Full wwPDB X-ray Structure Validation Report ⓘ

Jan 27, 2024 – 03:46 PM EST

PDB ID	:	1ATI
Title	:	CRYSTAL STRUCTURE OF GLYCYL-TRNA SYNTHETASE FROM THERMUS THERMOPHILUS
Authors	:	Logan, D.T.; Mazauric, M.-H.; Kern, D.; Moras, D.
Deposited on	:	1996-04-23
Resolution	:	2.75 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:

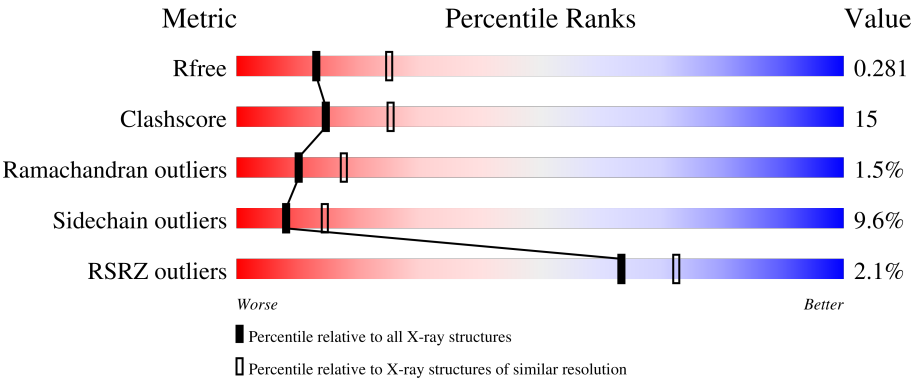
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation 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 2.75 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	1235 (2.78-2.74)
Clashscore	141614	1277 (2.78-2.74)
Ramachandran outliers	138981	1257 (2.78-2.74)
Sidechain outliers	138945	1257 (2.78-2.74)
RSRZ outliers	127900	1207 (2.78-2.74)

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	505	60% 23% 13%
1	B	505	57% 26% 14%
2	C	37	73% 27%
3	D	16	75% 25%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 7407 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 GLYCYL-TRNA SYNTHETASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	437	Total	C	N	O	S	0	0	0
			3568	2270	640	650	8			
1	B	436	Total	C	N	O	S	0	0	0
			3554	2259	638	649	8			

- Molecule 2 is a protein called GLYCYL-tRNA SYNTHETASE.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	37	Total	C	N	O	0	0	0
			184	110	37	37			

- Molecule 3 is a protein called GLYCYL-tRNA SYNTHETASE.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	D	16	Total	C	N	O	0	0	0
			78	46	16	16			

- Molecule 4 is water.

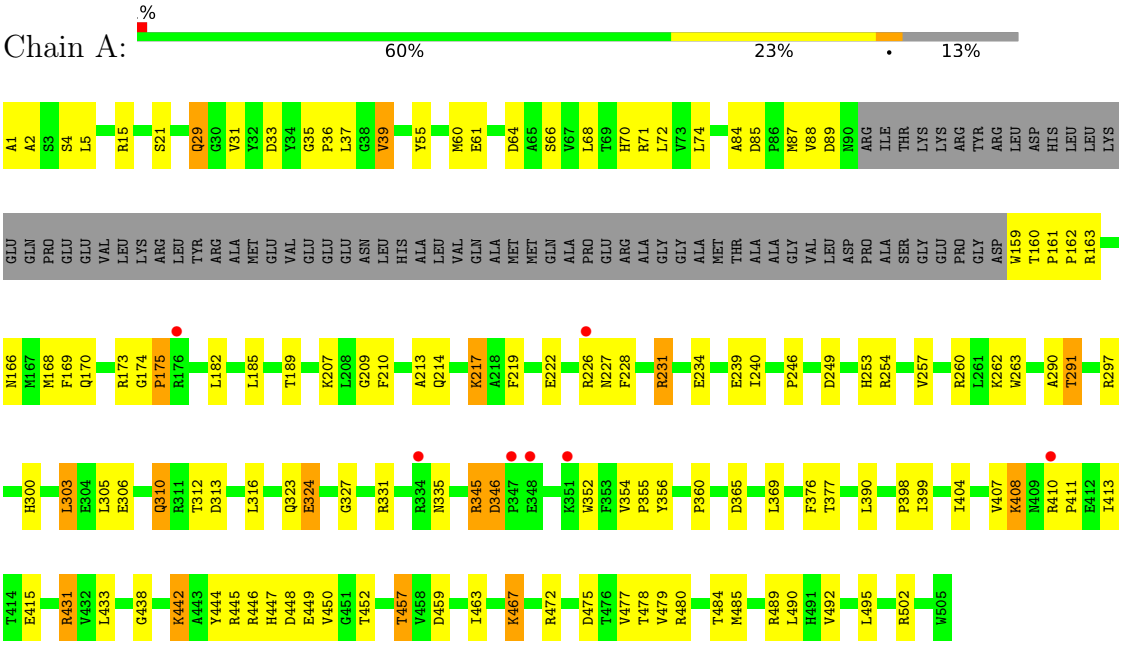
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	17	Total	O	0	0
			17	17		
4	B	6	Total	O	0	0
			6	6		

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.

