Full wwPDB X-ray Structure Validation Report ⓘ

Oct 15, 2023 – 07:13 AM EDT

PDB ID	:	8D3F
Title	:	Crystal structure of human STAT1 in complex with the repeat region from Toxoplasma protein TgIST
Authors	:	Huang, Z.; Liu, H.; Nix, J.C.; Amarasinghe, G.K.; Sibley, L.D.
Deposited on	:	2022-06-01
Resolution	:	2.97 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:

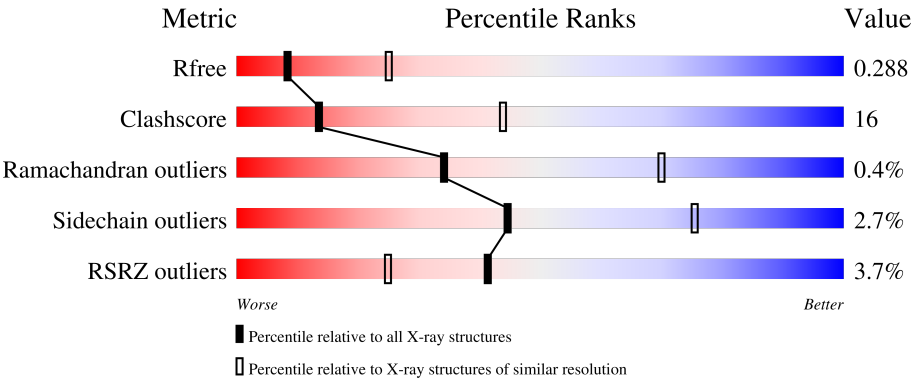
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation 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 2.97 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	2754 (3.00-2.96)
Clashscore	141614	3103 (3.00-2.96)
Ramachandran outliers	138981	2993 (3.00-2.96)
Sidechain outliers	138945	2996 (3.00-2.96)
RSRZ outliers	127900	2644 (3.00-2.96)

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	642	3% 60% 29% · 11%

2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 4360 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 Signal transducer and activator of transcription 1-alpha/beta, Inhibitor of STAT1-dependent transcription TgIST.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	572	4360	2786	732	823	19	0	0	0

There are 25 discrepancies between the modelled and reference sequences:

