Full wwPDB X-ray Structure Validation Report ⓘ

Oct 18, 2023 – 11:19 PM EDT

PDB ID	:	2QUK
Title	:	Crystal structures of human tryptophanyl-tRNA synthetase in complex with ATP(putative)
Authors	:	Shen, N.; Ding, J.P.
Deposited on	:	2007-08-06
Resolution	:	2.80 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:

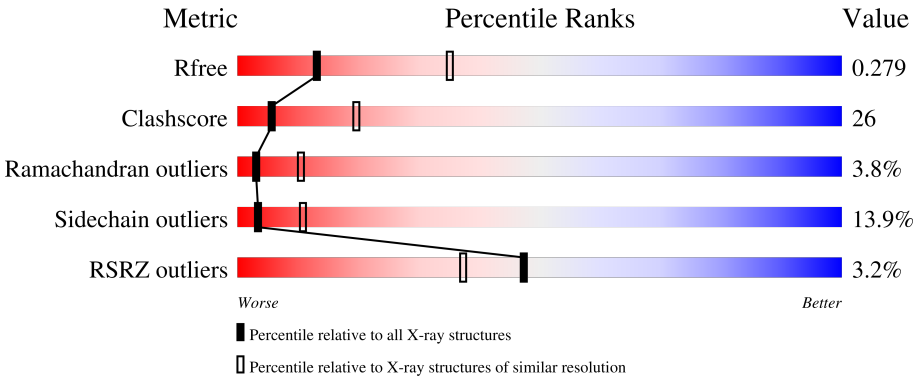
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation 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 2.80 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}	130704	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (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 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	477	3% 41% 31% 6% • 22%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 3064 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 Tryptophanyl-tRNA synthetase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	374	Total	C	N	O	S	0	0	0
			2994	1920	504	555	15			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	472	HIS	-	expression tag	UNP P23381
A	473	HIS	-	expression tag	UNP P23381
A	474	HIS	-	expression tag	UNP P23381
A	475	HIS	-	expression tag	UNP P23381
A	476	HIS	-	expression tag	UNP P23381
A	477	HIS	-	expression tag	UNP P23381

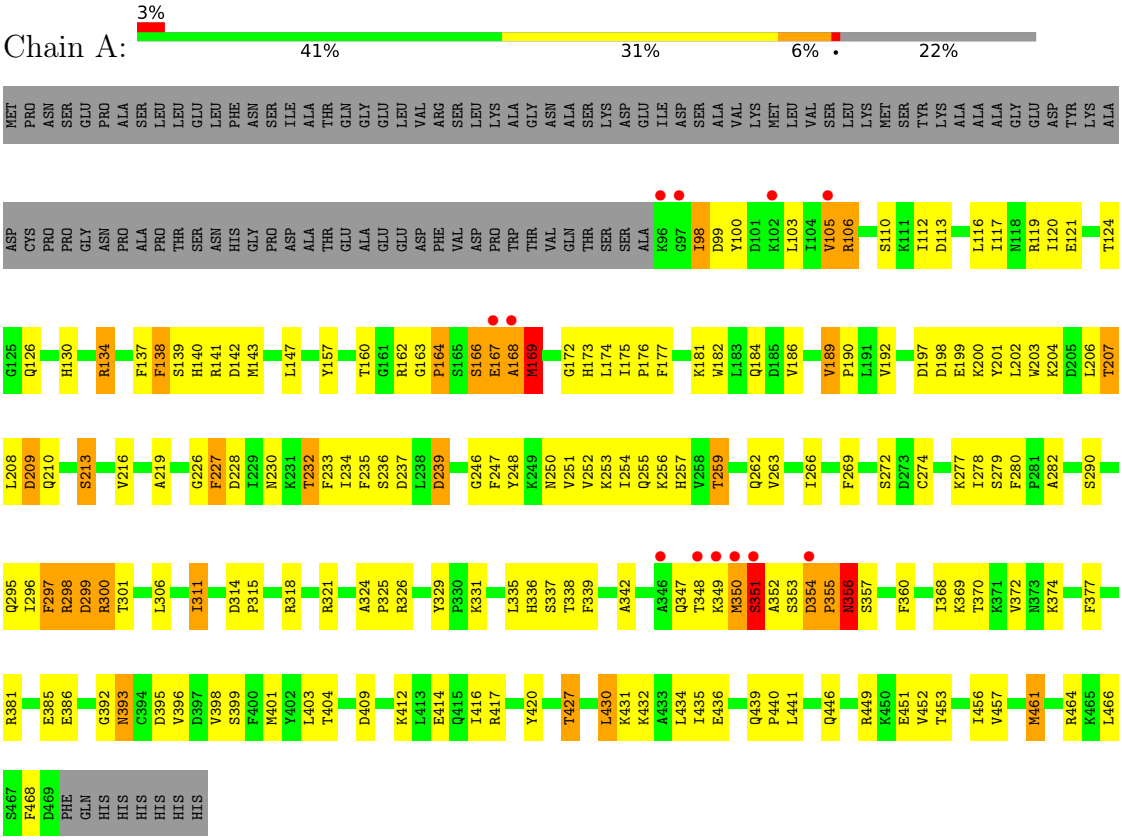
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	70	Total	O	0	0
			70	70		

