wwPDB X-ray Structure Validation Summary Report (i)

Aug 20, 2023 – 09:34 AM EDT

PDB ID	:	2NR0
Title	:	Crystal structure of pseudoudirinde synthase TruA in complex with leucyl tRNA
Authors	:	Hur, S.; Stroud, R.M.
Deposited on	:	2006-11-01
Resolution	:	3.90 Å(reported)

This is a wwPDB X-ray 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
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) 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 (1)) were used in the production of this report:

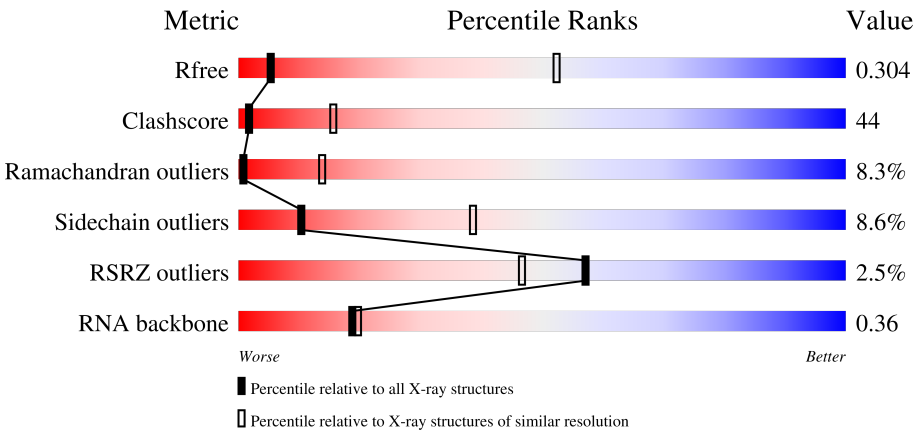
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.35
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.90 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))
R_{free}	130704	1002 (4.14-3.66)
Clashscore	141614	1004 (4.12-3.68)
Ramachandran outliers	138981	1021 (4.14-3.66)
Sidechain outliers	138945	1014 (4.14-3.66)
RSRZ outliers	127900	1275 (4.20-3.60)
RNA backbone	3102	1040 (4.76-3.00)

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 of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. 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% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	E	87	13%; 17%, 49%, 23%, •, 7%
1	F	87	10%; 7%, 40%, 28%, 8%, 17%
1	G	87	2%; 14%, 33%, 28%, •, 23%
1	H	87	10%; 21%, 32%, 18%, •, 25%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	A	270	30% 57% 10%
2	B	270	30% 56% 10%
2	C	270	30% 58% 9%
2	D	270	31% 57% 10%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 14269 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 leucyl tRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
1	E	81	1682	748	292	562	80	0	0	0
1	F	72	1544	687	266	518	73	0	2	0
1	G	67	1422	634	251	471	66	0	0	0
1	H	65	1343	595	236	448	64	0	0	0

- Molecule 2 is a protein called tRNA pseudouridine synthase A.

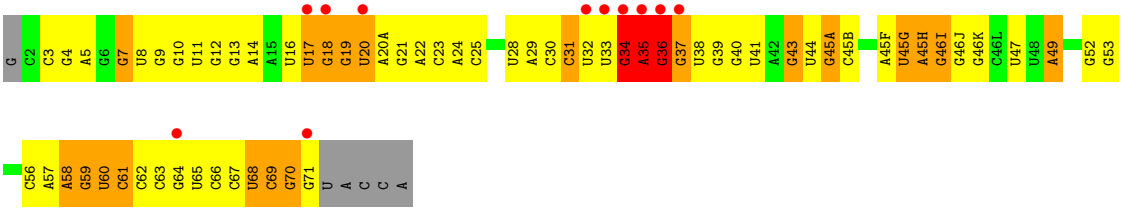
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	A	264	2071	1316	378	369	8	0	0	0
2	B	264	2082	1323	378	373	8	0	0	0
2	C	264	2056	1308	371	369	8	0	0	0
2	D	264	2069	1317	373	371	8	0	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes 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.