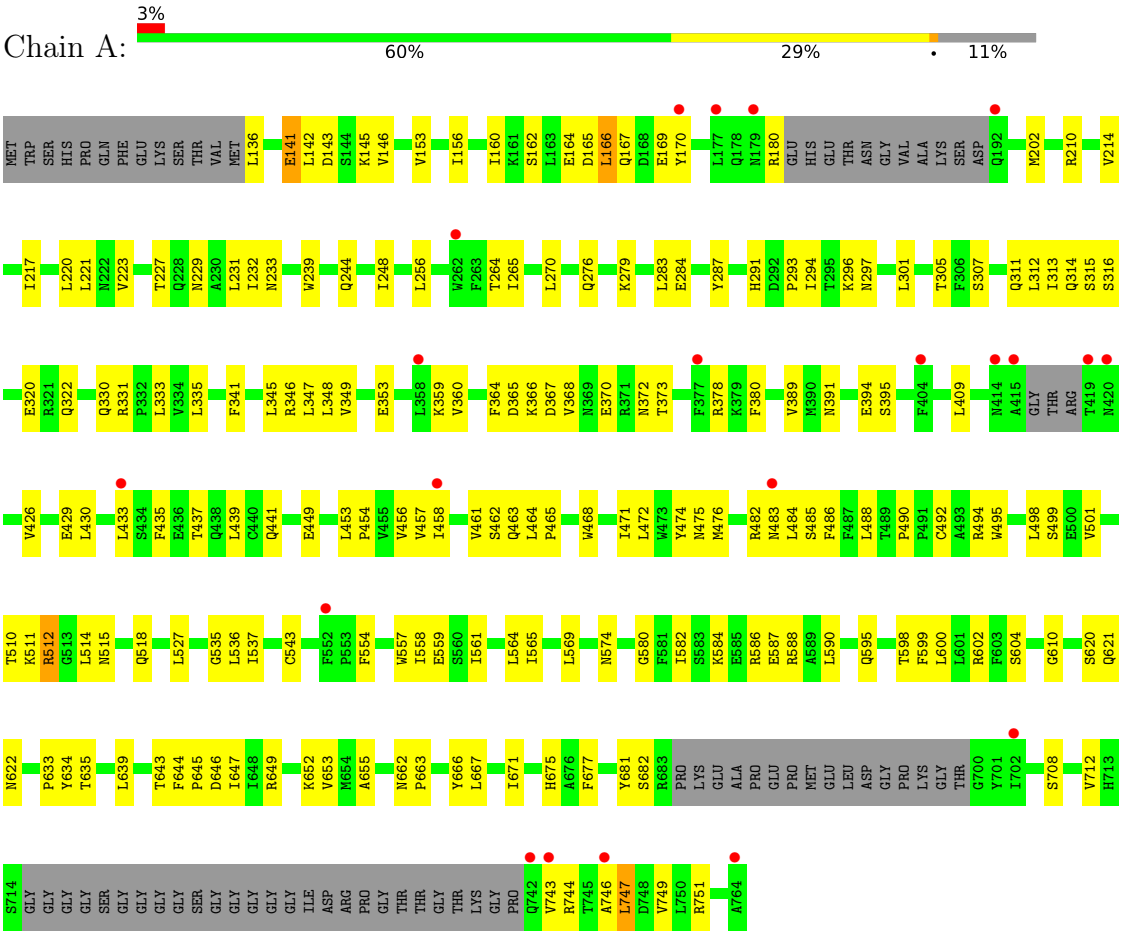
Chain	Residue	Modelled	Actual	Comment	Reference
A	123	MET	-	initiating methionine	UNP P42224
A	124	TRP	-	expression tag	UNP P42224
A	125	SER	-	expression tag	UNP P42224
A	126	HIS	-	expression tag	UNP P42224
A	127	PRO	-	expression tag	UNP P42224
A	128	GLN	-	expression tag	UNP P42224
A	129	PHE	-	expression tag	UNP P42224
A	130	GLU	-	expression tag	UNP P42224
A	131	LYS	-	expression tag	UNP P42224
A	714	SER	-	linker	UNP P42224
A	715	GLY	-	linker	UNP P42224
A	716	GLY	-	linker	UNP P42224
A	717	GLY	-	linker	UNP P42224
A	718	GLY	-	linker	UNP P42224
A	719	SER	-	linker	UNP P42224
A	720	GLY	-	linker	UNP P42224
A	721	GLY	-	linker	UNP P42224
A	722	GLY	-	linker	UNP P42224
A	723	GLY	-	linker	UNP P42224
A	724	SER	-	linker	UNP P42224
A	725	GLY	-	linker	UNP P42224
A	726	GLY	-	linker	UNP P42224
A	727	GLY	-	linker	UNP P42224
A	728	GLY	-	linker	UNP P42224
A	729	GLY	-	linker	UNP P42224

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: Signal transducer and activator of transcription 1-alpha/beta,Inhibitor of STAT1-dependent transcription TgIST

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α, β, γ	59.96Å 163.92Å 226.86Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.64 – 2.97 46.64 – 2.97	Depositor EDS
% Data completeness (in resolution range)	99.9 (46.64-2.97) 99.9 (46.64-2.97)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	0.18	Depositor
$< I/\sigma(I) >$ [1]	1.84 (at 2.96Å)	Xtriage
Refinement program	PHENIX 1.16_3549	Depositor
R, R_{free}	0.248 , 0.288 0.248 , 0.288	Depositor DCC
R_{free} test set	1160 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å^2)	79.6	Xtriage
Anisotropy	0.881	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 87.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	4360	wwPDB-VP
Average B, all atoms (Å^2)	95.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.46% 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	0.50	1/4450 (0.0%)	0.64	0/6074

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	543	CYS	CB-SG	8.35	1.96	1.82

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	4360	0	4062	135	0
All	All	4360	0	4062	135	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 16.

All (135) 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:564:LEU:HD22	1:A:569:LEU:HD11	1.45	0.98
1:A:564:LEU:HD12	1:A:610:GLY:O	1.70	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:564:LEU:HD22	1:A:569:LEU:CD1	2.08	0.83
1:A:465:PRO:HB3	1:A:559:GLU:HG3	1.61	0.82
1:A:313:ILE:HG22	1:A:349:VAL:HG11	1.58	0.82
1:A:333:LEU:HB3	1:A:471:ILE:HD12	1.64	0.77
1:A:586:ARG:O	1:A:590:LEU:HD12	1.85	0.77
1:A:380:PHE:HB3	1:A:409:LEU:HD21	1.66	0.76
1:A:378:ARG:CZ	1:A:426:VAL:HG23	2.22	0.70
1:A:561:ILE:O	1:A:565:ILE:HG13	1.92	0.69
1:A:430:LEU:HD23	1:A:454:PRO:HB2	1.74	0.68
1:A:598:THR:HA	1:A:666:TYR:O	1.94	0.68
1:A:746:ALA:HA	1:A:749:VAL:HG12	1.75	0.68
1:A:164:GLU:HG2	1:A:283:LEU:HD11	1.75	0.68
1:A:511:LYS:H	1:A:574:ASN:HD21	1.43	0.67
1:A:747:LEU:HD13	1:A:751:ARG:NH2	2.09	0.67
1:A:511:LYS:H	1:A:574:ASN:ND2	1.93	0.66
1:A:495:TRP:O	1:A:499:SER:HB3	1.95	0.66
1:A:492:CYS:HB2	1:A:536:LEU:HD22	1.77	0.65
1:A:162:SER:HA	1:A:165:ASP:HB2	1.79	0.64
1:A:598:THR:HG22	1:A:666:TYR:HB2	1.80	0.64
1:A:239:TRP:CZ2	1:A:256:LEU:HG	2.33	0.63
1:A:743:VAL:HG12	1:A:744:ARG:H	1.64	0.63
1:A:580:GLY:HA2	1:A:602:ARG:HA	1.81	0.62
1:A:584:LYS:O	1:A:588:ARG:HG3	2.00	0.61
1:A:498:LEU:HD12	1:A:537:ILE:HD13	1.82	0.61
1:A:586:ARG:HD2	1:A:590:LEU:HD11	1.82	0.60
1:A:600:LEU:HA	1:A:667:LEU:HD11	1.83	0.59
1:A:141:GLU:OE2	1:A:142:LEU:N	2.35	0.59
1:A:649:ARG:HB3	1:A:681:TYR:CE1	2.38	0.58
1:A:248:ILE:HB	1:A:472:LEU:CD2	2.34	0.58
1:A:223:VAL:O	1:A:227:THR:HG23	2.04	0.58
1:A:620:SER:OG	1:A:620:SER:O	2.22	0.58
1:A:461:VAL:HG13	1:A:464:LEU:HD12	1.85	0.57
1:A:652:LYS:HZ1	1:A:662:ASN:HB2	1.68	0.57
1:A:291:HIS:HA	1:A:296:LYS:HE3	1.86	0.57
1:A:634:TYR:CE2	1:A:647:ILE:HG21	2.40	0.56
1:A:667:LEU:HD22	1:A:677:PHE:HZ	1.69	0.56
1:A:599:PHE:O	1:A:667:LEU:HD12	2.05	0.56
1:A:214:VAL:HG11	1:A:297:ASN:OD1	2.06	0.56
1:A:378:ARG:NH1	1:A:426:VAL:HG23	2.21	0.55
1:A:141:GLU:OE1	1:A:145:LYS:HD2	2.05	0.55
1:A:366:LYS:HG2	1:A:367:ASP:OD1	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:301:LEU:O	1:A:305:THR:HG23	2.07	0.55
1:A:635:THR:O	1:A:639:LEU:HD12	2.06	0.55
1:A:515:ASN:OD1	1:A:518:GLN:HG3	2.08	0.54
1:A:667:LEU:HD22	1:A:677:PHE:CZ	2.42	0.53
1:A:510:THR:HB	1:A:574:ASN:HD21	1.72	0.53
1:A:153:VAL:HG13	1:A:220:LEU:HD11	1.90	0.53
1:A:587:GLU:HG3	1:A:600:LEU:HD11	1.91	0.52
1:A:276:GLN:HA	1:A:279:LYS:HD3	1.91	0.52
1:A:456:VAL:HG23	1:A:471:ILE:HD11	1.92	0.52
1:A:554:PHE:O	1:A:558:ILE:HD12	2.09	0.52
1:A:248:ILE:HD13	1:A:475:ASN:HB2	1.92	0.52
1:A:256:LEU:HD22	1:A:348:LEU:HD11	1.92	0.51
1:A:239:TRP:CH2	1:A:256:LEU:HG	2.45	0.51
1:A:360:VAL:HG12	1:A:437:THR:HB	1.92	0.51
1:A:145:LYS:HE3	1:A:227:THR:HG22	1.91	0.50
1:A:565:ILE:HA	1:A:569:LEU:HB2	1.93	0.50
1:A:391:ASN:OD1	1:A:394:GLU:HB2	2.12	0.50
1:A:595:GLN:O	1:A:598:THR:OG1	2.24	0.50
1:A:365:ASP:HB3	1:A:368:VAL:HG11	1.93	0.50
1:A:311:GLN:HA	1:A:314:GLN:HB2	1.92	0.50
1:A:322:GLN:CD	1:A:453:LEU:HD12	2.33	0.49
1:A:671:ILE:HD11	1:A:675:HIS:ND1	2.27	0.49
1:A:746:ALA:HA	1:A:749:VAL:CG1	2.42	0.49
1:A:331:ARG:HD2	1:A:468:TRP:CD2	2.48	0.49
1:A:284:GLU:HB2	1:A:294:ILE:HG21	1.94	0.49
1:A:646:ASP:OD2	1:A:682:SER:OG	2.13	0.49
1:A:256:LEU:HD13	1:A:346:ARG:HD3	1.94	0.49
1:A:166:LEU:HA	1:A:169:GLU:HG2	1.95	0.48
1:A:170:TYR:HA	1:A:202:MET:CE	2.43	0.48
1:A:494:ARG:HA	1:A:535:GLY:O	2.14	0.48
1:A:167:GLN:NE2	1:A:287:TYR:HB3	2.28	0.47
1:A:232:ILE:HD11	1:A:312:LEU:HA	1.95	0.47
1:A:364:PHE:HD2	1:A:433:LEU:HD13	1.78	0.47
1:A:335:LEU:O	1:A:457:VAL:HA	2.14	0.47
1:A:380:PHE:HB3	1:A:409:LEU:CD2	2.40	0.47
1:A:141:GLU:OE2	1:A:142:LEU:HB2	2.14	0.47
1:A:221:LEU:HD21	1:A:305:THR:HG22	1.97	0.47
1:A:264:THR:OG1	1:A:349:VAL:O	2.28	0.47
1:A:495:TRP:HB2	1:A:527:LEU:HD11	1.97	0.47
1:A:320:GLU:OE2	1:A:346:ARG:NH1	2.47	0.47
1:A:378:ARG:HD3	1:A:429:GLU:CD	2.35	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:347:LEU:HD12	1:A:347:LEU:HA	1.80	0.46
1:A:557:TRP:CE3	1:A:558:ILE:HG13	2.51	0.46
1:A:378:ARG:HD3	1:A:429:GLU:OE1	2.16	0.46
1:A:667:LEU:O	1:A:671:ILE:HG22	2.16	0.46
1:A:488:LEU:C	1:A:490:PRO:HD3	2.36	0.45
1:A:330:GLN:C	1:A:331:ARG:HG2	2.36	0.45
1:A:141:GLU:CD	1:A:142:LEU:N	2.70	0.45
1:A:156:ILE:HD13	1:A:217:ILE:HG13	1.97	0.45
1:A:498:LEU:HA	1:A:501:VAL:HG22	1.98	0.45
1:A:652:LYS:NZ	1:A:662:ASN:HB2	2.32	0.45
1:A:210:ARG:HB3	1:A:293:PRO:HG2	2.00	0.45
1:A:345:LEU:HD11	1:A:435:PHE:CG	2.52	0.45
1:A:512:ARG:NH1	1:A:574:ASN:O	2.50	0.45
1:A:620:SER:O	1:A:622:ASN:N	2.51	0.44
1:A:649:ARG:HD2	1:A:681:TYR:CD1	2.52	0.44
1:A:498:LEU:HA	1:A:498:LEU:HD23	1.74	0.44
1:A:220:LEU:HA	1:A:223:VAL:HG12	1.99	0.44
1:A:335:LEU:HD22	1:A:341:PHE:CG	2.52	0.44
1:A:554:PHE:O	1:A:557:TRP:HB3	2.17	0.44
1:A:276:GLN:HA	1:A:279:LYS:CD	2.48	0.44
1:A:476:MET:SD	1:A:501:VAL:HG21	2.58	0.43
1:A:653:VAL:HG23	1:A:663:PRO:HD3	2.01	0.43
1:A:160:ILE:O	1:A:164:GLU:HG3	2.18	0.43
1:A:634:TYR:HE2	1:A:647:ILE:HG21	1.82	0.43
1:A:639:LEU:CD2	1:A:644:PHE:HB2	2.49	0.43
1:A:229:ASN:O	1:A:233:ASN:HB2	2.18	0.43
1:A:514:LEU:HA	1:A:514:LEU:HD23	1.69	0.43
1:A:639:LEU:HD21	1:A:644:PHE:HB2	2.01	0.43
1:A:270:LEU:HD23	1:A:270:LEU:HA	1.69	0.43
1:A:458:ILE:HB	1:A:463:GLN:HB2	2.01	0.43
1:A:655:ALA:HB2	1:A:712:VAL:HG22	2.00	0.42
1:A:146:VAL:HB	1:A:265:ILE:HD11	2.01	0.42
1:A:335:LEU:HD22	1:A:341:PHE:CB	2.49	0.42
1:A:430:LEU:HD11	1:A:486:PHE:CE2	2.54	0.42
1:A:483:ASN:O	1:A:484:LEU:HD23	2.20	0.42
1:A:316:SER:OG	1:A:348:LEU:N	2.51	0.42
1:A:231:LEU:HD12	1:A:231:LEU:HA	1.79	0.42
1:A:667:LEU:HD12	1:A:667:LEU:HA	1.62	0.42
1:A:474:TYR:OH	1:A:482:ARG:N	2.52	0.41
1:A:180:ARG:HH11	1:A:180:ARG:HG3	1.84	0.41
1:A:430:LEU:N	1:A:430:LEU:HD12	2.34	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:359:LYS:HB2	1:A:389:VAL:HG22	2.02	0.41
1:A:604:SER:HB2	1:A:633:PRO:HG2	2.02	0.41
1:A:353:GLU:H	1:A:353:GLU:HG3	1.53	0.41
1:A:370:GLU:HA	1:A:373:THR:OG1	2.21	0.41
1:A:232:ILE:HD13	1:A:315:SER:HB2	2.02	0.41
1:A:366:LYS:NZ	1:A:449:GLU:OE1	2.41	0.41
1:A:643:THR:OG1	1:A:645:PRO:HD2	2.20	0.41
1:A:439:LEU:HD11	1:A:441:GLN:HG3	2.02	0.40
1:A:244:GLN:HB2	1:A:475:ASN:HB3	2.03	0.40
1:A:747:LEU:O	1:A:751:ARG:HG3	2.21	0.40