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: Tryptophanyl-tRNA synthetase



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 6 2 2	Depositor
Cell constants a, b, c, α, β, γ	235.60Å 235.60Å 48.80Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.00 – 2.80 47.46 – 2.80	Depositor EDS
% Data completeness (in resolution range)	98.8 (50.00-2.80) 98.8 (47.46-2.80)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.61 (at 2.81Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.267 , 0.290 0.263 , 0.279	Depositor DCC
R_{free} test set	1019 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å^2)	59.0	Xtriage
Anisotropy	0.486	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 65.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	3064	wwPDB-VP
Average B, all atoms (Å^2)	67.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.77% 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	0.47	0/3067	0.76	5/4145 (0.1%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	351	SER	N-CA-C	9.94	137.83	111.00
1	A	351	SER	N-CA-CB	-8.31	98.03	110.50
1	A	356	ASN	N-CA-C	-6.13	94.45	111.00
1	A	168	ALA	N-CA-C	5.38	125.53	111.00
1	A	298	ARG	N-CA-C	-5.01	97.46	111.00

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	2994	0	2917	151	0
2	A	70	0	0	0	0
All	All	3064	0	2917	151	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 26.

All (151) 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:348:THR:HG22	1:A:350:MET:H	0.96	1.10
1:A:348:THR:HG22	1:A:350:MET:N	1.76	0.99
1:A:348:THR:HG21	1:A:350:MET:HG3	1.46	0.98
1:A:348:THR:HG22	1:A:349:LYS:H	1.25	0.97
1:A:259:THR:HG23	1:A:262:GLN:HE21	1.35	0.89
1:A:348:THR:HG22	1:A:349:LYS:N	1.88	0.89
1:A:351:SER:HB2	1:A:354:ASP:OD2	1.77	0.85
1:A:168:ALA:O	1:A:169:MET:HB3	1.77	0.84
1:A:207:THR:HG22	1:A:210:GLN:H	1.41	0.83
1:A:141:ARG:HG3	1:A:141:ARG:HH11	1.45	0.82
1:A:299:ASP:O	1:A:300:ARG:HB2	1.81	0.81
1:A:348:THR:CG2	1:A:350:MET:H	1.87	0.81
1:A:201:TYR:CD2	1:A:208:LEU:HD23	2.16	0.80
1:A:207:THR:HG22	1:A:210:GLN:N	2.02	0.75
1:A:228:ASP:O	1:A:232:THR:HG22	1.87	0.74
1:A:420:TYR:CE1	1:A:430:LEU:HD12	2.22	0.74
1:A:321:ARG:O	1:A:331:LYS:HE3	1.89	0.72
1:A:204:LYS:HB2	1:A:206:LEU:CD2	2.19	0.72
1:A:110:SER:HB2	1:A:140:HIS:CE1	2.25	0.71
1:A:290:SER:HB2	1:A:297:PHE:HD1	1.55	0.71
1:A:138:PHE:H	1:A:138:PHE:HD1	1.37	0.70
1:A:431:LYS:O	1:A:435:ILE:HG13	1.92	0.70
1:A:435:ILE:O	1:A:439:GLN:HG3	1.92	0.69
1:A:348:THR:CG2	1:A:349:LYS:H	2.05	0.68
1:A:124:THR:HG21	1:A:186:VAL:CG1	2.24	0.68
1:A:355:PRO:O	1:A:356:ASN:HB2	1.94	0.68
1:A:342:ALA:CB	1:A:350:MET:HB2	2.23	0.67
1:A:348:THR:CG2	1:A:350:MET:HG3	2.24	0.66
1:A:140:HIS:HD2	1:A:143:MET:HB3	1.59	0.66
