Full wwPDB X-ray Structure Validation Report ⓘ

Nov 16, 2023 – 02:09 AM JST

PDB ID	:	6KHR
Title	:	Structure of glycinamide-RNase-transformylase T from Mycobacterium tuberculosis
Authors	:	Chen, C.; Wang, J.
Deposited on	:	2019-07-16
Resolution	:	2.79 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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 ⓘ 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 ⓘ) were used in the production of this report:

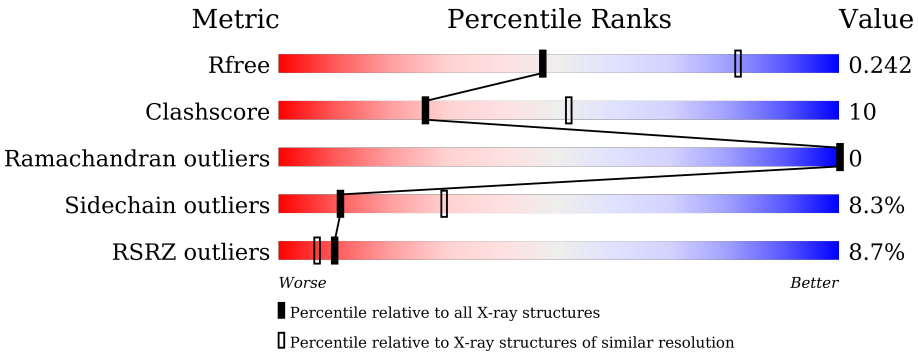
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.79 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	4107 (2.80-2.76)
Clashscore	141614	4575 (2.80-2.76)
Ramachandran outliers	138981	4487 (2.80-2.76)
Sidechain outliers	138945	4489 (2.80-2.76)
RSRZ outliers	127900	4027 (2.80-2.76)

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	A	420	7% 65% 15% · 17%
1	B	420	6% 58% 16% · 24%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 4920 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 Formate-dependent phosphoribosylglycinamide formyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	349	Total	C	N	O	S	0	0	0
			2543	1604	450	478	11			
1	B	320	Total	C	N	O	S	0	0	0
			2343	1476	414	442	11			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP P95197
A	2	VAL	-	expression tag	UNP P95197
B	1	MET	-	initiating methionine	UNP P95197
B	2	VAL	-	expression tag	UNP P95197

- Molecule 2 is water.

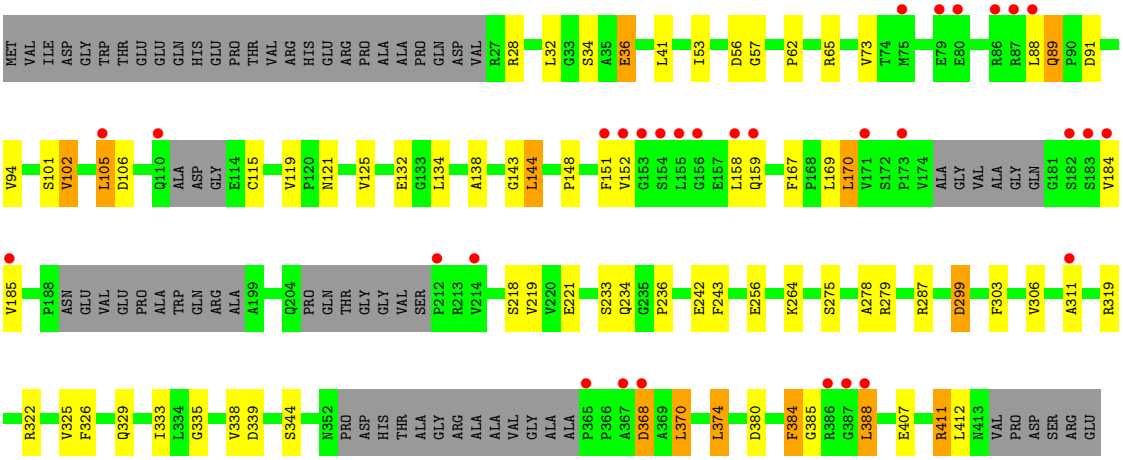
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	15	Total	O	0	0
			15	15		
2	B	19	Total	O	0	0
			19	19		

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.

