wwPDB NMR Structure Validation Summary Report

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PDB ID	:	2LGZ
Title	:	Solution structure of STT3P
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This is a wwPDB NMR Structure Validation Summary 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 (i) symbol.

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

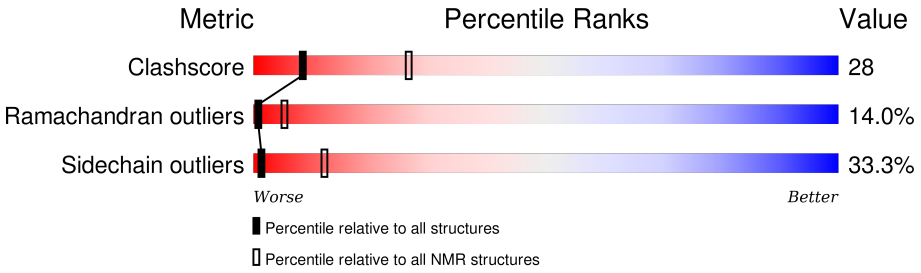
Cyrange	:	Kirchner and Güntert (2011)
NmrClust	:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Mogul	:	unknown
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	rb-20027457
Ideal 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 (i)

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

The overall completeness of chemical shifts assignment is 36%.

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 <=5%

Mol	Chain	Length	Quality of chain
1	A	273	16% 53% 7% 23%

2 Ensemble composition and analysis

This entry contains 10 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: *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:21-A:146, A:153-A:166, A:189-A:197, A:202-A:261 (209)	1.52	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 3 clusters and 1 single-model cluster was found.

Cluster number	Models
1	4, 5, 7, 8, 10
2	3, 9
3	1, 2
Single-model clusters	6

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 4340 atoms, of which 2124 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3.

Mol	Chain	Residues	Atoms						Trace
1	A	273	Total	C	H	N	O	S	0
			4340	1395	2124	392	423	6	

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	EXPRESSION TAG	UNP P39007
A	2	GLY	-	EXPRESSION TAG	UNP P39007
A	3	SER	-	EXPRESSION TAG	UNP P39007
A	4	SER	-	EXPRESSION TAG	UNP P39007
A	5	HIS	-	EXPRESSION TAG	UNP P39007
A	6	HIS	-	EXPRESSION TAG	UNP P39007
A	7	HIS	-	EXPRESSION TAG	UNP P39007
A	8	HIS	-	EXPRESSION TAG	UNP P39007
A	9	HIS	-	EXPRESSION TAG	UNP P39007
A	10	HIS	-	EXPRESSION TAG	UNP P39007
A	11	SER	-	EXPRESSION TAG	UNP P39007
A	12	SER	-	EXPRESSION TAG	UNP P39007
A	13	GLY	-	EXPRESSION TAG	UNP P39007
A	14	LEU	-	EXPRESSION TAG	UNP P39007
A	15	VAL	-	EXPRESSION TAG	UNP P39007
A	16	PRO	-	EXPRESSION TAG	UNP P39007
A	17	ARG	-	EXPRESSION TAG	UNP P39007
A	18	GLY	-	EXPRESSION TAG	UNP P39007
A	19	SER	-	EXPRESSION TAG	UNP P39007
A	105	ASN	MET	CONFLICT	UNP P39007
A	145	ASN	MET	CONFLICT	UNP P39007
A	231	ASN	MET	CONFLICT	UNP P39007

