2	0.50	2.36	5	1
1:A:92:LEU:H	1:A:92:LEU:HD23	0.50	1.67	13	1
1:A:67:THR:HG23	1:A:90:GLN:HG2	0.49	1.82	4	3
1:A:65:VAL:HG23	1:A:91:ILE:C	0.49	2.32	17	1
1:A:92:LEU:HD21	1:A:121:ASN:ND2	0.49	2.22	17	1
1:A:87:LYS:HB2	1:A:104:ILE:HD12	0.49	1.85	5	3
1:A:130:ILE:HD11	1:A:145:ILE:HG13	0.49	1.82	19	1
1:A:33:VAL:HG23	1:A:49:SER:C	0.49	2.32	5	17
1:A:68:PHE:CE2	1:A:76:TYR:CD2	0.49	3.00	2	3
1:A:33:VAL:HG12	1:A:99:LEU:CD1	0.49	2.28	15	2
1:A:66:TRP:O	1:A:90:GLN:HA	0.49	2.07	11	14
1:A:36:VAL:HG23	1:A:48:LEU:HD11	0.49	1.83	19	3
1:A:129:GLU:HG3	1:A:144:VAL:HG22	0.49	1.82	1	1
1:A:49:SER:O	1:A:66:TRP:HZ2	0.49	1.91	17	10
1:A:99:LEU:HD13	1:A:124:LEU:CD2	0.49	2.38	7	1
1:A:88:HIS:CD2	1:A:132:VAL:HG11	0.49	2.43	17	16
1:A:78:LEU:HD13	1:A:84:LEU:HD23	0.49	1.83	8	1
1:A:43:ILE:HD12	1:A:143:LEU:HD11	0.48	1.83	2	1
1:A:109:THR:HG22	1:A:130:ILE:CG2	0.48	2.38	2	15
1:A:33:VAL:HG21	1:A:50:ALA:CB	0.48	2.38	17	1
1:A:88:HIS:CD2	1:A:132:VAL:CG1	0.48	2.97	18	17
1:A:83:ARG:NE	1:A:136:VAL:HG21	0.48	2.23	12	1
1:A:48:LEU:HD11	1:A:68:PHE:CZ	0.48	2.43	17	1
1:A:88:HIS:NE2	1:A:132:VAL:HB	0.48	2.23	14	15
1:A:43:ILE:HG21	1:A:76:TYR:CE1	0.48	2.43	18	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:101:LEU:CD1	1:A:130:ILE:HD11	0.48	2.36	11	1
1:A:42:GLN:HG3	1:A:43:ILE:N	0.47	2.23	2	1
1:A:111:LEU:HD13	1:A:128:ASP:OD2	0.47	2.09	4	2
1:A:36:VAL:HG23	1:A:48:LEU:HD13	0.47	1.84	11	1
1:A:78:LEU:CD2	1:A:84:LEU:HD13	0.47	2.33	17	1
1:A:36:VAL:CG2	1:A:76:TYR:CE1	0.47	2.97	7	1
1:A:48:LEU:HB3	1:A:66:TRP:CE2	0.47	2.45	17	9
1:A:68:PHE:CG	1:A:76:TYR:HB3	0.47	2.45	11	2
1:A:101:LEU:HD11	1:A:130:ILE:CD1	0.47	2.39	9	3
1:A:68:PHE:CG	1:A:76:TYR:CB	0.47	2.97	13	1
1:A:36:VAL:HG21	1:A:68:PHE:HE2	0.47	1.69	10	6
1:A:43:ILE:HG21	1:A:76:TYR:CE2	0.47	2.45	5	4
1:A:68:PHE:CD2	1:A:76:TYR:HB2	0.47	2.45	8	7
1:A:38:CYS:SG	1:A:43:ILE:HD13	0.47	2.50	14	1
1:A:131:THR:CG2	1:A:140:ILE:CG2	0.46	2.93	20	20
1:A:142:SER:O	1:A:143:LEU:HD22	0.46	2.10	6	6
1:A:84:LEU:CD2	1:A:88:HIS:CE1	0.46	2.99	2	2
1:A:42:GLN:CD	1:A:141:LEU:HD12	0.46	2.35	18	1
1:A:91:ILE:N	1:A:91:ILE:HD12	0.46	2.25	11	1
1:A:124:LEU:CD2	1:A:145:ILE:HG21	0.46	2.40	11	2
1:A:99:LEU:HD23	1:A:100:LEU:H	0.46	1.70	16	1
1:A:124:LEU:HD23	1:A:147:ILE:CD1	0.46	2.40	2	1
1:A:117:GLU:O	1:A:120:SER:OG	0.46	2.32	5	1