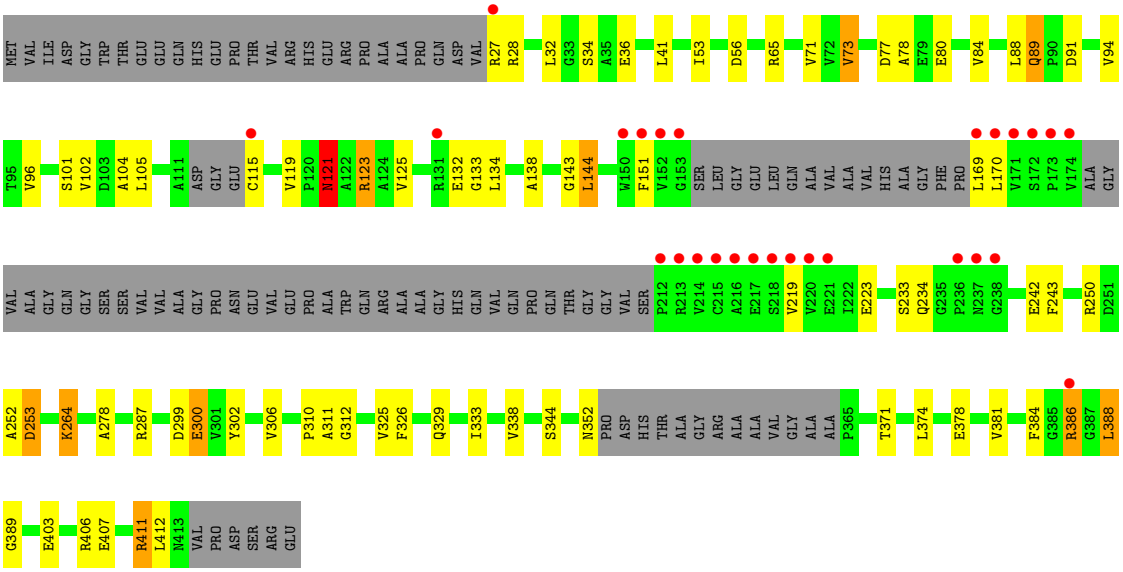
• Molecule 1: Formate-dependent phosphoribosylglycinamide formyltransferase

Chain A:



• Molecule 1: Formate-dependent phosphoribosylglycinamide formyltransferase

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α, β, γ	103.13Å 103.13Å 148.69Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	48.72 – 2.79 48.72 – 2.79	Depositor EDS
% Data completeness (in resolution range)	99.2 (48.72-2.79) 99.2 (48.72-2.79)	Depositor EDS
R_{merge}	0.27	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.18 (at 2.77Å)	Xtriage
Refinement program	PHENIX 1.14rc3_3206	Depositor
R, R_{free}	0.217 , 0.242 0.217 , 0.242	Depositor DCC
R_{free} test set	1137 reflections (4.89%)	wwPDB-VP
Wilson B-factor (Å^2)	57.1	Xtriage
Anisotropy	0.291	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 62.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.029 for -h,-k,l	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	4920	wwPDB-VP
Average B, all atoms (Å^2)	63.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.77% 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

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	0.59	1/2579 (0.0%)	0.70	4/3513 (0.1%)
1	B	0.66	1/2374 (0.0%)	0.71	1/3234 (0.0%)
All	All	0.62	2/4953 (0.0%)	0.71	5/6747 (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	B	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	36	GLU	C-N	8.10	1.49	1.34
1	B	378	GLU	CD-OE2	-5.09	1.20	1.25

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	299	ASP	CB-CA-C	-8.03	94.35	110.40
1	A	121	ASN	CB-CA-C	-7.21	95.98	110.40
1	A	256	GLU	CB-CA-C	-5.56	99.28	110.40
1	B	121	ASN	CB-CA-C	5.39	121.18	110.40
1	A	385	GLY	C-N-CA	-5.07	109.03	121.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	384	PHE	Peptide

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	A	2543	0	2581	55	1
1	B	2343	0	2392	55	1
2	A	15	0	0	7	0
2	B	19	0	0	9	0
All	All	4920	0	4973	102	1

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 10.

