wwPDB X-ray Structure Validation Summary Report (i)

Feb 1, 2016 – 05:38 AM GMT

PDB ID	:	2RHB
Title	:	Crystal structure of Nsp15-H234A mutant- Hexamer in asymmetric unit
Authors	:	Palaninathan, S.; Bhardwaj, K.; Alcantara, J.M.O.; Guarino, L.; Yi, L.L.; Kao, C.C.; Sacchettini, J.
Deposited on	:	2007-10-08
Resolution	:	2.80 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
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

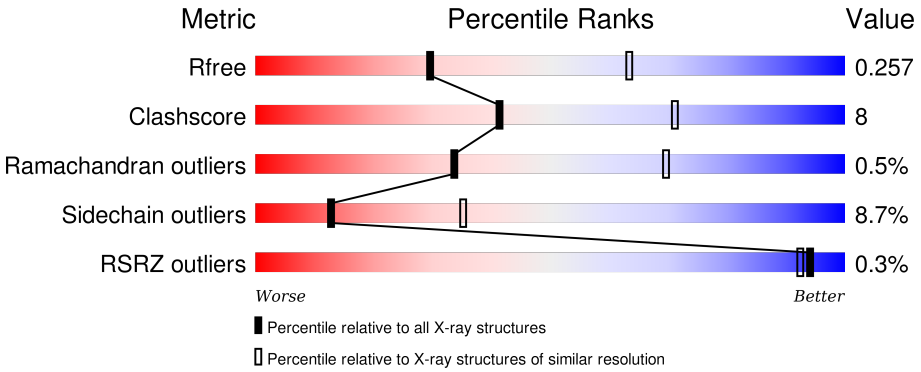
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

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 2.80 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}	91344	2393 (2.80-2.80)
Clashscore	102246	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)
RSRZ outliers	91569	2404 (2.80-2.80)

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. 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	A	353	76% 17%
1	B	353	% 79% 16%
1	C	353	78% 16%
1	D	353	78% 18%
1	E	353	% 77% 18%

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Mol	Chain	Length	Quality of chain
1	F	353	

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 16512 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 protein called Uridylate-specific endoribonuclease.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	345	Total	C	N	O	S	0	1	0
			2688	1717	437	522	12			
1	B	346	Total	C	N	O	S	0	0	0
			2689	1719	439	519	12			
1	C	345	Total	C	N	O	S	0	1	0
			2696	1723	439	522	12			
1	D	346	Total	C	N	O	S	0	0	0
			2681	1714	436	519	12			
1	E	346	Total	C	N	O	S	0	1	0
			2637	1676	436	513	12			
1	F	344	Total	C	N	O	S	0	1	0
			2680	1713	437	519	11			

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	HIS	-	expression tag	UNP P59641
A	-5	HIS	-	expression tag	UNP P59641
A	-4	HIS	-	expression tag	UNP P59641
A	-3	HIS	-	expression tag	UNP P59641
A	-2	HIS	-	expression tag	UNP P59641
A	-1	HIS	-	expression tag	UNP P59641
A	0	MET	-	expression tag	UNP P59641
A	234	ALA	HIS	engineered	UNP P59641
B	-6	HIS	-	expression tag	UNP P59641
B	-5	HIS	-	expression tag	UNP P59641
B	-4	HIS	-	expression tag	UNP P59641
B	-3	HIS	-	expression tag	UNP P59641
B	-2	HIS	-	expression tag	UNP P59641
B	-1	HIS	-	expression tag	UNP P59641
B	0	MET	-	expression tag	UNP P59641
B	234	ALA	HIS	engineered	UNP P59641
C	-6	HIS	-	expression tag	UNP P59641

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-5	HIS	-	expression tag	UNP P59641
C	-4	HIS	-	expression tag	UNP P59641
C	-3	HIS	-	expression tag	UNP P59641
C	-2	HIS	-	expression tag	UNP P59641
C	-1	HIS	-	expression tag	UNP P59641
C	0	MET	-	expression tag	UNP P59641
C	234	ALA	HIS	engineered	UNP P59641
D	-6	HIS	-	expression tag	UNP P59641
D	-5	HIS	-	expression tag	UNP P59641
D	-4	HIS	-	expression tag	UNP P59641
D	-3	HIS	-	expression tag	UNP P59641
D	-2	HIS	-	expression tag	UNP P59641
D	-1	HIS	-	expression tag	UNP P59641
D	0	MET	-	expression tag	UNP P59641
D	234	ALA	HIS	engineered	UNP P59641
E	-6	HIS	-	expression tag	UNP P59641
E	-5	HIS	-	expression tag	UNP P59641
E	-4	HIS	-	expression tag	UNP P59641
E	-3	HIS	-	expression tag	UNP P59641
E	-2	HIS	-	expression tag	UNP P59641
E	-1	HIS	-	expression tag	UNP P59641
E	0	MET	-	expression tag	UNP P59641
E	234	ALA	HIS	engineered	UNP P59641
F	-6	HIS	-	expression tag	UNP P59641
F	-5	HIS	-	expression tag	UNP P59641
F	-4	HIS	-	expression tag	UNP P59641
F	-3	HIS	-	expression tag	UNP P59641
F	-2	HIS	-	expression tag	UNP P59641
F	-1	HIS	-	expression tag	UNP P59641
F	0	MET	-	expression tag	UNP P59641
F	234	ALA	HIS	engineered	UNP P59641

- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	107	Total O 107 107	0	0
2	B	111	Total O 111 111	0	0
2	C	77	Total O 77 77	0	0
2	D	52	Total O 52 52	0	0

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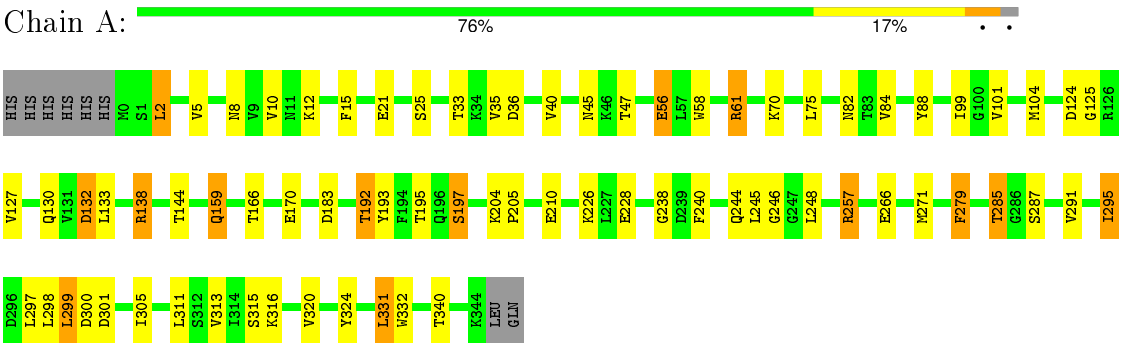
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	E	48	Total O 48 48	0	0
2	F	46	Total O 46 46	0	0

3 Residue-property plots (i)

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.

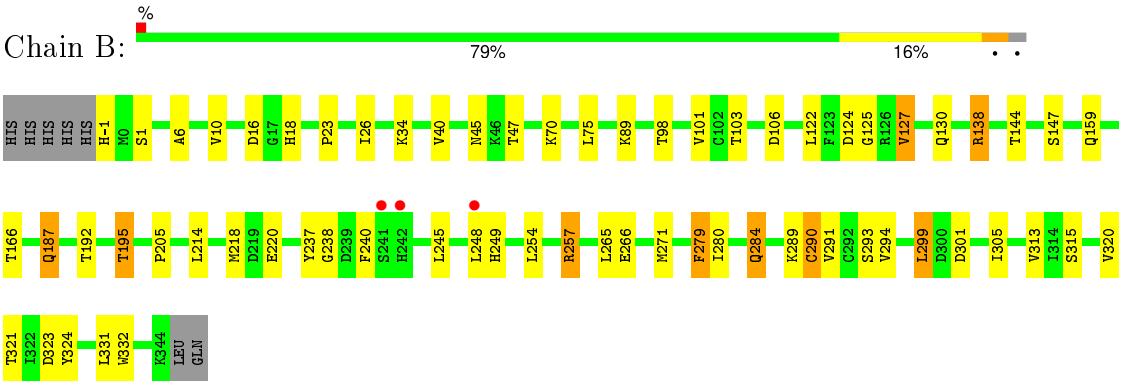
- Molecule 1: Uridylate-specific endoribonuclease

Chain A:



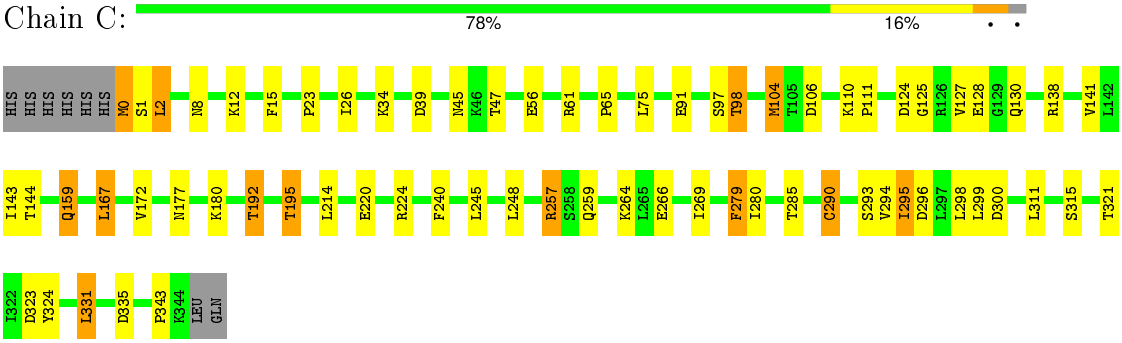
- Molecule 1: Uridylate-specific endoribonuclease

Chain B:



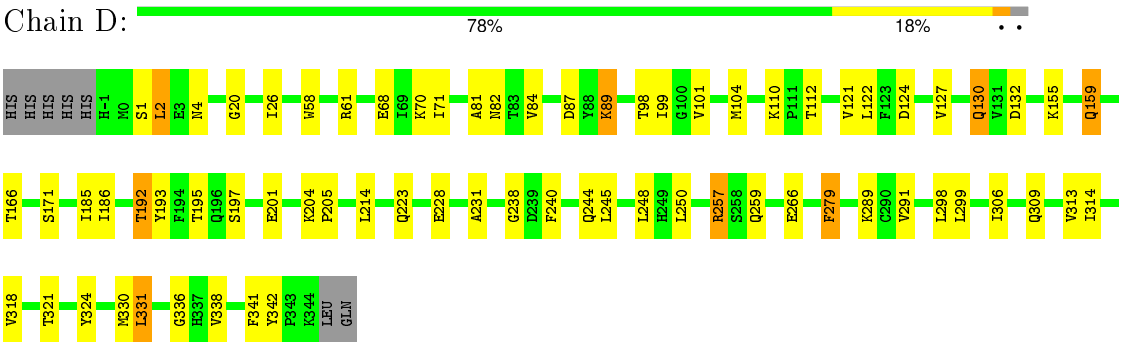
- Molecule 1: Uridylate-specific endoribonuclease

Chain C:



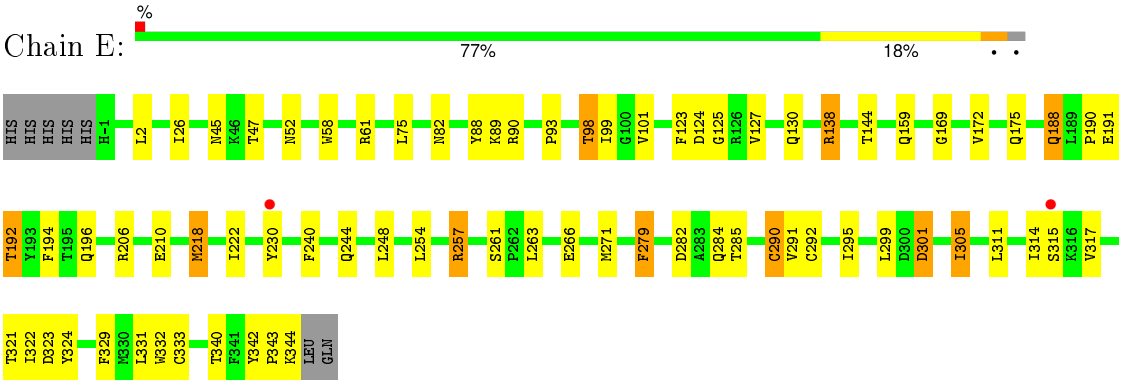
- Molecule 1: Uridylate-specific endoribonuclease

Chain D:



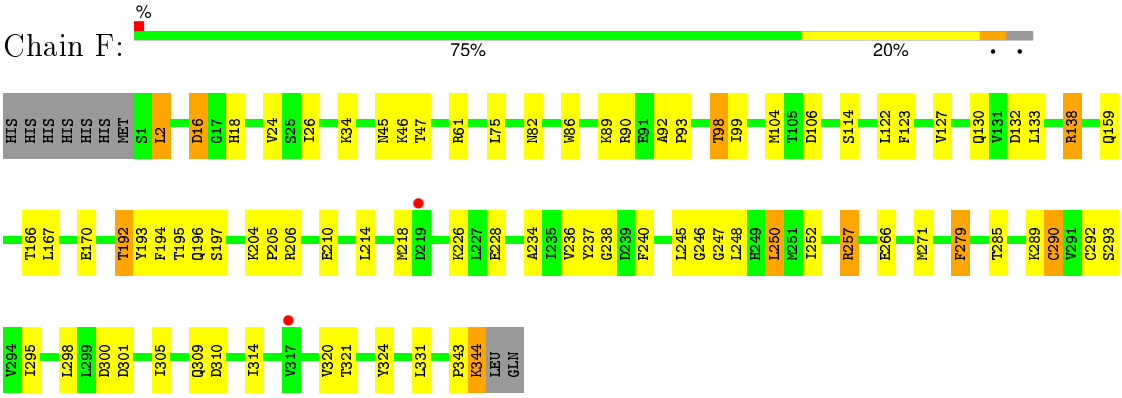
- Molecule 1: Uridylate-specific endoribonuclease

Chain E:



- Molecule 1: Uridylate-specific endoribonuclease

Chain F:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α, β, γ	305.76Å 305.76Å 88.74Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.00 – 2.80 34.01 – 2.65	Depositor EDS
% Data completeness (in resolution range)	92.0 (50.00-2.80) 86.7 (34.01-2.65)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.70 (at 2.65Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.198 , 0.260 0.206 , 0.257	Depositor DCC
R_{free} test set	3507 reflections (5.27%)	DCC
Wilson B-factor (Å^2)	49.6	Xtriage
Anisotropy	0.106	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.28 , 41.3	EDS
Estimated twinning fraction	0.025 for h,-h-k,-l	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Outliers	0 of 78182 reflections	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	16512	wwPDB-VP
Average B, all atoms (Å^2)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.87% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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	A	0.34	0/2745	0.53	0/3725
1	B	0.34	0/2742	0.55	0/3720
1	C	0.35	0/2753	0.56	0/3733
1	D	0.34	0/2733	0.53	0/3709
1	E	0.35	0/2691	0.51	0/3654
1	F	0.34	0/2738	0.53	0/3715
All	All	0.34	0/16402	0.53	0/22256

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 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 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	A	2688	0	2659	41	0
1	B	2689	0	2668	54	0
1	C	2696	0	2681	46	0
1	D	2681	0	2654	53	0
1	E	2637	0	2564	45	0
1	F	2680	0	2659	51	0
2	A	107	0	0	0	0
2	B	111	0	0	1	0
2	C	77	0	0	1	0
2	D	52	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	E	48	0	0	1	0
2	F	46	0	0	0	0
All	All	16512	0	15885	270	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 8.

The worst 5 of 270 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:D:192:THR:HG21	1:D:324:TYR:H	1.23	1.02
1:D:98:THR:HG21	1:D:101:VAL:HB	1.40	1.01
1:F:192:THR:HG21	1:F:324:TYR:H	1.24	1.00
1:B:98:THR:HG22	1:B:106:ASP:OD1	1.62	0.99
1:E:192:THR:HG21	1:E:324:TYR:H	1.26	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
1	A	344/353 (98%)	330 (96%)	12 (4%)	2 (1%)	30 65
1	B	344/353 (98%)	330 (96%)	13 (4%)	1 (0%)	46 79
1	C	344/353 (98%)	326 (95%)	15 (4%)	3 (1%)	21 55
1	D	344/353 (98%)	325 (94%)	17 (5%)	2 (1%)	30 65
1	E	345/353 (98%)	325 (94%)	18 (5%)	2 (1%)	30 65
1	F	343/353 (97%)	326 (95%)	17 (5%)	0	100 100
All	All	2064/2118 (98%)	1962 (95%)	92 (4%)	10 (0%)	34 69

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	295	ILE
1	D	336	GLY
1	C	128	GLU
1	D	291	VAL
1	A	226	LYS

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
1	A	299/309 (97%)	267 (89%)	32 (11%)	8 24
1	B	298/309 (96%)	277 (93%)	21 (7%)	19 47
1	C	301/309 (97%)	273 (91%)	28 (9%)	11 32
1	D	296/309 (96%)	274 (93%)	22 (7%)	17 43
1	E	285/309 (92%)	267 (94%)	18 (6%)	22 53
1	F	298/309 (96%)	264 (89%)	34 (11%)	7 21
All	All	1777/1854 (96%)	1622 (91%)	155 (9%)	13 35

5 of 155 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	257	ARG
1	D	132	ASP
1	F	271	MET
1	C	279	PHE
1	C	321	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 43 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	45	ASN
1	D	284	GLN

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Mol	Chain	Res	Type
1	F	159	GLN
1	D	130	GLN
1	D	159	GLN

5.3.3 RNA

There are no RNA molecules in this entry.

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

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

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

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, 95^{th} 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	A	345/353 (97%)	-0.62	0 100 100	35, 50, 68, 74	0
1	B	346/353 (98%)	-0.57	3 (0%) 85 79	34, 47, 75, 93	0
1	C	345/353 (97%)	-0.50	0 100 100	38, 54, 73, 79	0
1	D	346/353 (98%)	-0.48	0 100 100	37, 63, 86, 92	0
1	E	346/353 (98%)	-0.28	2 (0%) 90 86	38, 70, 99, 107	0
1	F	344/353 (97%)	-0.22	2 (0%) 90 86	39, 76, 99, 104	0
All	All	2072/2118 (97%)	-0.44	7 (0%) 94 92	34, 59, 91, 107	0

The worst 5 of 7 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	230	TYR	3.0
1	B	242	HIS	2.9
1	E	315	SER	2.7
1	B	241	SER	2.6
1	F	219	ASP	2.5

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

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

6.3 Carbohydrates

There are no carbohydrates in this entry.

6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.