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	562/642 (88%)	517 (92%)	43 (8%)	2 (0%)	34 70

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	621	GLN
1	A	582	ILE

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	444/577 (77%)	432 (97%)	12 (3%)	44 75

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	136	LEU
1	A	141	GLU
1	A	143	ASP
1	A	166	LEU
1	A	307	SER
1	A	372	ASN
1	A	395	SER
1	A	462	SER
1	A	485	SER
1	A	512	ARG
1	A	708	SER
1	A	747	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	158	HIS
1	A	233	ASN
1	A	272	GLN
1	A	328	HIS
1	A	431	HIS
1	A	548	ASN
1	A	574	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	572/642 (89%)	0.36	21 (3%) 41 25	63, 89, 144, 187	0

All (21) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	415	ALA	4.4
1	A	414	ASN	4.4
1	A	419	THR	3.3
1	A	377	PHE	3.3
1	A	433	LEU	2.9
1	A	742	GLN	2.9
1	A	702	ILE	2.8
1	A	746	ALA	2.7
1	A	262	TRP	2.7
1	A	764	ALA	2.6
1	A	177	LEU	2.5
1	A	179	ASN	2.5
1	A	743	VAL	2.5
1	A	192	GLN	2.4
1	A	483	ASN	2.4
1	A	420	ASN	2.4
1	A	358	LEU	2.3
1	A	458	ILE	2.3
1	A	404	PHE	2.2
1	A	170	TYR	2.1
1	A	552	PHE	2.1

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 (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.