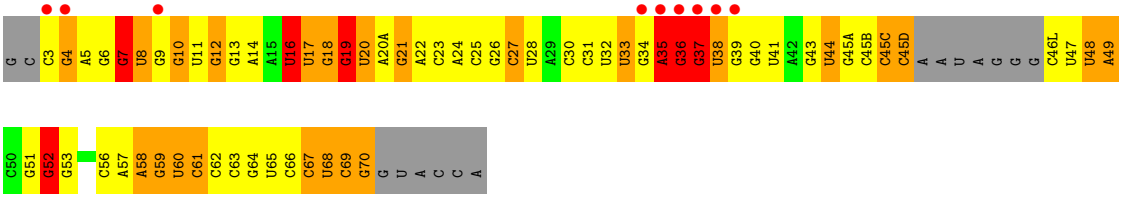
- Molecule 1: leucyl tRNA

Chain E:



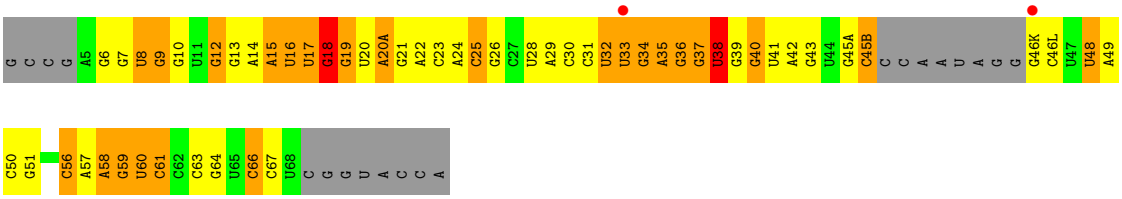
- Molecule 1: leucyl tRNA

Chain F:



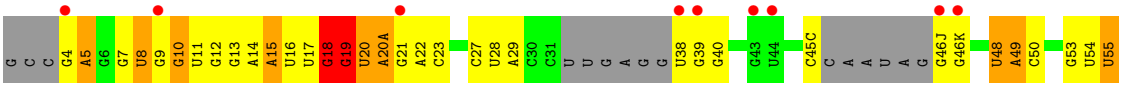
- Molecule 1: leucyl tRNA

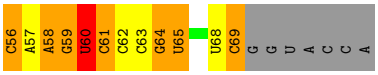
Chain G:



- Molecule 1: leucyl tRNA

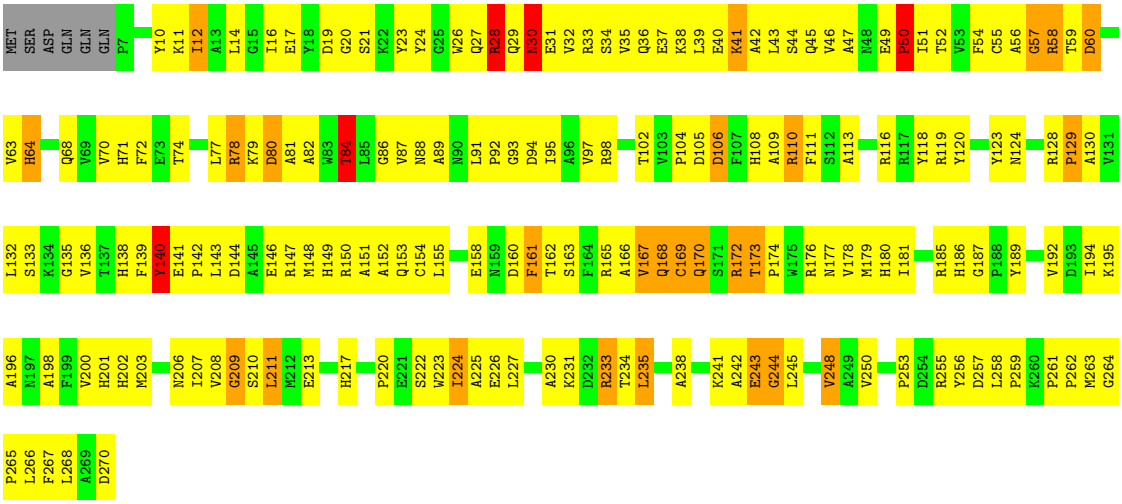
Chain H:





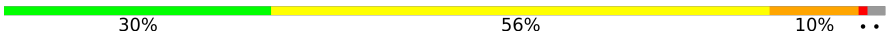
- Molecule 2: tRNA pseudouridine synthase A

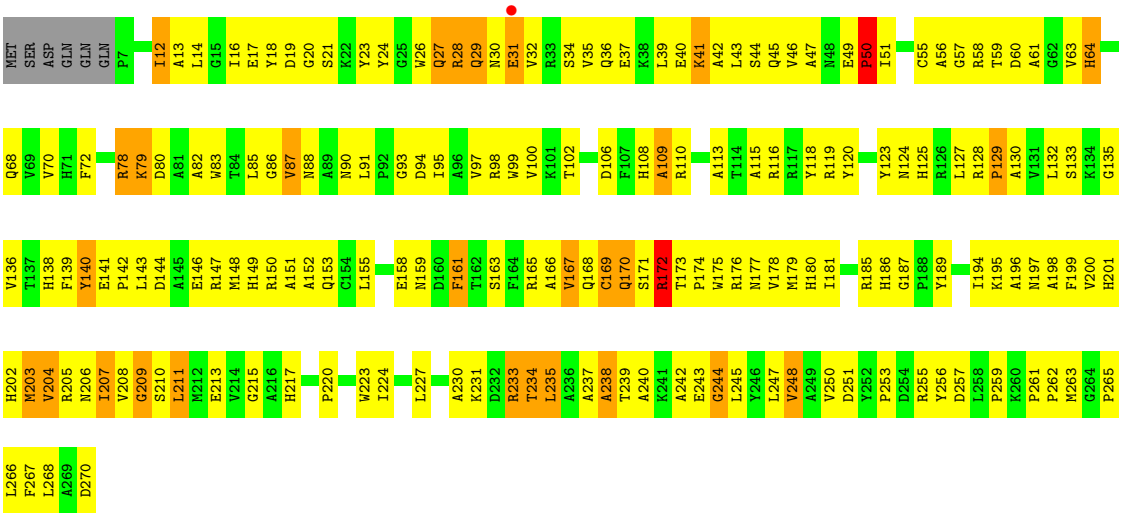
Chain A:



- Molecule 2: tRNA pseudouridine synthase A

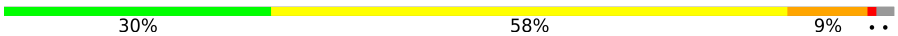
Chain B:

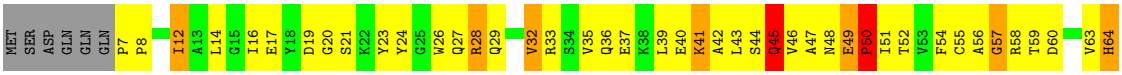


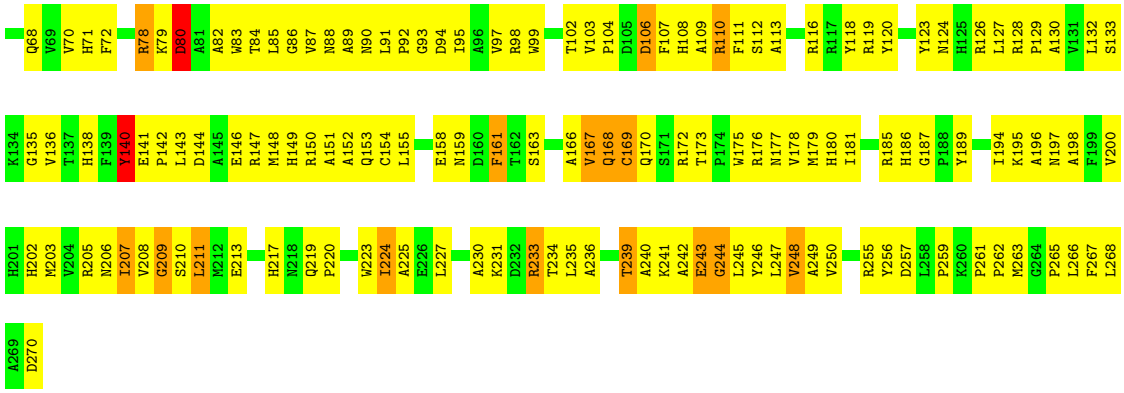


- Molecule 2: tRNA pseudouridine synthase A

Chain C:

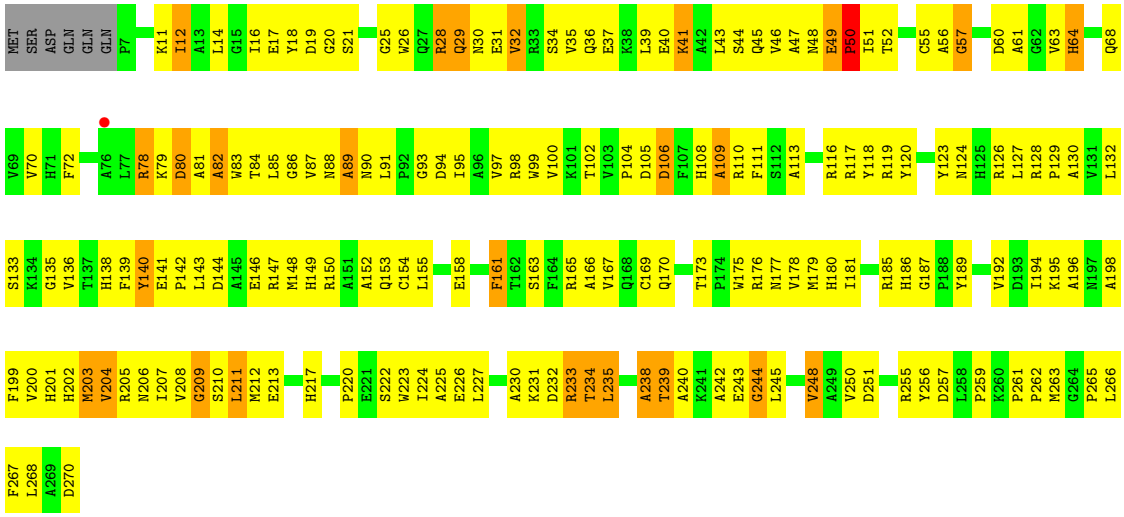






- Molecule 2: tRNA pseudouridine synthase A

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	65.03Å 149.29Å 291.99Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 3.90 65.58 – 3.82	Depositor EDS
% Data completeness (in resolution range)	89.4 (50.00-3.90) 88.3 (65.58-3.82)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.21	Depositor
$< I/\sigma(I) >$ [1]	4.27 (at 3.77Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.298 , 0.350 0.260 , 0.304	Depositor DCC
R_{free} test set	1361 reflections (4.84%)	wwPDB-VP
Wilson B-factor (Å^2)	74.8	Xtriage
Anisotropy	0.792	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.24 , 31.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.84	EDS
Total number of atoms	14269	wwPDB-VP
Average B, all atoms (Å^2)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.82% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality (i)

5.1 Standard geometry (i)

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	E	0.62	1/1877 (0.1%)	0.81	4/2922 (0.1%)
1	F	0.65	0/1723	0.90	5/2683 (0.2%)
1	G	0.61	0/1588	0.77	2/2473 (0.1%)
1	H	0.58	0/1495	0.81	3/2323 (0.1%)
2	A	0.62	0/2127	0.69	0/2899
2	B	0.61	0/2138	0.72	0/2913
2	C	0.60	0/2111	0.72	0/2879
2	D	0.60	0/2125	0.68	0/2897
All	All	0.61	1/15184 (0.0%)	0.76	14/21989 (0.1%)

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 outliers	#Planarity outliers
1	F	0	4
1	G	0	1
1	H	0	2
All	All	0	7

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	35	A	O3'-P	-7.94	1.51	1.61

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	F	35	A	P-O3'-C3'	11.98	134.08	119.70
1	F	36	G	OP1-P-OP2	-7.85	107.83	119.60
1	H	19	G	N9-C1'-C2'	7.30	123.49	114.00
1	F	16	U	N1-C1'-C2'	6.90	122.97	114.00

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	E	34	G	OP1-P-OP2	-6.62	109.67	119.60

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	F	19	G	Sidechain
1	F	36	G	Sidechain
1	F	37	G	Sidechain
1	F	52	G	Sidechain
1	G	38	U	Sidechain

5.2 Too-close contacts (i)

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 hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	1682	0	846	92	0
1	F	1544	0	779	108	0
1	G	1422	0	718	91	0
1	H	1343	0	678	52	0
2	A	2071	0	2012	202	0
2	B	2082	0	2029	203	0
2	C	2056	0	1988	208	0
2	D	2069	0	2012	204	0
All	All	14269	0	11062	1103	0

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.

The worst 5 of 1103 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:34:G:H4'	1:E:35:A:OP1	1.48	1.13
1:H:58:A:H4'	1:H:59:G:OP1	1.45	1.10
2:B:88:ASN:HA	2:B:91:LEU:HD12	1.38	1.06

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:28:ARG:HG2	2:C:29:GLN:H	1.20	1.03
1:H:15:A:H61	1:H:48:U:H3	1.02	0.99

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 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 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	262/270 (97%)	195 (74%)	46 (18%)	21 (8%)	1	15
2	B	262/270 (97%)	192 (73%)	50 (19%)	20 (8%)	1	16
2	C	262/270 (97%)	193 (74%)	44 (17%)	25 (10%)	0	11
2	D	262/270 (97%)	196 (75%)	45 (17%)	21 (8%)	1	15
All	All	1048/1080 (97%)	776 (74%)	185 (18%)	87 (8%)	1	14

5 of 87 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	58	ARG
2	A	80	ASP
2	A	109	ALA
2	A	167	VAL
2	A	243	GLU

5.3.2 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 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	210/223 (94%)	189 (90%)	21 (10%)	7	30
2	B	213/223 (96%)	192 (90%)	21 (10%)	8	31
2	C	207/223 (93%)	193 (93%)	14 (7%)	16	45
2	D	211/223 (95%)	195 (92%)	16 (8%)	13	42
All	All	841/892 (94%)	769 (91%)	72 (9%)	10	38

5 of 72 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	28	ARG
2	D	248	VAL
2	D	32	VAL
2	D	106	ASP
2	B	29	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 29 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	218	ASN
2	D	202	HIS
2	C	153	GLN
2	D	182	ASN
2	C	124	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	E	79/87 (90%)	26 (32%)	5 (6%)
1	F	68/87 (78%)	35 (51%)	9 (13%)
1	G	65/87 (74%)	27 (41%)	5 (7%)
1	H	59/87 (67%)	21 (35%)	5 (8%)
All	All	271/348 (77%)	109 (40%)	24 (8%)

5 of 109 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	E	3	C
1	E	8	U
1	E	10	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	E	17	U
1	E	18	G

5 of 24 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	G	18	G
1	G	58	A
1	G	37	G
1	G	60	U
1	F	16	U

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	F	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	F	38:U	O3'	39[B]:G	P	10.17

6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	E	81/87 (93%)	0.47	11 (13%) 3 3	14, 62, 98, 105	4 (4%)
1	F	72/87 (82%)	0.77	9 (12%) 3 4	6, 44, 116, 134	8 (11%)
1	G	67/87 (77%)	0.20	2 (2%) 50 38	14, 52, 105, 121	2 (2%)
1	H	65/87 (74%)	0.80	9 (13%) 2 3	5, 53, 121, 138	2 (3%)
2	A	264/270 (97%)	-0.29	0 100 100	1, 12, 32, 50	0
2	B	264/270 (97%)	-0.32	1 (0%) 92 87	1, 12, 33, 50	0
2	C	264/270 (97%)	-0.36	0 100 100	1, 13, 34, 50	0
2	D	264/270 (97%)	-0.23	1 (0%) 92 87	1, 11, 34, 51	0
All	All	1341/1428 (93%)	-0.12	33 (2%) 57 47	1, 16, 79, 138	16 (1%)

The worst 5 of 33 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	3	C	8.3
1	E	17	U	5.2
1	H	43	G	4.4
1	G	46(K)	G	4.2
1	H	46(J)	G	3.6

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

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

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.