1:A:201:TYR:CE2	1:A:208:LEU:HD23	2.30	0.65
1:A:296:ILE:HG23	1:A:464:ARG:O	1.98	0.64
1:A:412:LYS:O	1:A:416:ILE:HG13	1.98	0.63
1:A:173:HIS:O	1:A:177:PHE:HD2	1.82	0.63
1:A:236:SER:HB3	1:A:239:ASP:HB2	1.80	0.63
1:A:227:PHE:HB3	1:A:232:THR:HG21	1.80	0.63
1:A:321:ARG:HB3	1:A:331:LYS:HE2	1.80	0.63
1:A:296:ILE:C	1:A:297:PHE:HD2	2.02	0.62
1:A:369:LYS:HA	1:A:435:ILE:HD13	1.83	0.61
1:A:141:ARG:HG3	1:A:141:ARG:NH1	2.16	0.61
1:A:248:TYR:O	1:A:252:VAL:HG23	2.01	0.60
1:A:130:HIS:O	1:A:134:ARG:HG3	2.02	0.60
1:A:116:LEU:O	1:A:120:ILE:HG13	2.02	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:140:HIS:CD2	1:A:143:MET:HB3	2.38	0.59
1:A:113:ASP:O	1:A:117:ILE:HG13	2.03	0.59
1:A:119:ARG:HG2	1:A:147:LEU:HD13	1.84	0.58
1:A:124:THR:HG21	1:A:186:VAL:HG13	1.85	0.58
1:A:197:ASP:OD2	1:A:236:SER:OG	2.20	0.58
1:A:207:THR:HG23	1:A:209:ASP:H	1.69	0.58
1:A:141:ARG:HD2	1:A:321:ARG:NH2	2.18	0.58
1:A:175:ILE:HB	1:A:176:PRO:CD	2.33	0.58
1:A:138:PHE:CD1	1:A:138:PHE:N	2.71	0.57
1:A:274:CYS:SG	1:A:277:LYS:HG3	2.44	0.57
1:A:233:PHE:CZ	1:A:235:PHE:HB3	2.39	0.57
1:A:168:ALA:HB3	1:A:360:PHE:CD1	2.40	0.57
1:A:393:ASN:HD21	1:A:395:ASP:HB2	1.69	0.57
1:A:162:ARG:O	1:A:164:PRO:HD3	2.05	0.57
1:A:199:GLU:HB2	1:A:280:PHE:CZ	2.39	0.57
1:A:290:SER:HB2	1:A:297:PHE:CD1	2.40	0.56
1:A:182:TRP:CE2	1:A:186:VAL:HG21	2.41	0.56
1:A:140:HIS:HD2	1:A:143:MET:CB	2.18	0.55
1:A:173:HIS:O	1:A:177:PHE:CD2	2.59	0.55
1:A:139:SER:HB2	1:A:336:HIS:HB2	1.87	0.55
1:A:157:TYR:CB	1:A:190:PRO:HG2	2.36	0.55
1:A:139:SER:HB2	1:A:336:HIS:CD2	2.42	0.54
1:A:137:PHE:CE2	1:A:337:SER:HB3	2.42	0.54
1:A:353:SER:O	1:A:354:ASP:C	2.46	0.54
1:A:168:ALA:O	1:A:169:MET:CB	2.46	0.54
1:A:297:PHE:N	1:A:297:PHE:CD2	2.75	0.54
1:A:234:ILE:O	1:A:461:MET:HA	2.08	0.53
1:A:401:MET:O	1:A:404:THR:HB	2.08	0.53
1:A:452:VAL:O	1:A:452:VAL:HG13	2.09	0.53
1:A:355:PRO:O	1:A:356:ASN:CB	2.56	0.52
1:A:299:ASP:O	1:A:300:ARG:CB	2.54	0.52
1:A:297:PHE:HD2	1:A:297:PHE:N	2.07	0.52
1:A:296:ILE:HG21	1:A:466:LEU:HG	1.92	0.52
1:A:189:VAL:HG22	1:A:190:PRO:HD2	1.92	0.52
1:A:368:ILE:O	1:A:372:VAL:HG23	2.11	0.51
1:A:124:THR:CG2	1:A:186:VAL:HG13	2.41	0.51
1:A:142:ASP:OD1	1:A:321:ARG:NH1	2.44	0.50
1:A:324:ALA:HB3	1:A:325:PRO:HD3	1.93	0.50
1:A:381:ARG:HD2	1:A:386:GLU:OE2	2.12	0.50
1:A:255:GLN:HE21	1:A:279:SER:HB2	1.77	0.50
1:A:372:VAL:HG12	1:A:431:LYS:HG3	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:198:ASP:OD2	1:A:237:ASP:HB3	2.12	0.49
1:A:339:PHE:HD1	1:A:349:LYS:HZ2	1.58	0.49
1:A:174:LEU:O	1:A:175:ILE:C	2.50	0.49
1:A:157:TYR:HB2	1:A:190:PRO:HG2	1.95	0.49
1:A:314:ASP:N	1:A:315:PRO:HD2	2.27	0.49
1:A:449:ARG:O	1:A:452:VAL:HG12	2.13	0.49
1:A:301:THR:HG21	1:A:329:TYR:HE1	1.78	0.48