1:A:136:VAL:HG11	1:A:139:ASP:HB2	0.46	1.86	5	1
1:A:83:ARG:O	1:A:107:ASN:ND2	0.46	2.49	13	3
1:A:92:LEU:HD22	1:A:102:ASN:HB2	0.46	1.87	13	1
1:A:111:LEU:C	1:A:111:LEU:HD12	0.46	2.35	17	13
1:A:49:SER:O	1:A:64:LYS:CE	0.46	2.64	17	16
1:A:91:ILE:HG23	1:A:101:LEU:HD22	0.46	1.88	12	1
1:A:69:GLY:CA	1:A:78:LEU:HD11	0.46	2.41	1	1
1:A:67:THR:HA	1:A:90:GLN:HG2	0.46	1.87	19	1
1:A:89:PHE:CZ	1:A:143:LEU:HD13	0.46	2.44	19	1
1:A:43:ILE:HG12	1:A:78:LEU:HD23	0.46	1.88	3	1
1:A:81:ILE:CD1	1:A:141:LEU:HD12	0.46	2.40	11	1
1:A:36:VAL:HG22	1:A:145:ILE:CD1	0.46	2.41	20	1
1:A:130:ILE:CG1	1:A:145:ILE:HD11	0.45	2.41	8	2
1:A:65:VAL:CG1	1:A:91:ILE:O	0.45	2.64	13	11
1:A:43:ILE:HD13	1:A:78:LEU:CD2	0.45	2.39	6	1
1:A:91:ILE:CD1	1:A:145:ILE:HD11	0.45	2.40	19	1
1:A:48:LEU:HG	1:A:66:TRP:CD1	0.45	2.46	15	8
1:A:84:LEU:N	1:A:84:LEU:CD1	0.45	2.78	1	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:69:GLY:CA	1:A:78:LEU:HD12	0.45	2.40	4	1
1:A:92:LEU:HD13	1:A:121:ASN:OD1	0.45	2.11	3	1
1:A:83:ARG:CZ	1:A:136:VAL:HG21	0.45	2.41	12	1
1:A:88:HIS:O	1:A:105:SER:N	0.45	2.50	13	15
1:A:31:ASN:O	1:A:49:SER:HB3	0.45	2.12	17	2
1:A:118:LYS:O	1:A:119:ASN:C	0.45	2.60	5	9
1:A:124:LEU:CD2	1:A:145:ILE:HD13	0.45	2.42	8	1
1:A:124:LEU:HD23	1:A:147:ILE:HG12	0.45	1.88	3	2
1:A:92:LEU:CD2	1:A:102:ASN:HB2	0.45	2.41	11	1
1:A:68:PHE:O	1:A:88:HIS:N	0.45	2.50	19	16
1:A:99:LEU:HB3	1:A:124:LEU:HD13	0.45	1.87	1	1
1:A:48:LEU:HD21	1:A:68:PHE:CZ	0.45	2.46	15	2
1:A:76:TYR:HE2	1:A:78:LEU:HD23	0.45	1.72	7	1
1:A:91:ILE:HG23	1:A:101:LEU:HD12	0.44	1.89	1	1
1:A:66:TRP:O	1:A:90:GLN:CG	0.44	2.66	13	9
1:A:92:LEU:HD21	1:A:121:ASN:HD22	0.44	1.72	19	3
1:A:35:ARG:HE	1:A:45:ILE:HG21	0.44	1.69	15	1
1:A:130:ILE:N	1:A:143:LEU:O	0.44	2.50	10	3
1:A:67:THR:HA	1:A:90:GLN:CG	0.44	2.43	3	1
1:A:68:PHE:CE2	1:A:76:TYR:CG	0.44	3.05	17	2
1:A:81:ILE:HD13	1:A:84:LEU:HD22	0.44	1.89	8	1
1:A:69:GLY:HA2	1:A:78:LEU:HD21	0.44	1.89	11	2
1:A:39:THR:HG23	1:A:144:VAL:HG21	0.44	1.89	9	1
1:A:88:HIS:NE2	1:A:132:VAL:CG1	0.44	2.81	20	11
1:A:101:LEU:HD12	1:A:124:LEU:HG	0.44	1.88	11	1
1:A:50:ALA:HB3	1:A:93:LEU:CD2	0.44	2.43	12	1
1:A:78:LEU:C	1:A:78:LEU:HD12	0.44	2.38	16	2
1:A:36:VAL:HG11	1:A:68:PHE:CZ	0.44	2.48	7	1
1:A:110:TRP:O	1:A:130:ILE:HG23	0.43	2.13	19	3
1:A:117:GLU:O	1:A:120:SER:HB2	0.43	2.13	14	11
