



Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 09:08 AM GMT

PDB ID : 1SER
Title : THE 2.9 ANGSTROMS CRYSTAL STRUCTURE OF T. THERMOPHILUS
SERYL-TRNA SYNTHETASE COMPLEXED WITH TRNA SER
Authors : Biou, S.; Cusack, V.; Yaremchuk, A.; Tukalo, M.
Deposited on : 1994-02-21
Resolution : 2.90 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

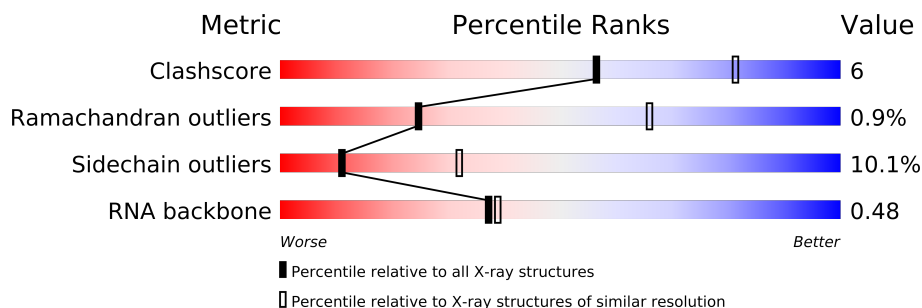
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 21963
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.90 Å.

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)	Similar resolution (#Entries, resolution range(Å))
Clashscore	79885	1326 (2.90-2.90)
Ramachandran outliers	78287	1290 (2.90-2.90)
Sidechain outliers	78261	1292 (2.90-2.90)
RNA backbone	1838	1055 (3.40-2.40)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	T	94	
2	A	421	
2	B	421	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7780 atoms, of which 0 are hydrogen and 0 are deuterium.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called TRNASER.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	T	65	Total	C	N	O	P	60	0	0
			1381	613	247	456	65			

- Molecule 2 is a protein called PROTEIN (SERYL-TRNA SYNTHETASE (E.C.6.1.1.11)).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	372	Total	C	N	O	S	30	0	0
			2982	1901	531	539	11			
2	B	421	Total	C	N	O	S	0	0	0
			3373	2143	606	613	11			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	208	TYR	THR	CONFLICT	UNP P34945
B	708	TYR	THR	CONFLICT	UNP P34945

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	T	1	Total	O	0	0
			1	1		
3	A	14	Total	O	0	0
			14	14		
3	B	29	Total	O	0	0
			29	29		

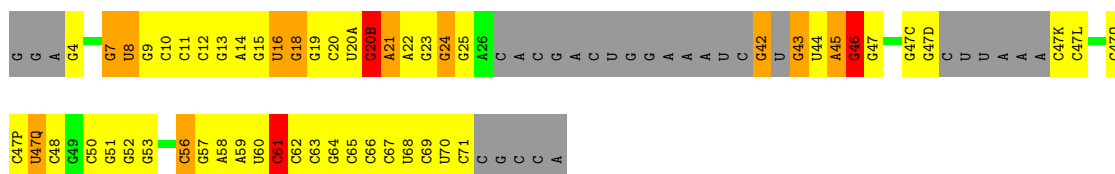
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-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. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

Note EDS was not executed.

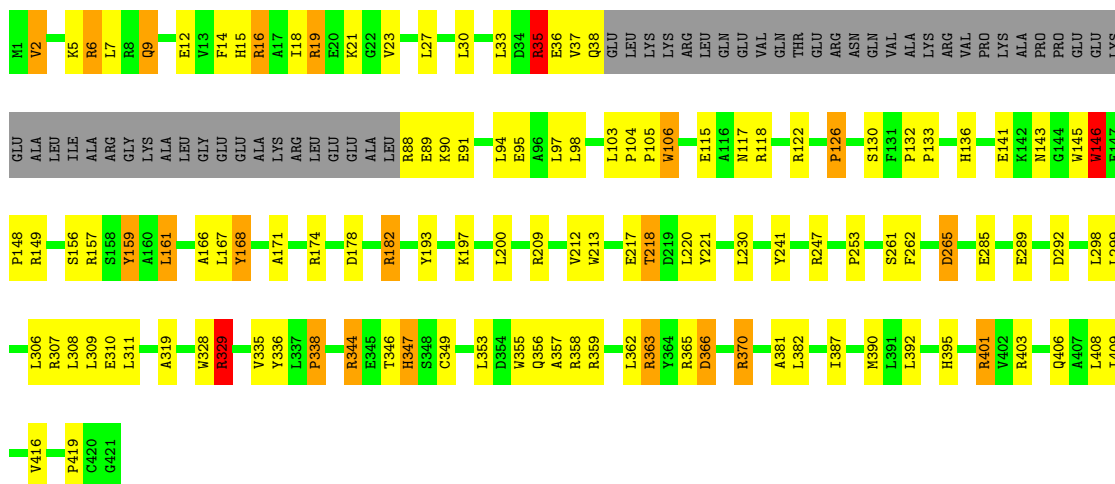
- Molecule 1: TRNASER

Chain T: 