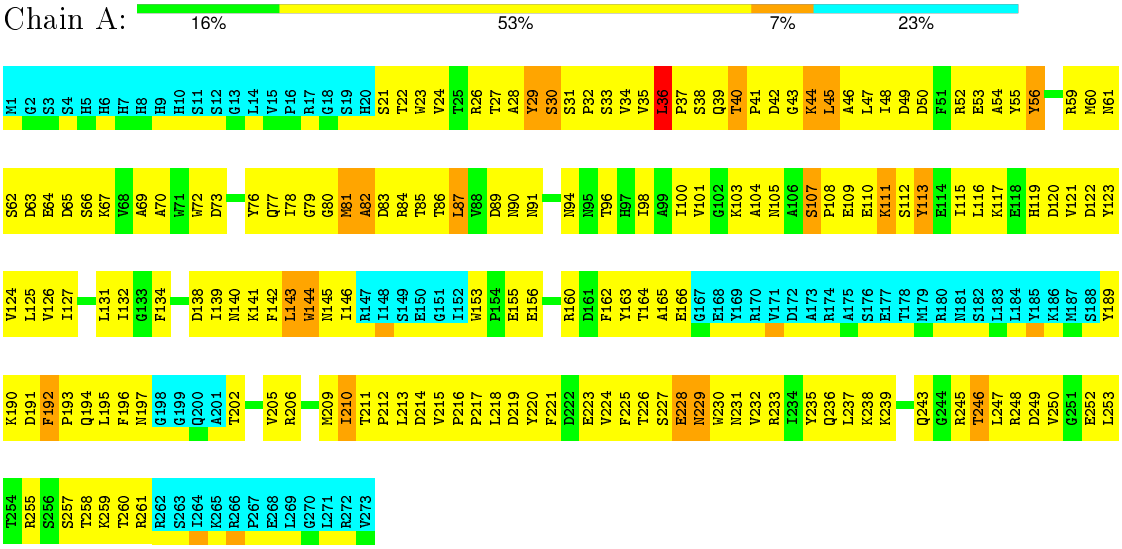
4 Residue-property plots

4.1 Average score per residue in the NMR ensemble

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

- Molecule 1: Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3

Chain A:

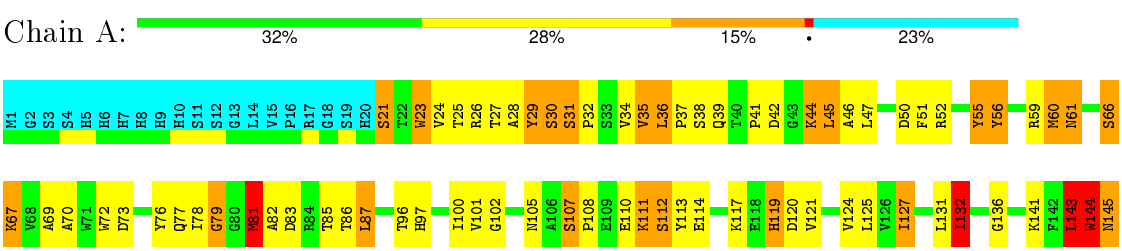


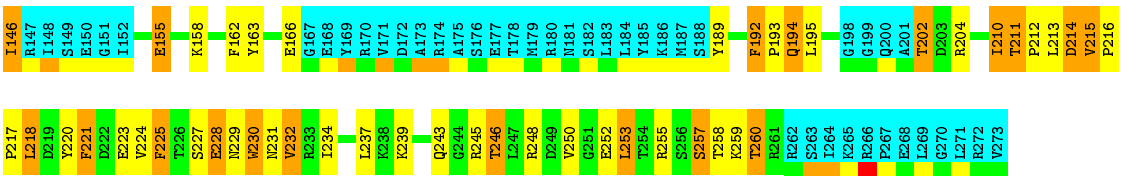
4.2 Residue scores for the representative (medoid) model from the NMR ensemble

The representative model is number 4. Colouring as in section 4.1 above.

- Molecule 1: Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3

Chain A:




I146 R147 I148 S149 E150 G151 I152 E155 K158 F162 Y163 E166 G167 E168 Y169 R170 V171 D172 A173 R174 A175 S176 E177 T178 M179 R180 N181 S182 L183 L184 Y185 K186 M187 S188 Y189 F192 P193 Q194 L195 G198 G199 Q200 A201 T202 D203 R204 I210 T211 P212 L213 D214 V215 P216
P217 L218 D219 Y220 F221 D222 E223 V224 F225 T226 S227 E228 N229 W230 N231 V232 R233 I234 L237 K238 K239 Q243 G244 R245 T246 I247 R248 D249 V250 G251 E252 L253 T254 R255 S256 S257 T258 K259 T260 R261 R262 S263 I264 K265 R266 P267 E268 L269 G270 L271 R272 V273

5 Refinement protocol and experimental data overview

The models were refined using the following method: *torsion angle 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
CYANA	refinement	3.0

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)	2lgz_cs.str
Number of chemical shift lists	1
Total number of shifts	1187
Number of shifts mapped to atoms	1187
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	36%

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	1718	1633	1633	94±7
All	All	17180	16330	16330	940

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 28.