1:A:101:LEU:HD22	1:A:101:LEU:N	0.43	2.27	2	1
1:A:90:GLN:CG	1:A:104:ILE:HD13	0.43	2.43	12	1
1:A:43:ILE:CD1	1:A:143:LEU:HD21	0.43	2.44	17	2
1:A:101:LEU:HD12	1:A:124:LEU:CG	0.43	2.44	11	1
1:A:76:TYR:HE1	1:A:78:LEU:HD23	0.43	1.73	15	1
1:A:136:VAL:HG11	1:A:139:ASP:HB3	0.43	1.90	5	1
1:A:33:VAL:HG21	1:A:50:ALA:HB3	0.43	1.90	17	1
1:A:124:LEU:N	1:A:124:LEU:CD1	0.43	2.82	2	3
1:A:100:LEU:HD13	1:A:122:GLN:C	0.43	2.37	19	1
1:A:129:GLU:CG	1:A:143:LEU:O	0.43	2.67	2	3
1:A:124:LEU:HD21	1:A:147:ILE:CG1	0.43	2.44	20	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:92:LEU:HD11	1:A:100:LEU:CD2	0.43	2.44	20	1
1:A:88:HIS:CG	1:A:105:SER:HB3	0.43	2.49	16	1
1:A:64:LYS:O	1:A:66:TRP:CZ3	0.43	2.72	17	1
1:A:143:LEU:N	1:A:143:LEU:CD1	0.43	2.82	10	1
1:A:101:LEU:CD1	1:A:124:LEU:HD13	0.43	2.43	19	1
1:A:130:ILE:O	1:A:143:LEU:HD12	0.42	2.13	14	2
1:A:49:SER:O	1:A:64:LYS:HE2	0.42	2.14	15	2
1:A:42:GLN:OE1	1:A:141:LEU:HD11	0.42	2.14	1	1
1:A:48:LEU:CD2	1:A:66:TRP:CG	0.42	3.03	5	6
1:A:83:ARG:HG2	1:A:133:GLY:CA	0.42	2.44	13	1
1:A:89:PHE:CD1	1:A:89:PHE:N	0.42	2.87	3	2
1:A:109:THR:CG2	1:A:130:ILE:CG2	0.42	2.97	14	6
1:A:124:LEU:HD22	1:A:145:ILE:HG21	0.42	1.90	12	1
1:A:89:PHE:HA	1:A:104:ILE:HG12	0.42	1.91	15	3
1:A:124:LEU:HD21	1:A:147:ILE:HG13	0.42	1.89	19	1
1:A:99:LEU:N	1:A:99:LEU:CD1	0.42	2.80	7	1
1:A:43:ILE:CD1	1:A:78:LEU:CB	0.42	2.98	2	1
1:A:65:VAL:HA	1:A:91:ILE:O	0.42	2.15	4	3
1:A:43:ILE:CD1	1:A:78:LEU:HD22	0.42	2.42	6	1
1:A:93:LEU:HD13	1:A:93:LEU:O	0.42	2.15	1	1
1:A:70:ARG:N	1:A:86:ASN:O	0.42	2.53	13	2
1:A:70:ARG:HD2	1:A:81:ILE:O	0.42	2.14	13	1
1:A:66:TRP:N	1:A:91:ILE:O	0.42	2.48	20	7
1:A:81:ILE:HD12	1:A:81:ILE:H	0.42	1.75	12	1
1:A:103:ASP:OD2	1:A:117:GLU:O	0.42	2.38	6	1
1:A:111:LEU:HD22	1:A:116:VAL:HG13	0.42	1.92	8	1
1:A:147:ILE:HD12	1:A:147:ILE:H	0.42	1.73	1	2
1:A:117:GLU:O	1:A:120:SER:CB	0.42	2.67	5	1
1:A:123:LEU:C	1:A:123:LEU:HD13	0.42	2.40	17	1
1:A:83:ARG:CD	1:A:139:ASP:CB	0.42	2.97	19	1
1:A:129:GLU:HA	1:A:143:LEU:O	0.41	2.15	14	4
1:A:90:GLN:O	1:A:102:ASN:N	0.41	2.50	14	3
1:A:33:VAL:HG11	1:A:93:LEU:HD13	0.41	1.90	12	1
1:A:92:LEU:O	1:A:99:LEU:HD23	0.41	2.14	2	1
1:A:103:ASP:OD1	1:A:103:ASP:N	0.41	2.52	10	2
1:A:92:LEU:HD12	1:A:92:LEU:H	0.41	1.73	8	1
1:A:101:LEU:HD11	1:A:130:ILE:CG1	0.41	2.45	9	1
1:A:103:ASP:HB3	1:A:109:THR:HB	0.41	1.91	9	1
1:A:67:THR:HG21	1:A:87:LYS:NZ	0.41	2.29	10	1
1:A:43:ILE:HG21	1:A:76:TYR:CZ	0.41	2.50	6	1
1:A:66:TRP:O	1:A:90:GLN:HG2	0.41	2.15	9	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:83:ARG:NH1	1:A:136:VAL:HG21	0.41	2.31	16	1
1:A:33:VAL:HG13	1:A:99:LEU:HD11	0.41	1.92	17	1
1:A:36:VAL:HG11	1:A:68:PHE:HE2	0.41	1.72	12	2
1:A:78:LEU:C	1:A:78:LEU:CD2	0.41	2.94	1	1
1:A:88:HIS:CD2	1:A:105:SER:HB3	0.41	2.51	5	2
1:A:100:LEU:HD23	1:A:121:ASN:CG	0.41	2.40	6	1
1:A:130:ILE:O	1:A:143:LEU:CD1	0.41	2.69	7	1
1:A:78:LEU:HD13	1:A:84:LEU:CD2	0.41	2.45	8	1
1:A:40:THR:CG2	1:A:142:SER:OG	0.41	2.68	17	1
1:A:46:ARG:HB2	1:A:76:TYR:CZ	0.41	2.51	2	1
1:A:101:LEU:N	1:A:101:LEU:CD2	0.41	2.83	2	1
1:A:68:PHE:CB	1:A:89:PHE:CE2	0.41	3.04	8	1
1:A:83:ARG:HG3	1:A:139:ASP:HB3	0.41	1.92	11	1
1:A:66:TRP:O	1:A:91:ILE:N	0.41	2.51	13	1
1:A:141:LEU:HD23	1:A:141:LEU:C	0.41	2.41	3	1
1:A:88:HIS:CE1	1:A:105:SER:CB	0.41	3.04	18	3
1:A:130:ILE:HD11	1:A:145:ILE:HG12	0.41	1.92	4	1
1:A:120:SER:OG	1:A:122:GLN:NE2	0.41	2.54	6	1
1:A:124:LEU:HD11	1:A:145:ILE:CG2	0.41	2.45	7	1
1:A:101:LEU:HD12	1:A:101:LEU:O	0.41	2.15	16	1
1:A:35:ARG:N	1:A:146:PHE:O	0.41	2.54	18	1
1:A:111:LEU:HD12	1:A:111:LEU:C	0.41	2.40	18	1
1:A:69:GLY:C	1:A:78:LEU:HD21	0.41	2.41	20	1
1:A:71:ASN:ND2	1:A:86:ASN:ND2	0.41	2.69	11	1
1:A:84:LEU:HD22	1:A:88:HIS:ND1	0.40	2.31	2	1
1:A:34:CYS:O	1:A:48:LEU:HB2	0.40	2.17	9	1
1:A:117:GLU:CG	1:A:120:SER:CB	0.40	2.99	12	1
1:A:40:THR:HG21	1:A:142:SER:H	0.40	1.76	17	2
1:A:33:VAL:CG2	1:A:50:ALA:CB	0.40	2.98	17	1
1:A:33:VAL:CG1	1:A:93:LEU:CD1	0.40	2.98	10	1
1:A:68:PHE:N	1:A:89:PHE:O	0.40	2.46	12	1
1:A:85:SER:O	1:A:86:ASN:C	0.40	2.64	17	1
1:A:43:ILE:CD1	1:A:143:LEU:HD11	0.40	2.46	2	1
1:A:101:LEU:HD23	1:A:124:LEU:HD11	0.40	1.93	12	1
1:A:32:ILE:CG2	1:A:48:LEU:O	0.40	2.69	13	1
1:A:84:LEU:CD2	1:A:132:VAL:CG2	0.40	2.97	5	1
1:A:125:SER:CB	1:A:128:ASP:HB2	0.40	2.46	9	1
1:A:101:LEU:HD12	1:A:124:LEU:HD21	0.40	1.92	11	1
1:A:76:TYR:CD1	1:A:76:TYR:C	0.40	2.99	15	1
1:A:66:TRP:CD1	1:A:75:ASP:CG	0.40	3.00	10	1
1:A:110:TRP:O	1:A:131:THR:N	0.40	2.53	14	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:35:ARG:CG	1:A:45:ILE:CG2	0.40	3.00	15	1
1:A:49:SER:O	1:A:64:LYS:NZ	0.40	2.55	16	1