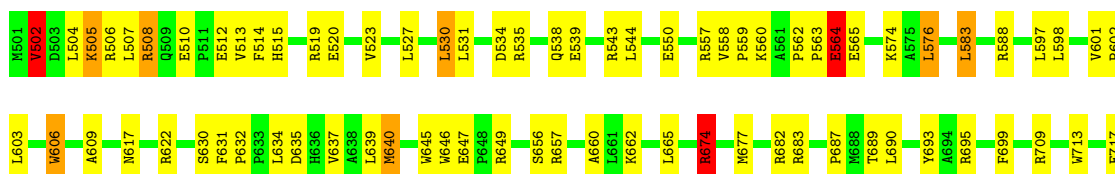
- Molecule 2: PROTEIN (SERYL-TRNA SYNTHETASE (E.C.6.1.1.11))

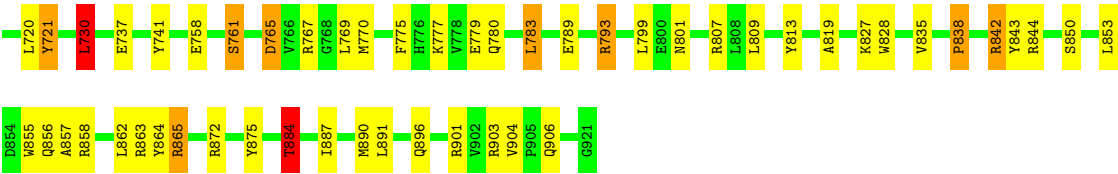
Chain A: 



- Molecule 2: PROTEIN (SERYL-TRNA SYNTHETASE (E.C.6.1.1.11))

Chain B: 





4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	124.50Å 128.90Å 121.20Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 2.90	Depositor
% Data completeness (in resolution range)	92.9 (10.00-2.90)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.194 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	7780	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 5MU, H2U, PSU

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 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	T	1.54	6/1472 (0.4%)	2.24	96/2290 (4.2%)
2	A	0.86	0/3053	1.60	53/4138 (1.3%)
2	B	0.90	0/3448	1.73	75/4667 (1.6%)
All	All	1.03	6/7973 (0.1%)	1.80	224/11095 (2.0%)

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	T	58	A	C5'-C4'	6.34	1.58	1.51
1	T	18	G	P-O5'	6.24	1.66	1.59
1	T	18	G	C2'-C1'	-6.12	1.46	1.53
1	T	50	C	P-O5'	6.07	1.65	1.59
1	T	18	G	N9-C8	-5.48	1.34	1.37
1	T	46	G	C4'-C3'	-5.07	1.47	1.52