All (102) 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:A:169:LEU:HB2	1:A:185:VAL:HG13	1.34	1.07
1:A:299:ASP:CG	1:B:253:ASP:OD1	1.95	1.05
1:A:169:LEU:CB	1:A:185:VAL:HG13	1.92	0.98
1:A:299:ASP:OD2	1:B:253:ASP:OD1	1.80	0.97
1:B:352:ASN:OD1	2:B:501:HOH:O	1.85	0.93
1:B:352:ASN:CG	2:B:501:HOH:O	2.10	0.89
1:B:133:GLY:O	2:B:502:HOH:O	1.89	0.88
1:A:299:ASP:OD1	1:B:253:ASP:OD1	1.93	0.86
1:B:310:PRO:O	2:B:503:HOH:O	1.95	0.84
1:B:352:ASN:O	2:B:504:HOH:O	1.97	0.82
1:A:170:LEU:HD23	1:A:219:VAL:HG22	1.59	0.82
1:A:299:ASP:OD2	1:B:252:ALA:HB1	1.82	0.79
1:B:123:ARG:HH11	1:B:123:ARG:HG3	1.47	0.79
1:B:41:LEU:HD13	1:B:329:GLN:HG3	1.65	0.79
1:A:41:LEU:HD13	1:A:329:GLN:HG3	1.65	0.78
1:A:279:ARG:NE	2:A:501:HOH:O	1.94	0.75
1:A:335:GLY:O	2:A:502:HOH:O	2.05	0.73
1:B:311:ALA:C	2:B:503:HOH:O	2.32	0.68
1:A:28:ARG:NH2	1:A:88:LEU:O	2.26	0.68
1:B:28:ARG:NH2	1:B:88:LEU:O	2.26	0.68
1:B:123:ARG:HH11	1:B:123:ARG:CG	2.08	0.67
1:A:303:PHE:O	2:A:505:HOH:O	2.12	0.67
1:B:388:LEU:HD22	1:B:389:GLY:N	2.10	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:311:ALA:O	2:A:504:HOH:O	2.12	0.66
1:A:169:LEU:CB	1:A:185:VAL:CG1	2.72	0.65
1:B:300:GLU:OE2	1:B:302:TYR:OH	2.15	0.64
1:A:170:LEU:HD23	1:A:219:VAL:CG2	2.26	0.64
1:A:36:GLU:HG2	1:A:384:PHE:CG	2.33	0.63
1:A:368:ASP:OD1	1:A:368:ASP:N	2.31	0.62
1:B:121:ASN:C	1:B:121:ASN:HD22	2.02	0.61
1:A:152:VAL:HG21	1:A:158:LEU:HG	1.81	0.60
1:A:89:GLN:NE2	1:A:115:CYS:SG	2.74	0.60
1:A:233:SER:HA	1:A:287:ARG:HG2	1.84	0.60
1:B:89:GLN:NE2	1:B:115:CYS:SG	2.74	0.59
1:B:233:SER:HA	1:B:287:ARG:HG2	1.84	0.58
1:A:119:VAL:HG11	1:A:333:ILE:HA	1.85	0.58
1:A:370:LEU:HD22	1:A:374:LEU:HD22	1.87	0.57
1:B:170:LEU:HG	1:B:219:VAL:HG22	1.87	0.57
1:A:169:LEU:HB3	1:A:185:VAL:CG1	2.34	0.56
1:B:78:ALA:HA	1:B:104:ALA:HB2	1.88	0.55
1:B:94:VAL:HG13	1:B:119:VAL:O	2.06	0.55
1:A:384:PHE:CD2	1:A:388:LEU:HD12	2.43	0.54
1:B:28:ARG:NH1	1:B:53:ILE:HD11	2.24	0.53
1:A:299:ASP:HB3	1:B:250:ARG:HH22	1.73	0.53
1:A:28:ARG:N	1:A:91:ASP:OD2	2.39	0.53
1:B:371:THR:O	2:B:505:HOH:O	2.19	0.53
1:A:221:GLU:HB3	1:B:403:GLU:OE1	2.09	0.52
1:A:132:GLU:HG2	1:A:151:PHE:CE2	2.45	0.51
1:A:28:ARG:NH1	1:A:53:ILE:HD11	2.24	0.51
1:B:132:GLU:HG2	1:B:151:PHE:CE2	2.45	0.51
1:A:279:ARG:CD	2:A:501:HOH:O	2.53	0.50
1:A:148:PRO:HB2	1:A:218:SER:HB2	1.94	0.50
1:B:253:ASP:OD1	1:B:253:ASP:N	2.44	0.49
1:B:170:LEU:HG	1:B:219:VAL:CG2	2.43	0.49
1:B:386:ARG:O	1:B:386:ARG:HG3	2.13	0.49
1:B:134:LEU:HD21	1:B:306:VAL:HG12	1.95	0.48
1:A:134:LEU:HD21	1:A:306:VAL:HG12	1.95	0.48
1:B:27:ARG:N	2:B:508:HOH:O	2.45	0.48
1:A:101:SER:O	1:A:105:LEU:HD22	2.14	0.48
1:B:119:VAL:HG11	1:B:333:ILE:HA	1.94	0.48
1:A:325:VAL:O	1:A:329:GLN:HG2	2.14	0.47
1:B:102:VAL:HG12	1:B:125:VAL:HG12	1.96	0.47
1:B:77:ASP:HB3	1:B:80:GLU:HB2	1.95	0.47
1:B:28:ARG:N	1:B:91:ASP:OD2	2.39	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:325:VAL:O	1:B:329:GLN:HG2	2.14	0.47
1:B:123:ARG:CG	1:B:123:ARG:NH1	2.72	0.46
1:A:34:SER:O	1:A:62:PRO:HD2	2.16	0.45
1:A:53:ILE:HD13	1:A:88:LEU:HD23	1.99	0.45
1:B:73:VAL:HG21	1:B:84:VAL:HG21	1.99	0.44
1:B:326:PHE:HA	1:B:329:GLN:HG2	1.99	0.44
1:A:242:GLU:HA	2:A:503:HOH:O	2.17	0.44
1:A:275:SER:O	1:A:279:ARG:HG3	2.18	0.44
1:A:143:GLY:CA	1:B:264:LYS:HE2	2.48	0.44
1:A:326:PHE:HA	1:A:329:GLN:HG2	1.99	0.44
1:A:138:ALA:O	1:A:144:LEU:HB2	2.19	0.43
1:A:384:PHE:HD2	1:A:388:LEU:HD12	1.83	0.43
1:B:53:ILE:HD13	1:B:88:LEU:HD23	1.99	0.43
1:A:242:GLU:HG3	1:A:338:VAL:HG23	2.01	0.43
1:A:243:PHE:N	2:A:503:HOH:O	2.10	0.43
1:B:36:GLU:HG2	1:B:388:LEU:HD12	2.00	0.43
1:B:71:VAL:HG12	1:B:73:VAL:CG2	2.49	0.43
1:A:167:PHE:HE1	1:A:185:VAL:HG22	1.83	0.43
1:B:138:ALA:O	1:B:144:LEU:HB2	2.18	0.43
1:B:94:VAL:HG21	1:B:333:ILE:HD13	2.01	0.43
1:B:101:SER:HB3	1:B:104:ALA:HB3	2.00	0.42
1:B:242:GLU:HG3	1:B:338:VAL:HG23	2.01	0.42
1:A:102:VAL:HG12	1:A:125:VAL:HG12	2.01	0.42
1:A:56:ASP:OD1	1:A:57:GLY:N	2.46	0.42
1:A:94:VAL:HG21	1:A:333:ILE:HD13	2.01	0.42
1:A:279:ARG:NH2	1:B:223:GLU:OE2	2.53	0.42
1:A:184:VAL:O	1:A:184:VAL:HG23	2.20	0.41
1:B:34:SER:HB2	1:B:56:ASP:HB2	2.01	0.41
1:B:312:GLY:N	2:B:503:HOH:O	2.51	0.41
1:B:243:PHE:HZ	1:B:278:ALA:HB2	1.86	0.41
1:B:169:LEU:O	1:B:170:LEU:HD23	2.21	0.41
1:B:388:LEU:HD22	1:B:389:GLY:H	1.85	0.41
1:A:169:LEU:HA	1:A:169:LEU:HD23	1.86	0.41
1:A:322:ARG:NH2	1:A:339:ASP:OD2	2.54	0.41
1:B:407:GLU:O	1:B:411:ARG:HG2	2.22	0.40
1:A:243:PHE:HZ	1:A:278:ALA:HB2	1.86	0.40
1:A:319:ARG:NH2	1:A:380:ASP:OD2	2.49	0.40
1:A:407:GLU:O	1:A:411:ARG:HG2	2.22	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:236:PRO:O	1:B:143:GLY:O[5_554]	1.86	0.34

