Full wwPDB NMR Structure Validation Report ⓘ

Jan 5, 2022 – 09:16 pm GMT

PDB ID	:	7B9X
Title	:	NMR2 structure of TRIM24-BD in complex with a precursor of IACS-9571
Authors	:	Orts, J.; Torres, F.; Milbradt, A.G.; Walser, R.
Deposited on	:	2020-12-14

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/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:
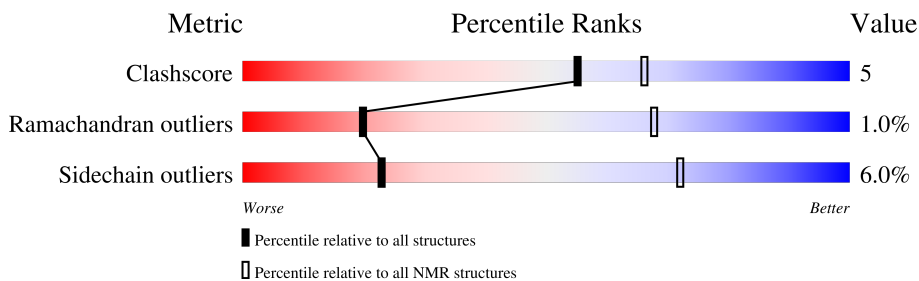
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:
SOLUTION NMR

The overall completeness of chemical shifts assignment is 1%.

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	Percentile Ranks	Value
Clashscore		5
Ramachandran outliers		1.0%
Sidechain outliers		6.0%

Worse   *Better*

▮ Percentile relative to all structures

▯ Percentile relative to all NMR structures

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 <=5%

Mol	Chain	Length	Quality of chain
1	A	106	88% 12%

2 Ensemble composition and analysis ⓘ

This entry contains 10 models. Model 6 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:901-A:1006 (106)	0.86	6

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

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

The models can be grouped into 2 clusters. No single-model clusters were found.

| Cluster number	Models
1	1, 4, 6, 7, 8, 9, 10
2	2, 3, 5

3 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 1839 atoms, of which 912 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Transcription intermediary factor 1-alpha.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	106	1757	573	873	138	167	6	0

- Molecule 2 is N-{6-[3-(4-Aminobutoxy)-5-propoxyphenoxy]-1,3-dimethyl-2-oxo-2,3-dihydro-1H-1,3-benzodiazol-5-yl}-3,4-dimethoxybenzene-1-sulfonamide (three-letter code: T52) (formula: $C_{30}H_{39}N_4O_8S$) (labeled as "Ligand of Interest" by depositor).


T52
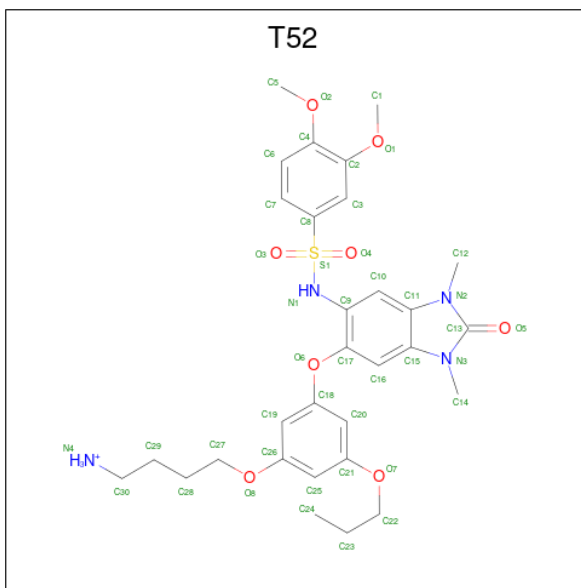
Mol	Chain	Residues	Atoms					
			Total	C	H	N	O	S
2	A	1	82	30	39	4	8	1

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: Transcription intermediary factor 1-alpha
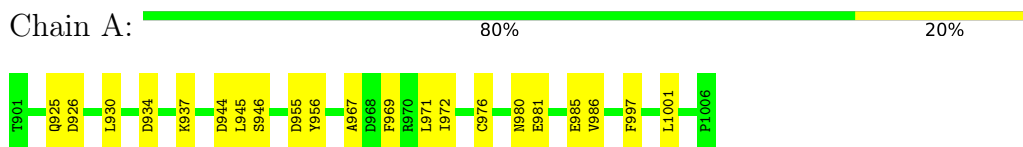
Chain A:
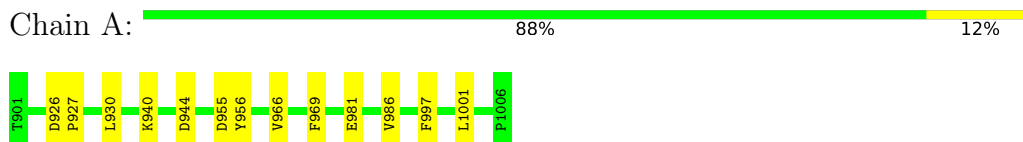
4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

• Molecule 1: Transcription intermediary factor 1-alpha

Chain A:

4.2.2 Score per residue for model 2

• Molecule 1: Transcription intermediary factor 1-alpha

Chain A:

4.2.3 Score per residue for model 3

• Molecule 1: Transcription intermediary factor 1-alpha

Chain A:

4.2.4 Score per residue for model 4

• Molecule 1: Transcription intermediary factor 1-alpha

Chain A:

4.2.5 Score per residue for model 5

• Molecule 1: Transcription intermediary factor 1-alpha

Chain A:

4.2.6 Score per residue for model 6 (medoid)

• Molecule 1: Transcription intermediary factor 1-alpha

Chain A:
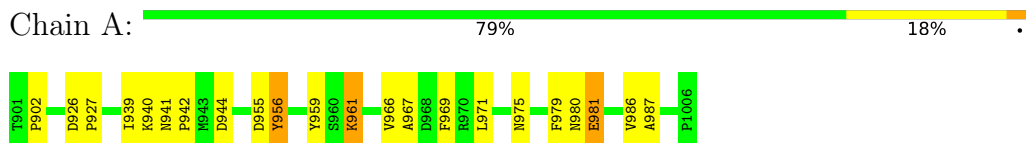
4.2.7 Score per residue for model 7

• Molecule 1: Transcription intermediary factor 1-alpha

Chain A:
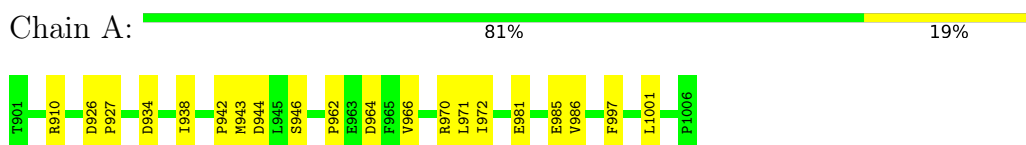
4.2.8   Score per residue for model 8

• Molecule 1: Transcription intermediary factor 1-alpha
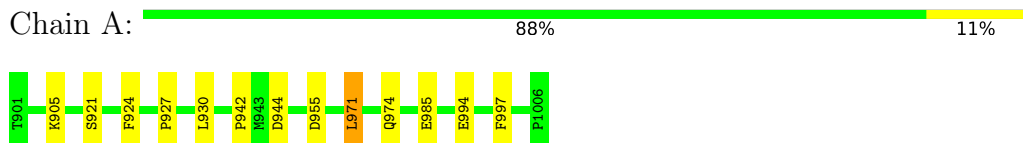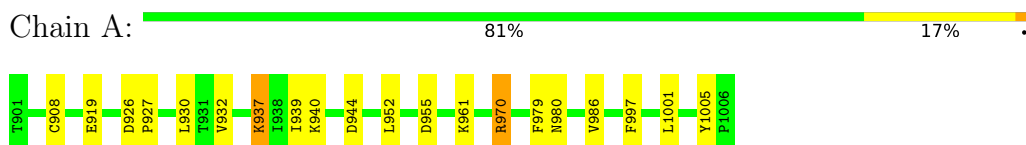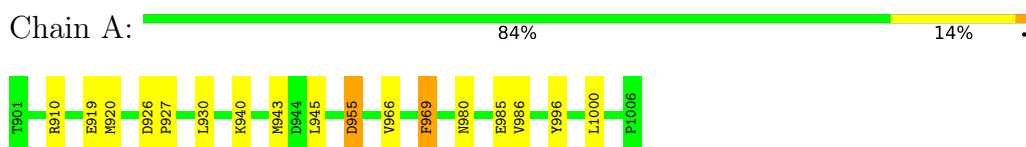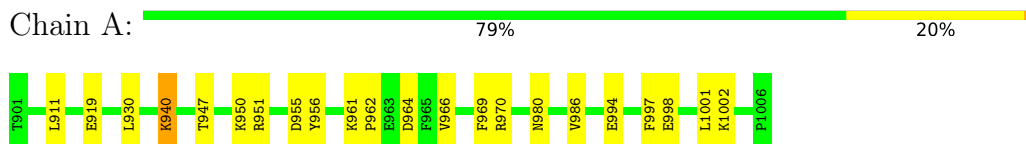
Chain A:
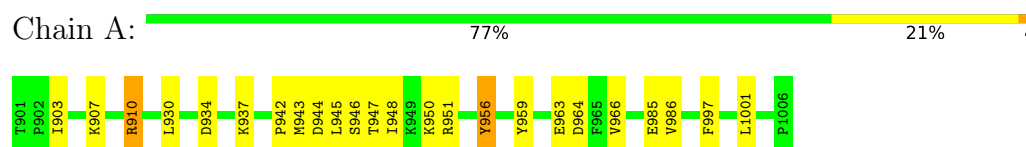
4.2.9   Score per residue for model 9

• Molecule 1: Transcription intermediary factor 1-alpha

Chain A:
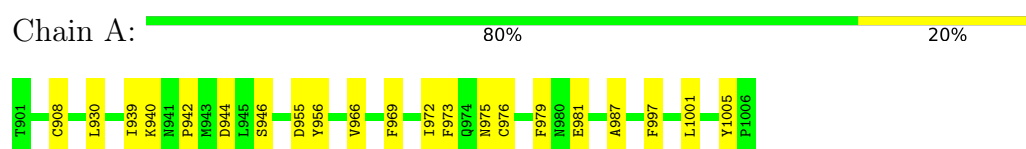
4.2.10   Score per residue for model 10

• Molecule 1: Transcription intermediary factor 1-alpha

Chain A:
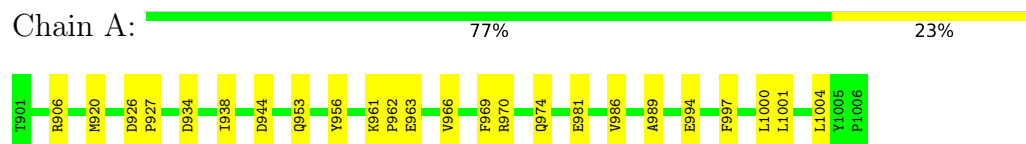
5   Refinement protocol and experimental data overview ⓘ

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

Of the 100 calculated structures, 10 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	3.9

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	62
Number of shifts mapped to atoms	62
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	1%

6   Model quality (i)

6.1   Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: T52

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	0.67±0.02	0±0/906 (0.0± 0.0%)	0.75±0.02	0±0/1224 (0.0± 0.0%)
All	All	0.67	0/9060 (0.0%)	0.75	4/12240 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	Chirality	Planarity
1	A	0.5±0.5	0.2±0.4
All	All	5	2

There are no bond-length outliers.

All unique angle outliers are listed below.

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})	Models	
								Worst	Total
1	A	955	ASP	N-CA-CB	5.25	120.06	110.60	5	4

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

Mol	Chain	Res	Type	Atoms	Models (Total)
1	A	983	ASP	CA	4
1	A	955	ASP	CA	1

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

Mol	Chain	Res	Type	Group	Models (Total)
1	A	970	ARG	Sidechain	1
1	A	906	ARG	Sidechain	1

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	884	873	870	10±3
2	A	43	39	0	1±1
All	All	9270	9120	8700	96

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 5.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models Worst	Total
1:A:966:VAL:HA	1:A:969:PHE:CE1	0.60	2.31	5	3
1:A:997:PHE:O	1:A:1001:LEU:HG	0.57	1.99	1	5
1:A:951:ARG:HA	1:A:951:ARG:NE	0.56	2.15	5	1
1:A:986:VAL:HA	2:A:1101:T52:C14	0.55	2.32	3	1
1:A:966:VAL:HA	1:A:969:PHE:CZ	0.55	2.37	9	3
1:A:986:VAL:HG13	2:A:1101:T52:C13	0.54	2.32	10	6
1:A:956:TYR:CD2	1:A:959:TYR:HB3	0.53	2.39	8	2
1:A:942:PRO:HA	1:A:975:ASN:OD1	0.53	2.03	6	1
1:A:956:TYR:CE2	1:A:959:TYR:HB3	0.52	2.39	8	1
1:A:980:ASN:HD22	1:A:986:VAL:HG12	0.51	1.65	4	1
1:A:980:ASN:ND2	1:A:986:VAL:HG12	0.51	2.21	4	2
1:A:940:LYS:HD2	1:A:940:LYS:N	0.51	2.21	9	1
1:A:944:ASP:OD2	1:A:946:SER:HB2	0.50	2.06	1	2
1:A:981:GLU:O	1:A:987:ALA:HB2	0.50	2.07	9	2
1:A:926:ASP:OD1	2:A:1101:T52:N4	0.49	2.45	10	3
1:A:980:ASN:HB3	1:A:986:VAL:HG12	0.49	1.85	3	2
1:A:947:THR:HA	1:A:950:LYS:CB	0.49	2.38	8	2
1:A:1001:LEU:HD22	1:A:1005:TYR:CE1	0.49	2.42	3	1
1:A:940:LYS:HB3	1:A:940:LYS:HZ3	0.49	1.68	6	1
1:A:937:LYS:HA	1:A:937:LYS:CE	0.48	2.38	3	1
1:A:967:ALA:O	1:A:971:LEU:HG	0.48	2.09	1	2

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models Worst	Total
1:A:910:ARG:NE	1:A:910:ARG:HA	0.48	2.23	8	1
1:A:903:ILE:O	1:A:907:LYS:HG3	0.48	2.09	8	1
1:A:908:CYS:HA	1:A:1005:TYR:OH	0.48	2.09	9	1
1:A:947:THR:HA	1:A:950:LYS:HB3	0.47	1.86	8	1
1:A:1000:LEU:O	1:A:1004:LEU:HG	0.47	2.09	10	1
1:A:940:LYS:HZ2	1:A:940:LYS:HB3	0.47	1.69	5	1
1:A:944:ASP:O	1:A:947:THR:HB	0.47	2.10	8	1
1:A:998:GLU:O	1:A:1002:LYS:HE2	0.47	2.09	5	1
1:A:934:ASP:O	1:A:938:ILE:HG12	0.47	2.09	7	2
1:A:963:GLU:O	1:A:966:VAL:HG12	0.47	2.09	8	1
1:A:926:ASP:OD2	2:A:1101:T52:N4	0.46	2.48	7	3
1:A:945:LEU:O	1:A:948:ILE:HG22	0.46	2.09	8	1
1:A:943:MET:O	1:A:972:ILE:HA	0.46	2.10	7	1
1:A:972:ILE:HA	1:A:975:ASN:OD1	0.45	2.10	9	1
1:A:940:LYS:HB3	1:A:940:LYS:NZ	0.45	2.26	6	2
1:A:980:ASN:CB	1:A:986:VAL:HG12	0.45	2.42	3	2
1:A:920:MET:SD	1:A:989:ALA:HA	0.45	2.52	10	1
1:A:994:GLU:HA	1:A:997:PHE:CE2	0.45	2.47	5	3
1:A:971:LEU:HA	1:A:974:GLN:NE2	0.44	2.27	2	1
1:A:951:ARG:HD3	1:A:964:ASP:OD1	0.44	2.13	5	1
1:A:944:ASP:OD2	1:A:946:SER:HB3	0.44	2.13	7	1
1:A:930:LEU:H	1:A:930:LEU:HD23	0.44	1.73	4	6
1:A:969:PHE:O	1:A:972:ILE:HG13	0.43	2.13	1	1
1:A:962:PRO:O	1:A:966:VAL:HG23	0.43	2.13	7	1
1:A:996:TYR:O	1:A:1000:LEU:HG	0.43	2.14	4	1
1:A:976:CYS:HB2	1:A:980:ASN:ND2	0.43	2.29	1	1
1:A:944:ASP:OD1	1:A:946:SER:HB3	0.43	2.14	9	1
1:A:902:PRO:HB3	1:A:955:ASP:OD1	0.42	2.14	6	1
1:A:940:LYS:O	1:A:942:PRO:HD3	0.42	2.14	9	1
1:A:919:GLU:HG3	1:A:920:MET:HG3	0.42	1.91	4	1
1:A:908:CYS:SG	1:A:952:LEU:HD11	0.41	2.55	3	1
1:A:937:LYS:HA	1:A:937:LYS:NZ	0.41	2.31	3	1
1:A:973:PHE:HA	1:A:976:CYS:SG	0.41	2.54	9	1
1:A:934:ASP:CG	1:A:937:LYS:HZ2	0.41	2.19	1	1
1:A:961:LYS:H	1:A:961:LYS:HD3	0.41	1.75	6	1
1:A:939:ILE:HB	1:A:979:PHE:CE1	0.41	2.50	3	1
1:A:921:SER:HA	1:A:924:PHE:CZ	0.41	2.50	2	1
1:A:953:GLN:HB3	1:A:956:TYR:CE2	0.41	2.51	10	1
1:A:934:ASP:CG	1:A:937:LYS:HD3	0.40	2.36	8	1
1:A:969:PHE:O	1:A:972:ILE:HG12	0.40	2.15	9	1
1:A:911:LEU:HD22	1:A:1001:LEU:HD21	0.40	1.94	5	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	104/106 (98%)	91±1 (88±1%)	12±1 (12±1%)	1±1 (1±1%)	20	68
All	All	1040/1060 (98%)	910 (88%)	120 (12%)	10 (1%)	20	68

All 3 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	927	PRO	6
1	A	962	PRO	2
1	A	942	PRO	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	100/100 (100%)	94±1 (94±1%)	6±1 (6±1%)	23	72
All	All	1000/1000 (100%)	940 (94%)	60 (6%)	23	72

All 28 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	956	TYR	5
1	A	985	GLU	5
1	A	981	GLU	4
1	A	944	ASP	4
1	A	961	LYS	4
1	A	970	ARG	4
1	A	955	ASP	3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Models (Total)
1	A	910	ARG	3
1	A	945	LEU	2
1	A	971	LEU	2
1	A	919	GLU	2
1	A	940	LYS	2
1	A	943	MET	2
1	A	939	ILE	2
1	A	979	PHE	2
1	A	964	ASP	2
1	A	925	GLN	1
1	A	905	LYS	1
1	A	930	LEU	1
1	A	942	PRO	1
1	A	932	VAL	1
1	A	937	LYS	1
1	A	997	PHE	1
1	A	969	PHE	1
1	A	941	ASN	1
1	A	951	ARG	1
1	A	963	GLU	1
1	A	974	GLN	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 ⓘ

1 ligand 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	T52	A	1101	-	43,46,46	2.78±0.05	12±1 (28±3%)

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	T52	A	1101	-	54,65,65	2.89±0.04	12±1 (22±1%)

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	T52	A	1101	-	-	0±0,29,29,29	0±0,4,4,4

All unique bond outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
2	A	1101	T52	O3-S1	9.72	1.32	1.43	6	10
2	A	1101	T52	O4-S1	9.12	1.53	1.43	10	10
2	A	1101	T52	C16-C17	7.18	1.49	1.36	4	10
2	A	1101	T52	S1-N1	5.82	1.73	1.63	5	10
2	A	1101	T52	C10-C9	4.55	1.46	1.37	5	10
2	A	1101	T52	C8-S1	4.26	1.69	1.76	1	10
2	A	1101	T52	C9-C17	4.18	1.49	1.40	1	10
2	A	1101	T52	C7-C8	4.06	1.45	1.38	6	10
2	A	1101	T52	C19-C26	3.53	1.45	1.38	9	10
2	A	1101	T52	C15-C11	2.92	1.32	1.39	6	10

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
2	A	1101	T52	C25-C26	2.68	1.43	1.38	9	3
2	A	1101	T52	C9-N1	2.68	1.38	1.42	7	3
2	A	1101	T52	C20-C21	2.56	1.43	1.38	2	5
2	A	1101	T52	C20-C18	2.45	1.43	1.38	4	1
2	A	1101	T52	C25-C21	2.45	1.43	1.38	3	4
2	A	1101	T52	C19-C18	2.15	1.42	1.38	8	2
2	A	1101	T52	O8-C26	2.10	1.42	1.37	9	1
2	A	1101	T52	C3-C2	2.06	1.42	1.38	5	1
2	A	1101	T52	C16-C15	2.01	1.36	1.40	9	1

All unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

| Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
2	A	1101	T52	O3-S1-C8	14.75	89.80	107.97	2	10
2	A	1101	T52	C8-S1-N1	8.06	116.98	106.83	4	10
2	A	1101	T52	O4-S1-C8	7.47	117.17	107.97	2	10
2	A	1101	T52	C9-C10-C11	7.27	115.04	121.32	9	10
2	A	1101	T52	C5-O2-C4	4.14	111.28	117.53	2	10
2	A	1101	T52	C1-O1-C2	4.07	111.38	117.53	5	10
2	A	1101	T52	O4-S1-O3	3.95	124.40	119.55	4	10
2	A	1101	T52	O1-C2-C4	3.63	120.47	115.41	2	10
2	A	1101	T52	O2-C4-C2	3.50	120.29	115.41	9	10
2	A	1101	T52	C7-C8-S1	3.35	123.41	119.77	6	10
2	A	1101	T52	C17-O6-C18	2.97	110.60	118.00	9	2
2	A	1101	T52	O2-C4-C6	2.77	119.63	124.37	6	10
2	A	1101	T52	O1-C2-C3	2.68	119.50	124.12	10	10
2	A	1101	T52	O4-S1-N1	2.07	101.56	106.73	10	1
2	A	1101	T52	C22-O7-C21	2.01	112.66	117.93	10	1

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be

highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand T52 A 1101

Bond lengths

Bond angles

Torsions

Rings
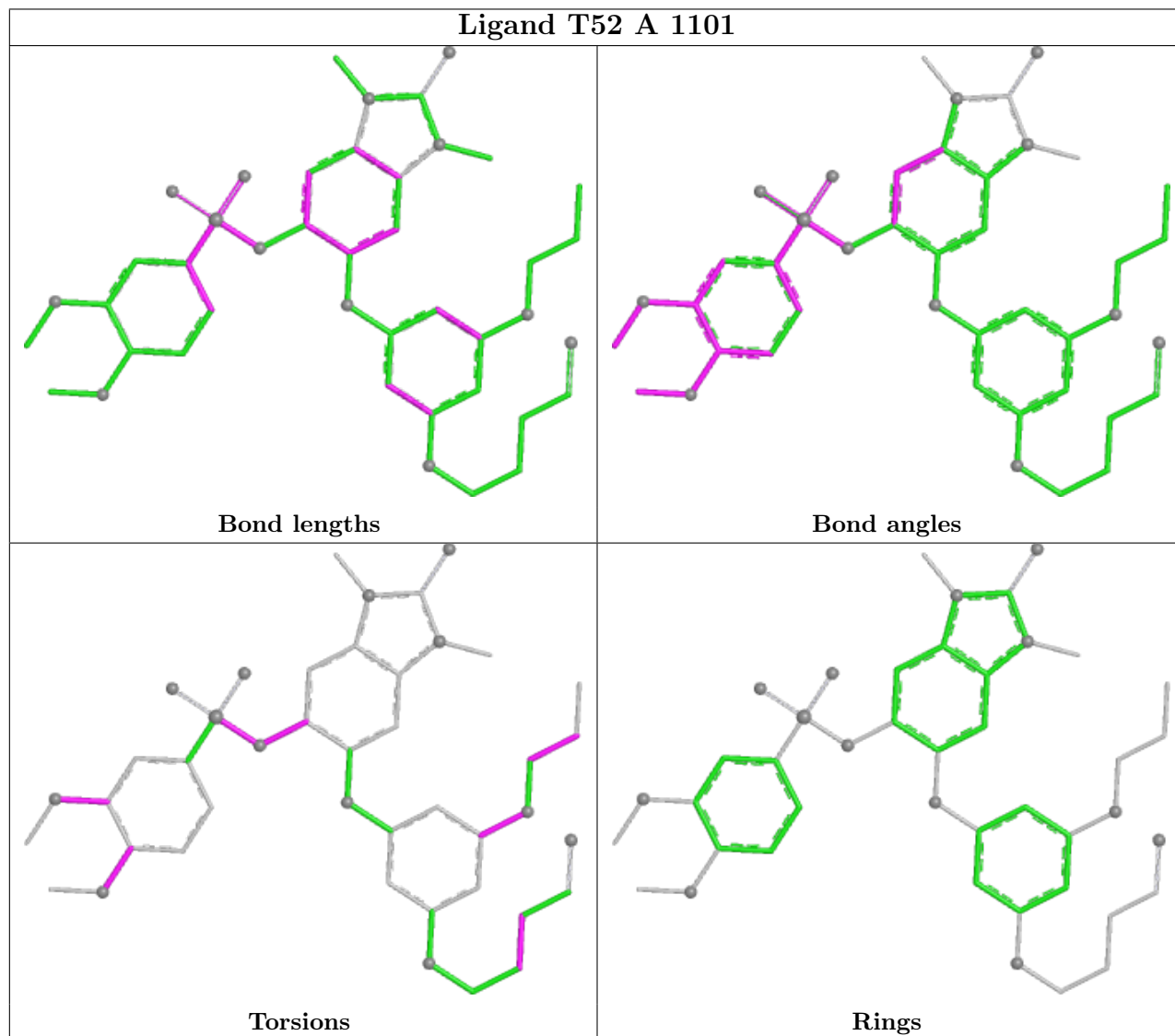
6.7 Other polymers ⓘ

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 ⓘ

The completeness of assignment taking into account all chemical shift lists is 1% for the well-defined parts and 1% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *assigned_chem_shift_list*

7.1.1 Bookkeeping ⓘ

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

Total number of shifts	62
Number of shifts mapped to atoms	62
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

7.1.2 Chemical shift referencing ⓘ

No chemical shift referencing corrections were calculated (not enough data).

7.1.3 Completeness of resonance assignments ⓘ

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 1%, i.e. 9 atoms were assigned a chemical shift out of a possible 1385. 0 out of 17 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	0/514 (0%)	0/204 (0%)	0/212 (0%)	0/98 (0%)
Sidechain	9/745 (1%)	9/441 (2%)	0/274 (0%)	0/30 (0%)
Aromatic	0/126 (0%)	0/67 (0%)	0/58 (0%)	0/1 (0%)
Overall	9/1385 (1%)	9/712 (1%)	0/544 (0%)	0/129 (0%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 1%, i.e. 9 atoms were assigned a chemical shift out of a possible 1385. 0 out of 17 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

WORLDWIDE
wwPDB
PROTEIN DATA BANK

	Total	^{1}H	^{13}C	^{15}N
Backbone	0/514 (0%)	0/204 (0%)	0/212 (0%)	0/98 (0%)
Sidechain	9/745 (1%)	9/441 (2%)	0/274 (0%)	0/30 (0%)
Aromatic	0/126 (0%)	0/67 (0%)	0/58 (0%)	0/1 (0%)
Overall	9/1385 (1%)	9/712 (1%)	0/544 (0%)	0/129 (0%)

7.1.4   Statistically unusual chemical shifts ⓘ

There are no statistically unusual chemical shifts.

7.1.5   Random Coil Index (RCI) plots ⓘ

No *random coil index* (RCI) plot could be generated from the current chemical shift list (assigned_chem_shift_list). RCI is only applicable to proteins.