6.3 Torsion angles [i](#)

6.3.1 Protein backbone [i](#)

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	105/151 (70%)	94±1 (89±1%)	8±1 (8±1%)	3±1 (3±1%)	5	38
2	B	0	-	-	-	-	-
All	All	2100/3220 (65%)	1874 (89%)	163 (8%)	63 (3%)	5	38

All 7 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	31	ASN	20
1	A	119	ASN	20
1	A	79	GLY	7
1	A	80	ASN	7
1	A	104	ILE	5
1	A	42	GLN	2
1	A	128	ASP	2

6.3.2 Protein sidechains [i](#)

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	95/137 (69%)	73±4 (77±4%)	22±4 (23±4%)	2	27
2	B	0	-	-	-	-

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	1900/2920 (65%)	1454 (77%)	446 (23%)	2 27

All 61 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	49	SER	20
1	A	67	THR	20
1	A	74	CYS	20
1	A	111	LEU	20
1	A	125	SER	19
1	A	146	PHE	18
1	A	31	ASN	15
1	A	99	LEU	15
1	A	46	ARG	15
1	A	120	SER	14
1	A	150	LYS	13
1	A	39	THR	12
1	A	68	PHE	12
1	A	126	GLN	12
1	A	35	ARG	12
1	A	105	SER	12
1	A	137	GLU	11
1	A	77	HIS	10
1	A	83	ARG	10
1	A	92	LEU	10
1	A	101	LEU	10
1	A	82	SER	9
1	A	51	ASP	8
1	A	78	LEU	8
1	A	145	ILE	7
1	A	87	LYS	7
1	A	136	VAL	7
1	A	141	LEU	6
1	A	47	ASP	6
1	A	80	ASN	5
1	A	142	SER	5
1	A	114	GLN	5
1	A	30	GLU	5
1	A	115	LYS	5
1	A	124	LEU	4
1	A	119	ASN	4

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Mol	Chain	Res	Type	Models (Total)
1	A	143	LEU	4
1	A	117	GLU	4
1	A	149	ASP	4
1	A	86	ASN	4
1	A	43	ILE	4
1	A	71	ASN	4
1	A	90	GLN	3
1	A	48	LEU	3
1	A	138	SER	3
1	A	93	LEU	2
1	A	148	ASN	2
1	A	89	PHE	2
1	A	139	ASP	2
1	A	38	CYS	2
1	A	130	ILE	2
1	A	36	VAL	1
1	A	42	GLN	1
1	A	107	ASN	1
1	A	85	SER	1
1	A	129	GLU	1
1	A	100	LEU	1
1	A	75	ASP	1
1	A	118	LYS	1
1	A	33	VAL	1
1	A	123	LEU	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
2	TPO	B	169	2	8,10,11	1.03±0.02	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
2	TPO	B	169	2	10,14,16	1.18±0.03	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
2	TPO	B	169	2	-	0±0,9,11,13	-

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 oligosaccharides in this entry.

6.6 Ligand geometry [i](#)

There are no ligands in this entry.

6.7 Other polymers [i](#)

There are no such molecules in this entry.

6.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

7 Chemical shift validation

No chemical shift data were provided