1:A:296:ILE:CG2	1:A:466:LEU:HG	2.43	0.48
1:A:393:ASN:HD22	1:A:396:VAL:H	1.61	0.48
1:A:439:GLN:N	1:A:440:PRO:HD2	2.28	0.48
1:A:137:PHE:CZ	1:A:337:SER:HB3	2.48	0.48
1:A:203:TRP:CE2	1:A:277:LYS:HD3	2.49	0.47
1:A:137:PHE:HA	1:A:336:HIS:O	2.15	0.47
1:A:206:LEU:N	1:A:206:LEU:HD22	2.29	0.47
1:A:392:GLY:HA3	1:A:420:TYR:CE2	2.50	0.47
1:A:253:LYS:O	1:A:257:HIS:HD2	1.98	0.47
1:A:105:VAL:HG12	1:A:106:ARG:N	2.30	0.47
1:A:112:ILE:HG13	1:A:138:PHE:C	2.36	0.47
1:A:453:THR:O	1:A:457:VAL:HG23	2.15	0.47
1:A:377:PHE:HB3	1:A:398:VAL:HG23	1.97	0.46
1:A:138:PHE:HD1	1:A:138:PHE:N	2.10	0.46
1:A:274:CYS:O	1:A:278:ILE:HD12	2.15	0.46
1:A:112:ILE:HG13	1:A:138:PHE:O	2.16	0.46
1:A:298:ARG:C	1:A:299:ASP:O	2.55	0.45
1:A:296:ILE:CG2	1:A:464:ARG:O	2.65	0.45
1:A:201:TYR:CZ	1:A:208:LEU:HB2	2.51	0.45
1:A:204:LYS:HB2	1:A:206:LEU:HD21	1.98	0.45
1:A:201:TYR:CE1	1:A:208:LEU:N	2.85	0.44
1:A:324:ALA:HB3	1:A:325:PRO:CD	2.48	0.44
1:A:414:GLU:HA	1:A:414:GLU:OE1	2.17	0.44
1:A:139:SER:HB2	1:A:336:HIS:HD2	1.83	0.44
1:A:216:VAL:O	1:A:219:ALA:HB3	2.18	0.44
1:A:420:TYR:HE1	1:A:427:THR:HA	1.83	0.44
1:A:210:GLN:O	1:A:213:SER:HB2	2.18	0.43
1:A:354:ASP:OD2	1:A:354:ASP:N	2.50	0.43
1:A:247:PHE:O	1:A:251:VAL:HG23	2.18	0.43
1:A:311:ILE:HD13	1:A:311:ILE:O	2.18	0.43
1:A:403:LEU:HD23	1:A:403:LEU:HA	1.93	0.43
1:A:377:PHE:HB3	1:A:398:VAL:CG2	2.48	0.43
1:A:370:THR:HG22	1:A:374:LYS:HG3	2.00	0.43
1:A:395:ASP:O	1:A:401:MET:CE	2.67	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:166:SER:O	1:A:167:GLU:O	2.37	0.42
1:A:207:THR:O	1:A:210:GLN:HB2	2.19	0.42
1:A:250:ASN:O	1:A:254:ILE:HG13	2.19	0.42
1:A:348:THR:HB	1:A:350:MET:HE3	2.00	0.42
1:A:335:LEU:HD23	1:A:335:LEU:HA	1.91	0.42
1:A:100:TYR:CZ	1:A:338:THR:HB	2.54	0.42
1:A:139:SER:CB	1:A:336:HIS:HD2	2.32	0.42
1:A:200:LYS:HA	1:A:200:LYS:HD3	1.89	0.42
1:A:98:ILE:O	1:A:98:ILE:HG12	2.16	0.42
1:A:395:ASP:O	1:A:401:MET:HE1	2.20	0.42
1:A:172:GLY:C	1:A:174:LEU:H	2.23	0.42
1:A:163:GLY:HA3	1:A:200:LYS:HE3	2.02	0.42
1:A:253:LYS:O	1:A:257:HIS:CD2	2.73	0.41
1:A:262:GLN:O	1:A:266:ILE:HD12	2.20	0.41
1:A:207:THR:HG23	1:A:209:ASP:N	2.34	0.41
1:A:263:VAL:HG23	1:A:269:PHE:HD2	1.85	0.41
1:A:453:THR:OG1	1:A:456:ILE:HG12	2.19	0.41
1:A:348:THR:CG2	1:A:349:LYS:N	2.63	0.41
1:A:140:HIS:CD2	1:A:143:MET:H	2.38	0.41
1:A:210:GLN:O	1:A:213:SER:N	2.53	0.41
1:A:181:LYS:HE2	1:A:226:GLY:HA3	2.02	0.41
1:A:280:PHE:O	1:A:282:ALA:N	2.53	0.41
1:A:342:ALA:HB1	1:A:350:MET:HB2	2.01	0.41
1:A:348:THR:CG2	1:A:350:MET:HA	2.51	0.41
1:A:409:ASP:OD2	1:A:412:LYS:HE2	2.21	0.41
1:A:184:GLN:NE2	1:A:227:PHE:HD1	2.19	0.40
1:A:306:LEU:HD11	1:A:335:LEU:HG	2.04	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	372/477 (78%)	324 (87%)	34 (9%)	14 (4%)	3 10

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	227	PHE
1	A	350	MET
1	A	167	GLU
1	A	299	ASP
1	A	352	ALA
1	A	356	ASN
1	A	169	MET
1	A	99	ASP
1	A	300	ARG
1	A	468	PHE
1	A	246	GLY
1	A	351	SER
1	A	357	SER
1	A	164	PRO

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	324/416 (78%)	279 (86%)	45 (14%)	3 11

All (45) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	98	ILE
1	A	103	LEU
1	A	105	VAL
1	A	106	ARG
1	A	121	GLU
1	A	126	GLN
1	A	134	ARG

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Mol	Chain	Res	Type
1	A	138	PHE
1	A	160	THR
1	A	166	SER
1	A	169	MET
1	A	189	VAL
1	A	192	VAL
1	A	202	LEU
1	A	207	THR
1	A	209	ASP
1	A	213	SER
1	A	230	ASN
1	A	232	THR
1	A	239	ASP
1	A	256	LYS
1	A	259	THR
1	A	272	SER
1	A	295	GLN
1	A	297	PHE
1	A	311	ILE
1	A	318	ARG
1	A	326	ARG
1	A	347	GLN
1	A	351	SER
1	A	354	ASP
1	A	355	PRO
1	A	385	GLU
1	A	393	ASN
1	A	399	SER
1	A	417	ARG
1	A	427	THR
1	A	430	LEU
1	A	432	LYS
1	A	434	LEU
1	A	436	GLU
1	A	441	LEU
1	A	446	GLN
1	A	451	GLU
1	A	461	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	140	HIS
1	A	170	HIS
1	A	255	GLN
1	A	262	GLN
1	A	295	GLN
1	A	336	HIS
1	A	344	GLN
1	A	393	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 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)

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	374/477 (78%)	0.03	12 (3%) 47 37	25, 61, 116, 172	0

All (12) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	97	GLY	3.6
1	A	168	ALA	3.4
1	A	348	THR	3.4
1	A	349	LYS	3.4
1	A	351	SER	2.9
1	A	350	MET	2.6
1	A	96	LYS	2.6
1	A	167	GLU	2.5
1	A	354	ASP	2.1
1	A	346	ALA	2.1
1	A	102	LYS	2.1
1	A	105	VAL	2.0

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 monosaccharides 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.