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	337/420 (80%)	321 (95%)	16 (5%)	0	100 100
1	B	310/420 (74%)	299 (96%)	11 (4%)	0	100 100
All	All	647/840 (77%)	620 (96%)	27 (4%)	0	100 100

There are no Ramachandran outliers to report.

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	262/316 (83%)	242 (92%)	20 (8%)	13 33
1	B	243/316 (77%)	221 (91%)	22 (9%)	9 25
All	All	505/632 (80%)	463 (92%)	42 (8%)	11 29

All (42) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	32	LEU
1	A	65	ARG
1	A	73	VAL

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Mol	Chain	Res	Type
1	A	89	GLN
1	A	102	VAL
1	A	105	LEU
1	A	106	ASP
1	A	144	LEU
1	A	159	GLN
1	A	170	LEU
1	A	234	GLN
1	A	264	LYS
1	A	344	SER
1	A	368	ASP
1	A	370	LEU
1	A	374	LEU
1	A	384	PHE
1	A	388	LEU
1	A	411	ARG
1	A	412	LEU
1	B	32	LEU
1	B	65	ARG
1	B	73	VAL
1	B	89	GLN
1	B	96	VAL
1	B	105	LEU
1	B	121	ASN
1	B	123	ARG
1	B	144	LEU
1	B	234	GLN
1	B	253	ASP
1	B	264	LYS
1	B	299	ASP
1	B	300	GLU
1	B	344	SER
1	B	374	LEU
1	B	381	VAL
1	B	386	ARG
1	B	388	LEU
1	B	406	ARG
1	B	411	ARG
1	B	412	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	121	ASN

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 monosaccharides 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	349/420 (83%)	0.41	31 (8%)	9	6	27, 58, 111, 184	0
1	B	320/420 (76%)	0.79	27 (8%)	11	7	28, 51, 142, 197	0
All	All	669/840 (79%)	0.59	58 (8%)	10	7	27, 54, 119, 197	0

All (58) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	171	VAL	21.0
1	B	170	LEU	17.2
1	B	153	GLY	15.3
1	B	169	LEU	15.0
1	B	173	PRO	14.2
1	B	212	PRO	13.0
1	B	152	VAL	12.3
1	B	214	VAL	11.8
1	B	174	VAL	10.8
1	A	386	ARG	8.4
1	B	150	TRP	7.4
1	B	151	PHE	7.4
1	A	185	VAL	7.3
1	B	217	GLU	7.3
1	B	215	CYS	7.2
1	B	216	ALA	7.2
1	B	172	SER	6.3
1	A	387	GLY	5.9
1	B	213	ARG	5.9
1	B	236	PRO	5.1
1	B	115	CYS	4.5
1	A	151	PHE	4.1
1	B	218	SER	4.0
1	A	79	GLU	3.8

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Mol	Chain	Res	Type	RSRZ
1	A	158	LEU	3.7
1	A	212	PRO	3.7
1	A	159	GLN	3.7
1	A	86	ARG	3.7
1	A	183	SER	3.6
1	A	152	VAL	3.5
1	A	367	ALA	3.4
1	A	182	SER	3.2
1	A	311	ALA	3.1
1	B	27	ARG	3.0
1	B	386	ARG	3.0
1	A	365	PRO	3.0
1	B	238	GLY	3.0
1	A	184	VAL	2.9
1	A	155	LEU	2.8
1	A	153	GLY	2.7
1	A	388	LEU	2.7
1	A	368	ASP	2.6
1	A	156	GLY	2.5
1	A	75	MET	2.5
1	A	87	ARG	2.5
1	B	219	VAL	2.4
1	A	214	VAL	2.4
1	B	237	ASN	2.4
1	A	171	VAL	2.3
1	A	173	PRO	2.3
1	B	220	VAL	2.3
1	B	131	ARG	2.2
1	A	110	GLN	2.2
1	A	80	GLU	2.2
1	B	221	GLU	2.2
1	A	105	LEU	2.2
1	A	154	SER	2.1
1	A	88	LEU	2.0

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.