5 of 664 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:191:ASP:O	1:A:192:PHE:HB2	0.95	1.56	1	2
1:A:45:LEU:HD23	1:A:121:VAL:HG12	0.89	1.45	3	1
1:A:216:PRO:N	1:A:217:PRO:HD2	0.87	1.85	9	7
1:A:45:LEU:HD21	1:A:121:VAL:HG13	0.87	1.44	5	4
1:A:213:LEU:HD13	1:A:218:LEU:HD21	0.81	1.51	1	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	209/273 (77%)	144±4 (69±2%)	36±4 (17±2%)	29±2 (14±1%)	1 5
All	All	2090/2730 (77%)	1442 (69%)	355 (17%)	293 (14%)	1 5

5 of 79 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	144	TRP	9
1	A	194	GLN	9
1	A	67	LYS	9
1	A	29	TYR	8
1	A	36	LEU	8

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	186/239 (78%)	124±6 (67±3%)	62±6 (33±3%)	1 12
All	All	1860/2390 (78%)	1241 (67%)	619 (33%)	1 12

5 of 160 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	248	ARG	10
1	A	81	MET	9
1	A	107	SER	9
1	A	30	SER	8
1	A	246	THR	8

6.3.3 RNA (i)

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 carbohydrates in this entry.

6.6 Ligand geometry

There are no ligands in this entry.

6.7 Other polymers

There are no such molecules in this entry.

6.8 Polymer linkage issues

There are no chain breaks in this entry.

7 Chemical shift validation

The completeness of assignment taking into account all chemical shift lists is 36% for the well-defined parts and 35% for the entire structure.

7.1 Chemical shift list 1

File name: 2lgz_cs.str

Chemical shift list name: *assigned_chem_shift_list_1*

7.1.1 Bookkeeping

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

Total number of shifts	1187
Number of shifts mapped to atoms	1187
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	6

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	243	0.08 ± 0.17	None needed (< 0.5 ppm)
$^{13}C_{\beta}$	227	0.90 ± 0.05	Should be applied
$^{13}C'$	244	-0.05 ± 0.08	None needed (< 0.5 ppm)
^{15}N	235	0.41 ± 0.13	None needed (< 0.5 ppm)

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 36%, i.e. 942 atoms were assigned a chemical shift out of a possible 2631. 0 out of 29 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	758/1027 (74%)	187/409 (46%)	385/418 (92%)	186/200 (93%)
Sidechain	182/1325 (14%)	0/773 (0%)	182/487 (37%)	0/65 (0%)

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	Total	^{1}H	^{13}C	^{15}N
Aromatic	2/279 (1%)	1/145 (1%)	0/124 (0%)	1/10 (10%)
Overall	942/2631 (36%)	188/1327 (14%)	567/1029 (55%)	187/275 (68%)

7.1.4 Statistically unusual chemical shifts (i)

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

Mol	Chain	Res	Type	Atom	Shift, *ppm*	Expected range, *ppm*	Z-score
1	A	230	TRP	HA	11.41	7.28 – 2.08	12.9
1	A	160	ARG	CA	31.54	68.35 – 45.25	-10.9
1	A	27	THR	CB	54.99	78.10 – 61.30	-8.8
1	A	147	ARG	CB	43.89	39.81 – 21.51	7.2
1	A	111	LYS	CB	43.91	41.68 – 23.88	6.3
1	A	55	TYR	CB	27.54	50.05 – 28.55	-5.5

7.1.5 Random Coil Index (RCI) plots (i)

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

Random coil index (RCI) for chain A: