



# wwPDB X-ray Structure Validation Summary Report

Mar 7, 2026 – 02:12 AM UTC

PDB ID : 3TBF / pdb\_00003tbf  
Title : C-terminal domain of glucosamine-fructose-6-phosphate aminotransferase from Francisella tularensis.  
Authors : Osipiuk, J.; Zhou, M.; Maltseva, N.; Kim, Y.; Papazisi, L.; Anderson, W.F.; Joachimiak, A.; Center for Structural Genomics of Infectious Diseases (CS-GID)  
Deposited on : 2011-08-05  
Resolution : 2.28 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](mailto: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  symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 2.0  
EDS : 3.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

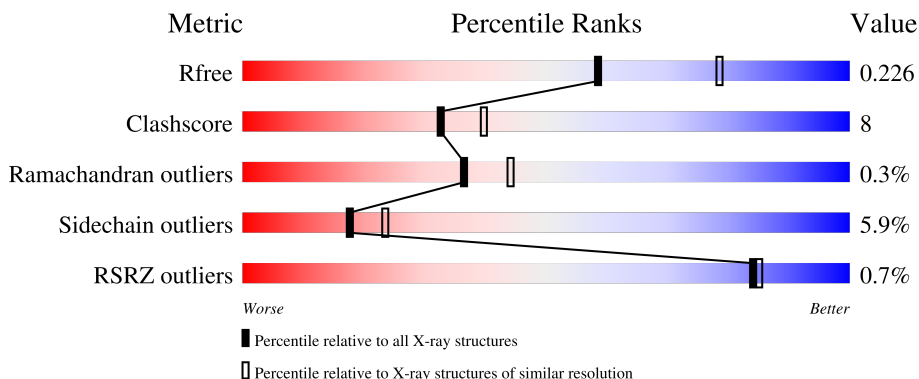
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*



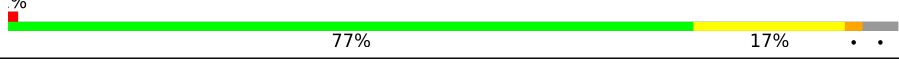

The reported resolution of this entry is 2.28 Å.

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))
$R_{free}$	180053	9078 (2.30-2.26)
Clashscore	190562	9802 (2.30-2.26)
Ramachandran outliers	187476	9690 (2.30-2.26)
Sidechain outliers	187428	9691 (2.30-2.26)
RSRZ outliers	180081	9085 (2.30-2.26)

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  $\geq 3$ , 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  $\leq 5\%$ . 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	372	 77% 18% . .
1	B	372	 % 73% 19% . 5%
1	C	372	 % 77% 17% . .
1	D	372	 78% 17% . .

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Mol	Chain	Length	Quality of chain
1	E	372	 78% 17% . .
1	F	372	 % 78% 17% . .
1	G	372	 % 72% 23% . .
1	H	372	 2% 71% 23% . .

## 2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 22905 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 Glucosamine--fructose-6-phosphate aminotransferase [isomerizing].

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	357	Total	C	N	O	S	Se	0	3	0
			2792	1786	456	539	5	6			
1	B	354	Total	C	N	O	S	Se	0	1	0
			2745	1755	447	532	5	6			
1	C	358	Total	C	N	O	S	Se	0	4	0
			2794	1787	455	539	7	6			
1	D	357	Total	C	N	O	S	Se	0	4	0
			2790	1785	455	537	7	6			
1	E	358	Total	C	N	O	S	Se	0	4	0
			2793	1786	455	538	8	6			
1	F	358	Total	C	N	O	S	Se	0	3	0
			2790	1786	455	536	7	6			
1	G	357	Total	C	N	O	S	Se	0	4	0
			2791	1785	454	539	7	6			
1	H	357	Total	C	N	O	S	Se	0	6	0
			2796	1786	456	541	7	6			

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	68	Total	O	0	1
			68	68		
2	B	66	Total	O	0	0
			66	66		
2	C	97	Total	O	0	0
			97	97		
2	D	97	Total	O	0	0
			97	97		
2	E	93	Total	O	0	0
			93	93		
2	F	85	Total	O	0	0
			85	85		