All (224) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	T	16	U	O4'-C1'-N1	-14.53	96.58	108.20
2	B	903	ARG	NE-CZ-NH2	-14.46	113.07	120.30
1	T	18	G	O4'-C1'-N9	13.52	119.02	108.20
2	B	657	ARG	NE-CZ-NH2	-12.82	113.89	120.30
2	B	657	ARG	NE-CZ-NH1	11.41	126.00	120.30
2	A	122	ARG	NE-CZ-NH2	-11.35	114.62	120.30
1	T	7	G	C5'-C4'-O4'	10.96	122.25	109.10
2	B	844	ARG	NE-CZ-NH2	-10.79	114.90	120.30
1	T	47(Q)	U	O4'-C1'-N1	10.66	116.72	108.20
1	T	15	G	O4'-C1'-N9	10.52	116.62	108.20
2	B	721	TYR	CB-CG-CD2	-10.50	114.70	121.00
1	T	52	G	O4'-C1'-N9	10.23	116.38	108.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	T	47(C)	G	O4'-C1'-N9	10.19	116.35	108.20
2	B	865	ARG	NE-CZ-NH2	-9.99	115.30	120.30
1	T	19	G	O4'-C1'-N9	-9.45	100.64	108.20
1	T	13	G	C5'-C4'-C3'	-9.37	101.01	116.00
2	A	146	TRP	CD1-CG-CD2	9.31	113.75	106.30
1	T	18	G	C5'-C4'-O4'	9.25	120.20	109.10
2	B	855	TRP	CD1-CG-CD2	9.22	113.68	106.30
2	B	606	TRP	CD1-CG-CD2	9.10	113.58	106.30
1	T	20	C	N1-C2-O2	9.06	124.34	118.90
2	A	106	TRP	CD1-CG-CD2	9.05	113.54	106.30
1	T	69	C	N1-C2-O2	9.04	124.32	118.90
2	B	646	TRP	CD1-CG-CD2	8.76	113.31	106.30
2	B	767	ARG	NE-CZ-NH1	8.76	124.68	120.30
1	T	24	G	P-O3'-C3'	8.71	130.15	119.70
1	T	47(O)	C	N1-C2-O2	8.61	124.06	118.90
2	B	695	ARG	NE-CZ-NH2	-8.57	116.01	120.30
2	B	901	ARG	NE-CZ-NH2	-8.54	116.03	120.30
1	T	10	C	N1-C2-O2	8.48	123.99	118.90
1	T	71	C	N1-C2-O2	8.46	123.97	118.90
2	A	145	TRP	CD1-CG-CD2	8.42	113.03	106.30
2	B	767	ARG	NE-CZ-NH2	-8.37	116.11	120.30
2	A	355	TRP	CD1-CG-CD2	8.21	112.87	106.30
2	B	844	ARG	NE-CZ-NH1	8.20	124.40	120.30
2	B	855	TRP	CE2-CD2-CG	-8.05	100.86	107.30
2	B	674	ARG	NE-CZ-NH1	7.98	124.29	120.30
1	T	64	G	O4'-C1'-N9	7.98	114.58	108.20
1	T	20(B)	G	O4'-C1'-N9	-7.96	101.83	108.20
2	A	328	TRP	CD1-CG-CD2	7.76	112.51	106.30
2	B	606	TRP	CE2-CD2-CG	-7.76	101.09	107.30
2	B	588	ARG	NE-CZ-NH1	7.66	124.13	120.30
1	T	69	C	O4'-C1'-N1	7.65	114.32	108.20
2	A	355	TRP	CE2-CD2-CG	-7.62	101.21	107.30
1	T	44	U	C5'-C4'-C3'	-7.59	103.86	116.00
1	T	11	C	N1-C2-O2	7.57	123.44	118.90
2	B	890	MET	CA-CB-CG	-7.54	100.49	113.30
2	B	713	TRP	CD1-CG-CD2	7.46	112.27	106.30
1	T	7	G	O4'-C1'-N9	7.41	114.13	108.20
1	T	66	C	N1-C2-O2	7.39	123.33	118.90
1	T	47(O)	C	N3-C2-O2	-7.36	116.75	121.90
2	A	363	ARG	NE-CZ-NH1	7.34	123.97	120.30
1	T	63	C	N1-C2-O2	7.33	123.30	118.90
1	T	50	C	N1-C2-O2	7.31	123.28	118.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	622	ARG	NE-CZ-NH1	7.30	123.95	120.30
2	A	328	TRP	CE2-CD2-CG	-7.26	101.49	107.30
2	B	646	TRP	CE2-CD2-CG	-7.20	101.54	107.30
2	B	828	TRP	CE2-CD2-CG	-7.20	101.54	107.30
2	A	145	TRP	CE2-CD2-CG	-7.14	101.58	107.30
2	A	106	TRP	CE2-CD2-CG	-7.14	101.59	107.30
2	B	530	LEU	CA-CB-CG	7.12	131.66	115.30
2	A	349	CYS	CA-CB-SG	-7.10	101.23	114.00
2	B	508	ARG	NE-CZ-NH1	7.09	123.84	120.30
1	T	46	G	O4'-C1'-N9	7.08	113.87	108.20
2	B	783	LEU	CA-CB-CG	7.03	131.47	115.30
1	T	4	G	C5'-C4'-C3'	-7.02	104.77	116.00
1	T	16	U	N3-C2-O2	-7.00	117.30	122.20
2	A	146	TRP	CE2-CD2-CG	-6.94	101.75	107.30
1	T	47	G	O4'-C1'-N9	6.94	113.75	108.20
2	A	247	ARG	NE-CZ-NH2	-6.94	116.83	120.30
1	T	61	C	N1-C2-O2	6.88	123.03	118.90
2	B	640	MET	CG-SD-CE	-6.85	89.24	100.20
1	T	66	C	N3-C2-O2	-6.85	117.11	121.90
1	T	69	C	N3-C2-O2	-6.85	117.11	121.90
2	A	213	TRP	CE2-CD2-CG	-6.83	101.84	107.30
2	B	713	TRP	CE2-CD2-CG	-6.82	101.85	107.30
2	B	709	ARG	NE-CZ-NH2	-6.73	116.93	120.30
2	B	828	TRP	CD1-CG-CD2	6.72	111.68	106.30
2	B	737	GLU	N-CA-CB	-6.72	98.51	110.60
2	A	403	ARG	NE-CZ-NH2	-6.71	116.94	120.30
1	T	16	U	P-O3'-C3'	6.71	127.75	119.70
2	A	344	ARG	NE-CZ-NH1	6.64	123.62	120.30
1	T	21	A	O4'-C1'-N9	6.64	113.51	108.20
2	A	307	ARG	NE-CZ-NH2	-6.62	116.99	120.30
2	B	645	TRP	CD1-CG-CD2	6.61	111.59	106.30
1	T	58	A	O4'-C1'-N9	6.57	113.45	108.20
2	B	858	ARG	NE-CZ-NH1	6.54	123.57	120.30
2	B	903	ARG	NE-CZ-NH1	6.54	123.57	120.30
1	T	16	U	C2-N1-C1'	6.50	125.50	117.70
1	T	16	U	N1-C1'-C2'	6.49	122.44	114.00
2	B	645	TRP	CE2-CD2-CG	-6.46	102.13	107.30
2	B	683	ARG	NE-CZ-NH1	6.43	123.52	120.30
1	T	65	C	N1-C2-O2	6.43	122.76	118.90
1	T	42	G	O4'-C1'-N9	6.43	113.34	108.20
2	B	856	GLN	CA-CB-CG	6.40	127.48	113.40
1	T	47(L)	C	N1-C2-O2	6.39	122.74	118.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	T	47(P)	C	O4'-C1'-N1	6.39	113.31	108.20
1	T	10	C	P-O3'-C3'	6.36	127.33	119.70
2	A	213	TRP	CD1-CG-CD2	6.36	111.39	106.30
2	B	557	ARG	NE-CZ-NH1	6.35	123.48	120.30
1	T	44	U	C5'-C4'-O4'	6.34	116.71	109.10
1	T	51	G	O4'-C1'-N9	6.34	113.27	108.20
1	T	56	C	N1-C2-O2	6.33	122.70	118.90
2	B	903	ARG	CG-CD-NE	-6.33	98.52	111.80
1	T	57	G	C8-N9-C4	-6.30	103.88	106.40
1	T	20	C	N3-C2-O2	-6.30	117.49	121.90
1	T	59	A	P-O3'-C3'	6.27	127.22	119.70
2	B	588	ARG	NE-CZ-NH2	-6.26	117.17	120.30
1	T	22	A	O4'-C1'-N9	6.25	113.20	108.20
1	T	47(K)	C	N1-C2-O2	6.24	122.65	118.90
2	B	709	ARG	NE-CZ-NH1	6.23	123.42	120.30
1	T	50	C	P-O3'-C3'	6.22	127.17	119.70
2	B	682	ARG	NE-CZ-NH2	-6.21	117.19	120.30
2	B	807	ARG	NE-CZ-NH1	6.18	123.39	120.30
1	T	45	A	C5'-C4'-O4'	6.18	116.52	109.10
1	T	23	G	C8-N9-C4	-6.17	103.93	106.40
1	T	14	A	O4'-C1'-N9	6.14	113.11	108.20
1	T	45	A	C8-N9-C4	-6.12	103.35	105.80
2	B	520	GLU	N-CA-CB	-6.11	99.60	110.60
2	A	370	ARG	NE-CZ-NH1	6.10	123.35	120.30
1	T	45	A	P-O3'-C3'	6.10	127.02	119.70
2	A	149	ARG	NE-CZ-NH1	6.09	123.34	120.30
1	T	50	C	N3-C2-O2	-6.06	117.66	121.90
2	A	359	ARG	NE-CZ-NH2	-6.05	117.27	120.30
2	B	843	TYR	CB-CG-CD2	-6.05	117.37	121.00
1	T	53	G	O4'-C1'-N9	6.04	113.04	108.20
2	A	2	VAL	CA-CB-CG2	-6.02	101.87	110.90
1	T	16	U	N1-C2-O2	6.02	127.01	122.80
2	A	168	TYR	CB-CG-CD2	-6.01	117.39	121.00
1	T	44	U	O3'-P-O5'	-6.00	92.59	104.00
1	T	47(P)	C	N1-C2-O2	5.98	122.49	118.90
2	A	146	TRP	CG-CD1-NE1	-5.97	104.13	110.10
2	A	157	ARG	NE-CZ-NH1	5.97	123.28	120.30
1	T	71	C	N1-C1'-C2'	-5.95	105.45	112.00
1	T	12	C	O4'-C1'-N1	5.95	112.96	108.20
2	A	401	ARG	NE-CZ-NH1	5.95	123.27	120.30
2	B	842	ARG	NE-CZ-NH2	-5.94	117.33	120.30
2	B	674	ARG	NE-CZ-NH2	-5.94	117.33	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	884	THR	N-CA-CB	-5.92	99.06	110.30
2	A	16	ARG	NE-CZ-NH1	5.91	123.25	120.30
2	A	19	ARG	NE-CZ-NH1	5.91	123.25	120.30
2	B	515	HIS	CA-CB-CG	-5.89	103.59	113.60
1	T	61	C	O4'-C1'-N1	5.89	112.91	108.20
2	A	358	ARG	NE-CZ-NH1	5.87	123.24	120.30
1	T	12	C	N1-C2-O2	5.85	122.41	118.90
1	T	16	U	C5'-C4'-O4'	-5.83	102.11	109.10
1	T	67	C	N3-C4-N4	5.82	122.08	118.00
2	B	863	ARG	NE-CZ-NH1	5.82	123.21	120.30
1	T	71	C	N3-C2-O2	-5.75	117.87	121.90
2	A	265	ASP	CA-C-N	-5.75	104.56	117.20
1	T	11	C	N3-C2-O2	-5.73	117.89	121.90
2	B	865	ARG	NE-CZ-NH1	5.71	123.16	120.30
2	B	506	ARG	NE-CZ-NH1	5.71	123.15	120.30
1	T	45	A	C2'-C3'-O3'	5.70	122.82	113.70
1	T	59	A	N1-C6-N6	5.69	122.01	118.60
1	T	11	C	O4'-C1'-N1	5.68	112.75	108.20
1	T	71	C	O4'-C1'-N1	5.67	112.74	108.20
1	T	20(B)	G	N9-C1'-C2'	5.64	121.33	114.00
2	A	212	VAL	CA-CB-CG2	-5.62	102.47	110.90
2	A	174	ARG	NE-CZ-NH1	5.60	123.10	120.30
2	A	159	TYR	CB-CG-CD2	-5.60	117.64	121.00
2	A	209	ARG	NE-CZ-NH1	5.58	123.09	120.30
1	T	42	G	C5'-C4'-O4'	5.57	115.79	109.10
2	A	106	TRP	CG-CD1-NE1	-5.56	104.54	110.10
2	A	145	TRP	CG-CD1-NE1	-5.55	104.55	110.10
1	T	47(P)	C	C5'-C4'-O4'	5.54	115.74	109.10
2	B	793	ARG	NE-CZ-NH1	5.52	123.06	120.30
1	T	65	C	O4'-C1'-N1	5.51	112.61	108.20
2	A	329	ARG	NE-CZ-NH1	5.51	123.05	120.30
1	T	70	U	N1-C1'-C2'	-5.49	105.96	112.00
2	A	307	ARG	NE-CZ-NH1	5.48	123.04	120.30
2	A	247	ARG	CB-CG-CD	-5.47	97.37	111.60
2	A	355	TRP	CG-CD2-CE3	5.47	138.82	133.90
2	B	765	ASP	N-CA-C	5.46	125.74	111.00
1	T	66	C	O4'-C1'-N1	5.45	112.56	108.20
2	B	872	ARG	NE-CZ-NH2	-5.41	117.59	120.30
2	A	401	ARG	NE-CZ-NH2	-5.41	117.60	120.30
1	T	69	C	N1-C1'-C2'	-5.41	106.05	112.00
1	T	13	G	C8-N9-C4	-5.38	104.25	106.40
1	T	43	G	O4'-C1'-N9	5.34	112.47	108.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	903	ARG	N-CA-CB	-5.33	101.01	110.60
1	T	16	U	C5'-C4'-C3'	-5.32	107.49	116.00
2	B	842	ARG	NE-CZ-NH1	5.32	122.96	120.30
1	T	8	U	N1-C1'-C2'	5.27	120.85	114.00
2	B	855	TRP	CG-CD2-CE3	5.27	138.64	133.90
2	A	118	ARG	NE-CZ-NH1	5.26	122.93	120.30
2	A	146	TRP	CB-CG-CD2	-5.24	119.78	126.60
2	A	392	LEU	CA-CB-CG	5.24	127.35	115.30
2	B	730	LEU	CA-CB-CG	5.24	127.35	115.30
1	T	67	C	C5-C4-N4	-5.23	116.54	120.20
2	B	682	ARG	NE-CZ-NH1	5.22	122.91	120.30
1	T	51	G	P-O5'-C5'	-5.21	112.56	120.90
2	B	519	ARG	NE-CZ-NH1	5.20	122.90	120.30
2	B	649	ARG	NE-CZ-NH2	-5.20	117.70	120.30
1	T	68	U	C5'-C4'-C3'	-5.18	107.72	116.00
2	A	174	ARG	NE-CZ-NH2	-5.17	117.71	120.30
1	T	60	U	N3-C2-O2	-5.17	118.58	122.20
1	T	47(D)	G	C8-N9-C4	-5.15	104.34	106.40
2	A	213	TRP	CG-CD2-CE3	5.15	138.53	133.90
2	B	662	LYS	O-C-N	-5.13	114.47	123.20
2	B	662	LYS	CA-C-N	5.13	126.46	116.20
2	A	356	GLN	CA-CB-CG	5.11	124.65	113.40
2	B	502	VAL	CA-CB-CG2	-5.11	103.23	110.90
1	T	45	A	O4'-C1'-N9	5.10	112.28	108.20
2	B	646	TRP	CG-CD1-NE1	-5.10	105.00	110.10
1	T	7	G	C8-N9-C4	-5.10	104.36	106.40
2	B	506	ARG	NE-CZ-NH2	-5.09	117.75	120.30
1	T	48	C	N1-C2-O2	5.09	121.95	118.90
2	A	292	ASP	CB-CG-OD1	5.08	122.88	118.30
2	B	835	VAL	CG1-CB-CG2	-5.08	102.78	110.90
2	A	347	HIS	CA-C-N	5.07	128.34	117.20
1	T	47(K)	C	N1-C1'-C2'	-5.06	106.43	112.00
2	B	864	TYR	CB-CG-CD2	-5.05	117.97	121.00
2	A	136	HIS	CA-CB-CG	5.05	122.19	113.60
2	B	606	TRP	CG-CD1-NE1	-5.05	105.05	110.10
2	A	370	ARG	NE-CZ-NH2	-5.04	117.78	120.30
2	A	344	ARG	NE-CZ-NH2	-5.04	117.78	120.30
1	T	13	G	N9-C1'-C2'	5.03	120.55	114.00
2	B	789	GLU	CA-CB-CG	5.03	124.46	113.40
2	B	813	TYR	CB-CG-CD1	-5.01	117.99	121.00
2	B	646	TRP	CB-CG-CD1	-5.01	120.49	127.00
1	T	67	C	N1-C2-O2	5.01	121.90	118.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	770	MET	CG-SD-CE	-5.01	92.19	100.20
2	B	535	ARG	NE-CZ-NH2	-5.00	117.80	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	T	1381	0	701	7	0
2	A	2982	0	2974	44	0
2	B	3373	0	3391	48	0
3	A	14	0	0	0	0
3	B	29	0	0	0	0
3	T	1	0	0	0	0
All	All	7780	0	7066	95	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 6.

All (95) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:A:21:LYS:HE3	2:A:105:PRO:HD3	1.51	0.92
2:A:36:GLU:HB3	2:A:90:LYS:HG2	1.74	0.70
2:B:550:GLU:HB3	2:B:576:LEU:HD21	1.75	0.67
2:A:382:LEU:HD21	2:A:387:ILE:HG21	1.80	0.64
2:B:558:VAL:N	2:B:559:PRO:HD2	2.13	0.64
2:B:693:TYR:HD1	2:B:720:LEU:HD22	1.64	0.62
2:B:775:PHE:HB2	2:B:884:THR:O	2.01	0.61
2:B:617:ASN:ND2	2:B:819:ALA:H	1.99	0.61
2:A:16:ARG:O	2:A:19:ARG:HB3	2.03	0.59
2:B:640:MET:HE1	2:B:769:LEU:HD11	1.84	0.59
2:B:857:ALA:HA	2:B:862:LEU:HD12	1.84	0.59
2:A:265:ASP:HB3	2:A:344:ARG:NH2	2.18	0.58

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:504:LEU:O	2:B:508:ARG:HG2	2.05	0.57
2:A:117:ASN:ND2	2:A:319:ALA:H	2.03	0.56
2:A:7:LEU:HD11	2:A:27:LEU:HD11	1.88	0.56
2:A:171:ALA:HB2	2:B:674:ARG:HH21	1.69	0.56
2:A:15:HIS:CE1	2:A:27:LEU:HB3	2.42	0.55
1:T:20(B):G:O6	1:T:47(Q):U:H2'	2.07	0.55
2:A:366:ASP:OD1	2:A:370:ARG:HB2	2.06	0.55
1:T:56:C:H1'	2:B:558:VAL:HG21	1.90	0.54
2:A:103:LEU:HD21	2:A:353:LEU:HD12	1.91	0.53
2:A:178:ASP:HB3	2:A:182:ARG:NH1	2.24	0.52
2:B:827:LYS:HD2	2:B:850:SER:HB3	1.92	0.52
2:A:406:GLN:HA	2:A:409:ILE:HD12	1.91	0.52
2:B:507:LEU:HD11	2:B:527:LEU:HD11	1.91	0.51
2:B:523:VAL:HG21	2:B:602:PRO:HG3	1.92	0.51
2:B:510:GLU:HB3	2:B:513:VAL:HG23	1.93	0.51
2:B:606:TRP:CD1	2:B:609:ALA:HB2	2.46	0.50
2:A:37:VAL:HG21	2:A:94:LEU:HD22	1.93	0.50
2:A:218:THR:HG22	2:A:220:LEU:H	1.75	0.50
2:A:18:ILE:HG23	2:A:23:VAL:HB	1.94	0.50
2:A:30:LEU:HD12	2:A:97:LEU:HB3	1.94	0.49
2:B:502:VAL:HG21	2:B:514:PHE:HE1	1.77	0.49
2:A:159:TYR:HD2	2:A:161:LEU:HD13	1.78	0.49
2:A:166:ALA:HB1	2:B:689:THR:HG23	1.95	0.49
2:B:523:VAL:HG21	2:B:602:PRO:CG	2.43	0.49
2:A:218:THR:CG2	2:A:220:LEU:H	2.26	0.49
2:B:502:VAL:HG21	2:B:514:PHE:CE1	2.48	0.49
2:A:347:HIS:HE1	2:A:381:ALA:O	1.96	0.49
2:B:603:LEU:HD21	2:B:853:LEU:HD12	1.95	0.48
2:B:853:LEU:O	2:B:875:TYR:HA	2.13	0.48
2:A:241:TYR:HB2	2:A:365:ARG:O	2.12	0.48
1:T:46:G:P	2:B:865:ARG:HH22	2.37	0.48
2:B:690:LEU:HD11	2:B:730:LEU:HD13	1.96	0.48
2:A:366:ASP:HB3	2:A:370:ARG:O	2.14	0.47
2:B:634:LEU:HB2	2:B:639:LEU:HD13	1.95	0.47
2:A:35:ARG:O	2:A:38:GLN:HG2	2.15	0.47
2:A:106:TRP:CE2	2:A:329:ARG:HD3	2.50	0.47
2:B:640:MET:CE	2:B:665:LEU:HD21	2.44	0.47
2:B:777:LYS:HE2	2:B:779:GLU:OE2	2.15	0.47
1:T:61:C:H2'	1:T:62:C:H6	1.79	0.47
1:T:42:G:H2'	1:T:43:G:O4'	2.15	0.46
2:B:558:VAL:N	2:B:559:PRO:CD	2.78	0.46
2:A:197:LYS:HA	2:A:200:LEU:HD12	1.97	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:T:20(B):G:H4'	1:T:21:A:O4'	2.16	0.46
2:A:33:LEU:O	2:A:37:VAL:HG23	2.17	0.45
2:A:126:PRO:HB3	2:A:336:TYR:CE2	2.52	0.45
2:A:311:LEU:HD13	2:A:335:VAL:HG11	1.99	0.45
2:A:104:PRO:HA	2:A:105:PRO:HD2	1.89	0.45
2:B:809:LEU:HG	2:B:891:LEU:HD21	1.99	0.44
2:A:346:THR:OG1	2:A:347:HIS:HD2	2.00	0.44
2:B:780:GLN:HE22	2:B:801:ASN:HB2	1.82	0.44
2:A:401:ARG:NH1	2:A:416:VAL:HG11	2.32	0.44
2:B:544:LEU:HA	2:B:583:LEU:HD23	1.98	0.44
1:T:61:C:H2'	1:T:62:C:C6	2.52	0.44
2:A:6:ARG:HA	2:A:9:GLN:HB3	1.99	0.44
2:B:639:LEU:HD21	2:B:896:GLN:HB3	2.00	0.43
2:B:647:GLU:HB3	2:B:660:ALA:HB3	2.00	0.43
2:A:146:TRP:O	2:A:148:PRO:HD3	2.18	0.43
2:B:677:MET:HE2	2:B:687:PRO:HB3	2.00	0.43
2:B:505:LYS:HD2	2:B:505:LYS:HA	1.82	0.43
2:B:758:GLU:HG3	2:B:761:SER:OG	2.19	0.43
2:B:504:LEU:HD13	2:B:598:LEU:HD11	2.01	0.43
2:A:265:ASP:HB3	2:A:344:ARG:HH21	1.84	0.42
2:B:699:PHE:CE2	2:B:721:TYR:HB2	2.54	0.42
2:A:132:PRO:HA	2:A:133:PRO:HD2	1.85	0.42
2:B:617:ASN:HD22	2:B:819:ALA:H	1.66	0.42
2:A:357:ALA:HA	2:A:362:LEU:HD12	2.01	0.42
2:A:2:VAL:HG21	2:A:14:PHE:CE1	2.54	0.42
2:B:631:PHE:HD2	2:B:632:PRO:O	2.02	0.42
2:B:601:VAL:HA	2:B:602:PRO:HD3	1.74	0.42
2:A:193:TYR:HA	2:A:221:TYR:O	2.20	0.41
2:B:693:TYR:CD1	2:B:720:LEU:HD22	2.49	0.41
2:B:562:PRO:O	2:B:564:GLU:N	2.52	0.41
2:A:310:GLU:O	2:A:395:HIS:HE1	2.03	0.41
2:B:574:LYS:HE3	2:B:574:LYS:HB3	1.91	0.40
2:B:543:ARG:HD3	2:B:543:ARG:HA	1.93	0.40
2:B:559:PRO:O	2:B:560:LYS:HB2	2.22	0.40
2:A:143:ASN:OD1	2:A:419:PRO:HG3	2.21	0.40
2:A:37:VAL:HG22	2:A:90:LYS:HB3	2.03	0.40
2:B:504:LEU:HD12	2:B:507:LEU:HD23	2.02	0.40
2:A:159:TYR:CD2	2:A:161:LEU:HD13	2.56	0.40
2:B:534:ASP:O	2:B:538:GLN:HG2	2.22	0.40
2:B:741:TYR:HB2	2:B:865:ARG:O	2.22	0.40
2:A:15:HIS:CD2	2:A:27:LEU:HD23	2.57	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 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 X-ray entries followed by that with respect to entries of similar resolution. 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	
2	A	368/421 (87%)	345 (94%)	20 (5%)	3 (1%)	27	68
2	B	419/421 (100%)	405 (97%)	10 (2%)	4 (1%)	22	63
All	All	787/842 (94%)	750 (95%)	30 (4%)	7 (1%)	25	66

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	765	ASP
2	A	35	ARG
2	B	564	GLU
2	A	126	PRO
2	A	338	PRO
2	B	838	PRO
2	B	563	PRO

5.3.2 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 X-ray entries followed by that with respect to entries of similar resolution. 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	
2	A	307/347 (88%)	269 (88%)	38 (12%)	7	19
2	B	347/347 (100%)	319 (92%)	28 (8%)	17	45
All	All	654/694 (94%)	588 (90%)	66 (10%)	11	32

All (66) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	5	LYS
2	A	6	ARG

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Mol	Chain	Res	Type
2	A	9	GLN
2	A	12	GLU
2	A	35	ARG
2	A	88	ARG
2	A	89	GLU
2	A	91	GLU
2	A	95	GLU
2	A	98	LEU
2	A	115	GLU
2	A	130	SER
2	A	141	GLU
2	A	146	TRP
2	A	156	SER
2	A	161	LEU
2	A	167	LEU
2	A	168	TYR
2	A	182	ARG
2	A	217	GLU
2	A	218	THR
2	A	230	LEU
2	A	253	PRO
2	A	261	SER
2	A	262	PHE
2	A	285	GLU
2	A	289	GLU
2	A	298	LEU
2	A	299	LEU
2	A	306	LEU
2	A	308	LEU
2	A	309	LEU
2	A	329	ARG
2	A	338	PRO
2	A	363	ARG
2	A	366	ASP
2	A	390	MET
2	A	408	LEU
2	B	502	VAL
2	B	505	LYS
2	B	512	GLU
2	B	530	LEU
2	B	531	LEU
2	B	539	GLU

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Mol	Chain	Res	Type
2	B	564	GLU
2	B	565	GLU
2	B	576	LEU
2	B	583	LEU
2	B	597	LEU
2	B	630	SER
2	B	635	ASP
2	B	637	VAL
2	B	656	SER
2	B	674	ARG
2	B	717	GLU
2	B	730	LEU
2	B	761	SER
2	B	783	LEU
2	B	793	ARG
2	B	799	LEU
2	B	838	PRO
2	B	842	ARG
2	B	884	THR
2	B	887	ILE
2	B	904	VAL
2	B	906	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
2	A	9	GLN
2	A	15	HIS
2	A	117	ASN
2	A	152	GLN
2	A	276	HIS
2	A	280	GLN
2	A	301	ASN
2	A	347	HIS
2	A	395	HIS
2	B	538	GLN
2	B	617	ASN
2	B	636	HIS
2	B	643	ASN
2	B	776	HIS
2	B	780	GLN
2	B	801	ASN

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Mol	Chain	Res	Type
2	B	879	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	T	61/94 (64%)	11 (18%)	5 (8%)

All (11) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	T	7	G
1	T	8	U
1	T	9	G
1	T	16	U
1	T	18	G
1	T	20(A)	H2U
1	T	20(B)	G
1	T	25	G
1	T	45	A
1	T	46	G
1	T	61	C

All (5) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	T	7	G
1	T	16	U
1	T	20(A)	H2U
1	T	24	G
1	T	45	A

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

3 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or 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 length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is

the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	H2U	T	20(A)	1	19,21,22	1.08	2 (10%)	27,30,33	1.15	2 (7%)
1	5MU	T	54	1	20,22,23	1.24	3 (15%)	25,32,35	1.22	2 (8%)
1	PSU	T	55	1	19,21,22	1.35	2 (10%)	23,30,33	2.98	7 (30%)

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
1	H2U	T	20(A)	1	-	0/8/38/39	0/2/2/2
1	5MU	T	54	1	-	0/6/25/26	0/2/2/2
1	PSU	T	55	1	-	0/8/25/26	0/2/2/2

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	T	55	PSU	C6-N1	4.17	1.36	1.32
1	T	54	5MU	O4'-C1'	2.98	1.45	1.41
1	T	20(A)	H2U	C5-C4	-2.63	1.43	1.50
1	T	54	5MU	C2-N1	2.34	1.40	1.38
1	T	54	5MU	C6-C5	-2.21	1.34	1.40
1	T	55	PSU	C6-C5	-2.14	1.34	1.38
1	T	20(A)	H2U	C2-N1	2.12	1.38	1.35

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	T	55	PSU	O4'-C1'-C5	11.64	124.03	109.55
1	T	55	PSU	C5-C4-N3	-3.98	111.61	118.86
1	T	55	PSU	C5-C1'-C2'	-3.83	108.85	115.61
1	T	54	5MU	C6-N1-C2	-3.52	121.41	122.41
1	T	20(A)	H2U	C5-C4-N3	-3.12	113.83	116.76
1	T	55	PSU	C6-C5-C4	3.05	123.24	116.72
1	T	20(A)	H2U	N3-C2-N1	-2.55	114.21	116.71
1	T	55	PSU	C6-C5-C1'	-2.51	116.77	121.36
1	T	55	PSU	C5'-C4'-C3'	-2.49	105.25	115.21
1	T	55	PSU	O3'-C3'-C4'	2.44	118.28	111.08
1	T	54	5MU	C6-C5-C4	2.38	120.89	115.11

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.