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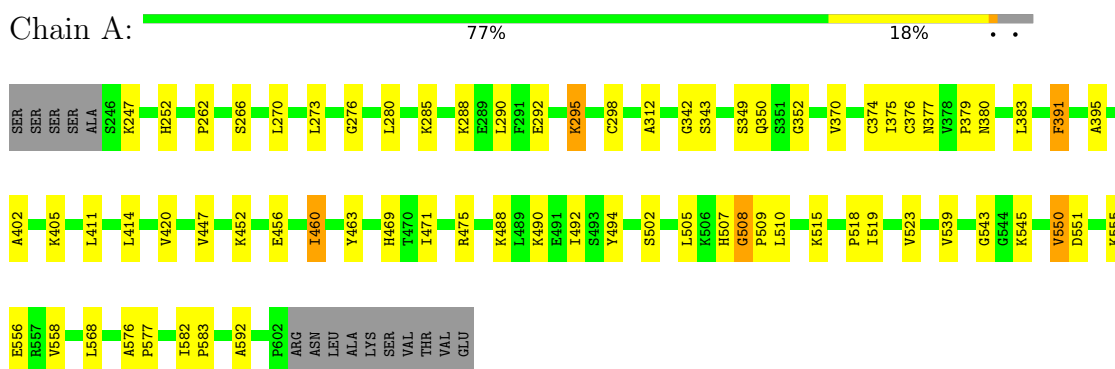
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<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>	<b>ZeroOcc</b>	<b>AltConf</b>
2	G	51	Total O 51 51	0	0
2	H	57	Total O 57 57	0	0

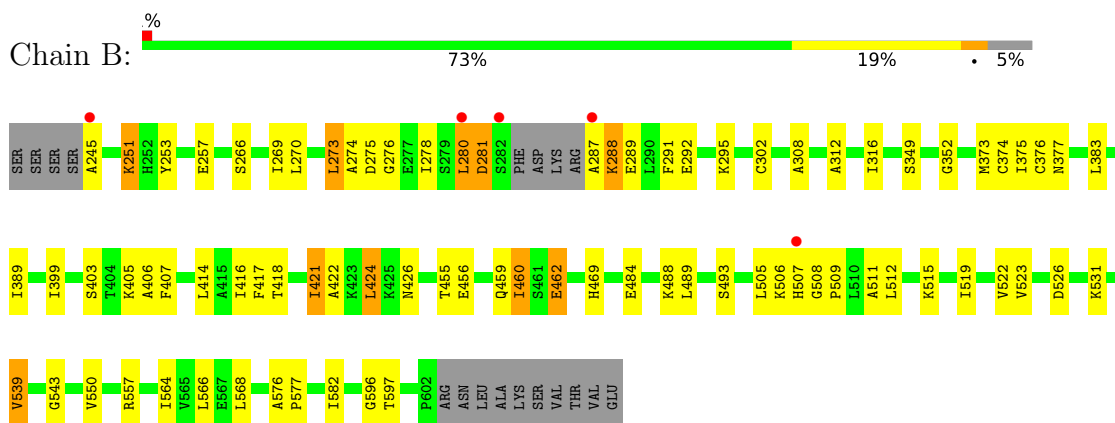
### 3 Residue-property plots

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.

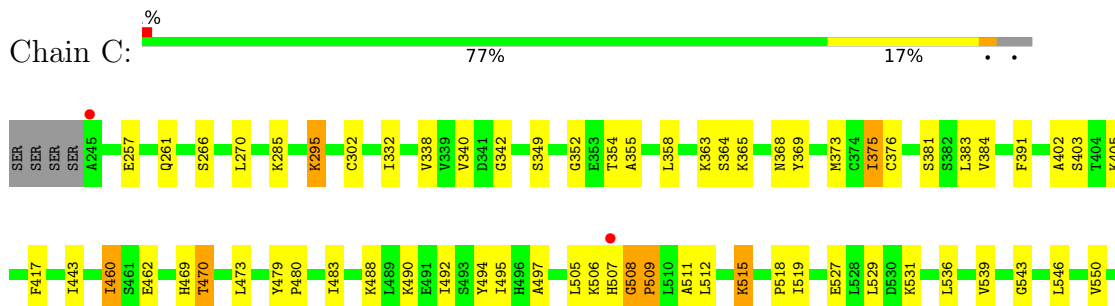
- Molecule 1: Glucosamine--fructose-6-phosphate aminotransferase [isomerizing]

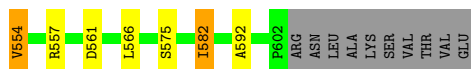


- Molecule 1: Glucosamine--fructose-6-phosphate aminotransferase [isomerizing]



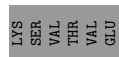
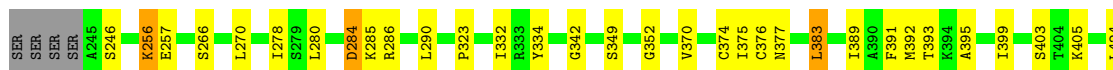
- Molecule 1: Glucosamine--fructose-6-phosphate aminotransferase [isomerizing]





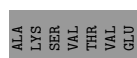
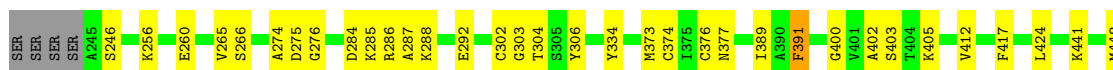
- Molecule 1: Glucosamine--fructose-6-phosphate aminotransferase [isomerizing]

Chain D: 78% 17%



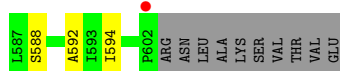
- Molecule 1: Glucosamine--fructose-6-phosphate aminotransferase [isomerizing]

Chain E: 78% 17%



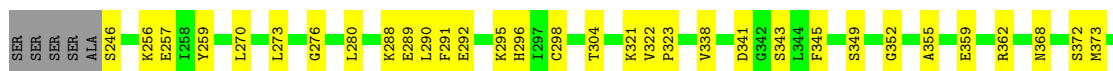
- Molecule 1: Glucosamine--fructose-6-phosphate aminotransferase [isomerizing]

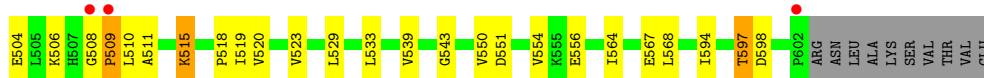
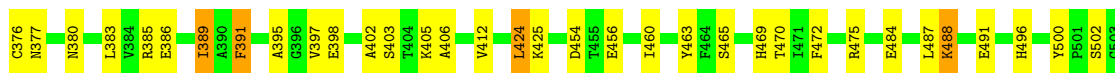
Chain F: 78% 17%



- Molecule 1: Glucosamine--fructose-6-phosphate aminotransferase [isomerizing]

Chain G: 72% 23%





● Molecule 1: Glucosamine--fructose-6-phosphate aminotransferase [isomerizing]



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	71.37Å 262.91Å 83.80Å 90.00° 91.32° 90.00°	Depositor
Resolution (Å)	45.80 – 2.28 45.80 – 2.28	Depositor EDS
% Data completeness (in resolution range)	74.7 (45.80-2.28) 74.7 (45.80-2.28)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.51 (at 2.29Å)	Xtrriage
Refinement program	REFMAC 5.5.0109	Depositor
R, $R_{free}$	0.172 , 0.232 0.169 , 0.226	Depositor DCC
$R_{free}$ test set	5213 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	27.1	Xtrriage
Anisotropy	0.474	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 33.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	0.031 for h,-k,-l	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	22905	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	31.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.42% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  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	A	1.10	0/2843	1.04	3/3837 (0.1%)
1	B	1.10	4/2787 (0.1%)	0.98	2/3762 (0.1%)
1	C	1.10	1/2847 (0.0%)	0.97	5/3842 (0.1%)
1	D	1.08	1/2842 (0.0%)	1.02	4/3833 (0.1%)
1	E	1.11	2/2846 (0.1%)	0.98	0/3841
1	F	1.07	0/2840	1.00	5/3833 (0.1%)
1	G	0.98	0/2844	0.98	3/3838 (0.1%)
1	H	1.04	0/2853	0.98	2/3849 (0.1%)
All	All	1.07	8/22702 (0.0%)	0.99	24/30635 (0.1%)

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	582	ILE	C-O	-6.83	1.18	1.24
1	E	582	ILE	CA-CB	6.14	1.57	1.54
1	B	316	ILE	CA-CB	-5.91	1.47	1.54
1	B	308	ALA	CA-CB	-5.49	1.44	1.53
1	E	471	ILE	CA-CB	-5.23	1.48	1.54

The worst 5 of 24 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	508	GLY	CA-C-N	9.77	129.53	119.56
1	G	508	GLY	C-N-CA	9.77	129.53	119.56
1	A	508	GLY	CA-C-N	9.12	128.86	119.56
1	A	508	GLY	C-N-CA	9.12	128.86	119.56
1	H	508	GLY	CA-C-N	7.07	128.68	119.84

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	2792	0	2840	39	0
1	B	2745	0	2792	47	0
1	C	2794	0	2847	42	0
1	D	2790	0	2850	38	0
1	E	2793	0	2847	41	0
1	F	2790	0	2847	47	0
1	G	2791	0	2841	62	0
1	H	2796	0	2852	62	0
2	A	68	0	0	0	0
2	B	66	0	0	2	0
2	C	97	0	0	0	0
2	D	97	0	0	2	0
2	E	93	0	0	4	0
2	F	85	0	0	2	0
2	G	51	0	0	1	0
2	H	57	0	0	0	0
All	All	22905	0	22716	355	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 355 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:302[B]:CYS:SG	1:F:507:HIS:NE2	2.35	0.99
1:E:302[B]:CYS:HG	1:F:507:HIS:HE2	0.88	0.88
1:H:257:GLU:HG2	1:H:405:LYS:HE2	1.63	0.81
1:D:374[A]:CYS:SG	1:D:376[A]:CYS:HB2	2.23	0.79
1:G:484:GLU:OE2	1:G:488:LYS:NZ	2.16	0.79

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	358/372 (96%)	348 (97%)	10 (3%)	0	100	100
1	B	351/372 (94%)	339 (97%)	11 (3%)	1 (0%)	36	44
1	C	360/372 (97%)	349 (97%)	8 (2%)	3 (1%)	16	18
1	D	359/372 (96%)	348 (97%)	11 (3%)	0	100	100
1	E	360/372 (97%)	350 (97%)	9 (2%)	1 (0%)	36	44
1	F	359/372 (96%)	348 (97%)	9 (2%)	2 (1%)	21	25
1	G	359/372 (96%)	343 (96%)	16 (4%)	0	100	100
1	H	359/372 (96%)	338 (94%)	19 (5%)	2 (1%)	21	25
All	All	2865/2976 (96%)	2763 (96%)	93 (3%)	9 (0%)	36	44

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	508	GLY
1	B	506	LYS
1	C	368	ASN
1	H	271	ALA
1	H	275	ASP

### 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	310/314 (99%)	293 (94%)	17 (6%)	19	26

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	304/314 (97%)	280 (92%)	24 (8%)	11	14
1	C	311/314 (99%)	290 (93%)	21 (7%)	14	18
1	D	310/314 (99%)	292 (94%)	18 (6%)	18	24
1	E	311/314 (99%)	299 (96%)	12 (4%)	28	41
1	F	310/314 (99%)	298 (96%)	12 (4%)	28	41
1	G	311/314 (99%)	290 (93%)	21 (7%)	14	18
1	H	312/314 (99%)	292 (94%)	20 (6%)	16	20
All	All	2479/2512 (99%)	2334 (94%)	145 (6%)	18	24

5 of 145 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	412	VAL
1	H	562	ASN
1	G	504	GLU
1	H	350	GLN
1	C	363	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 37 such sidechains are listed below:

Mol	Chain	Res	Type
1	G	469	HIS
1	H	469	HIS
1	G	525	ASN
1	G	585	GLN
1	C	525	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 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 oligosaccharides 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](#)

There are no chain breaks in this entry.

## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	351/372 (94%)	-0.46	0 <b>100</b> <b>100</b>	9, 24, 48, 58	3 (0%)
1	B	348/372 (93%)	-0.35	5 (1%) <b>73</b> <b>75</b>	12, 29, 52, 74	1 (0%)
1	C	352/372 (94%)	-0.42	2 (0%) <b>85</b> <b>86</b>	13, 27, 48, 67	4 (1%)
1	D	351/372 (94%)	-0.34	1 (0%) <b>90</b> <b>90</b>	14, 30, 52, 65	4 (1%)
1	E	352/372 (94%)	-0.44	1 (0%) <b>90</b> <b>90</b>	13, 26, 50, 66	4 (1%)
1	F	352/372 (94%)	-0.34	2 (0%) <b>85</b> <b>86</b>	13, 29, 51, 62	3 (0%)
1	G	351/372 (94%)	-0.17	3 (0%) <b>81</b> <b>82</b>	17, 35, 62, 77	4 (1%)
1	H	351/372 (94%)	-0.16	7 (1%) <b>65</b> <b>66</b>	14, 33, 63, 76	6 (1%)
All	All	2808/2976 (94%)	-0.34	21 (0%) <b>84</b> <b>85</b>	9, 29, 54, 77	29 (1%)

The worst 5 of 21 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	280	LEU	4.3
1	B	280	LEU	3.5
1	H	507	HIS	3.0
1	C	507	HIS	3.0
1	H	281	ASP	2.9

### 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 oligosaccharides in this entry.

## 6.4 Ligands

There are no ligands in this entry.

## 6.5 Other polymers

There are no such residues in this entry.