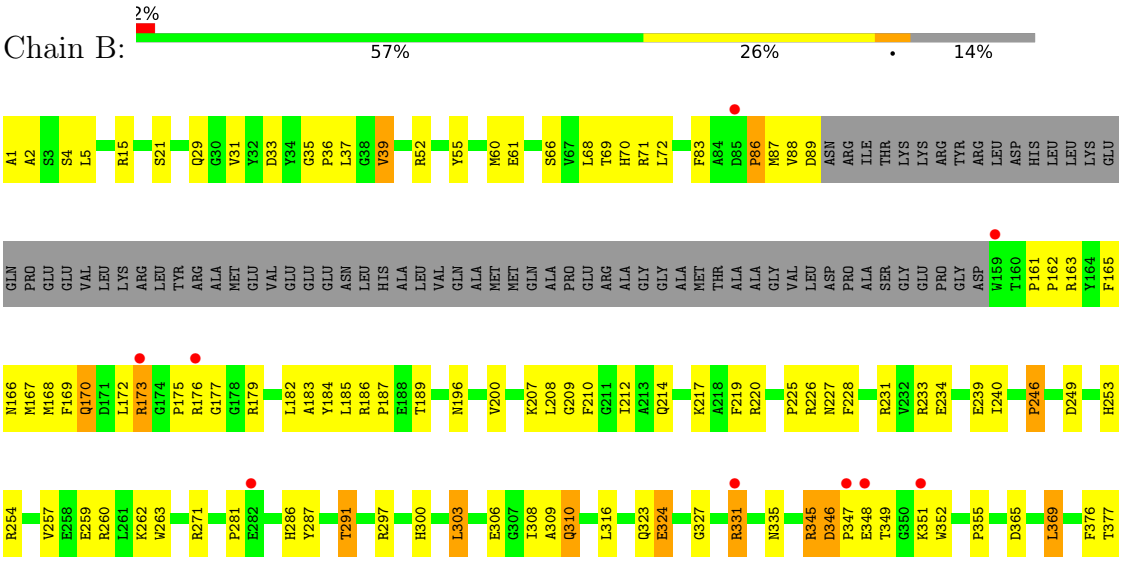
• Molecule 1: GLYCYL-TRNA SYNTHETASE

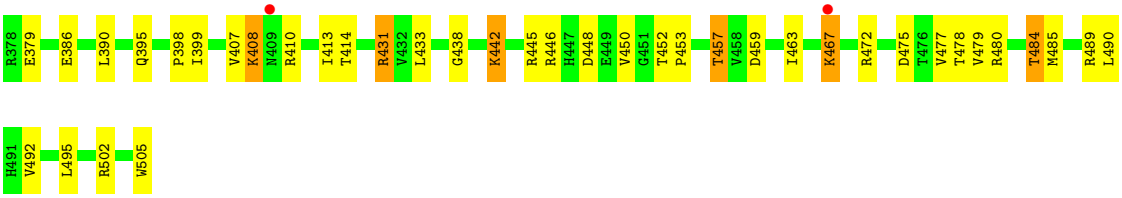
Chain A:



• Molecule 1: GLYCYL-TRNA SYNTHETASE

Chain B:





• Molecule 2: GLYCYL-tRNA SYNTHETASE

Chain C:

• Molecule 3: GLYCYL-tRNA SYNTHETASE

Chain D:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α, β, γ	126.90Å 255.30Å 105.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.75 19.98 – 2.71	Depositor EDS
% Data completeness (in resolution range)	84.3 (20.00-2.75) 81.3 (19.98-2.71)	Depositor EDS
R_{merge}	0.01	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.71 (at 2.71Å)	Xtriage
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.227 , 0.290 0.223 , 0.281	Depositor DCC
R_{free} test set	1832 reflections (4.82%)	wwPDB-VP
Wilson B-factor (Å^2)	63.6	Xtriage
Anisotropy	0.231	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.27 , 67.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	7407	wwPDB-VP
Average B, all atoms (Å^2)	71.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.23% 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	0.66	0/3653	0.85	1/4942 (0.0%)
1	B	0.69	0/3637	0.86	1/4919 (0.0%)
All	All	0.67	0/7290	0.85	2/9861 (0.0%)

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

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	209	GLY	N-CA-C	-9.38	89.66	113.10
1	B	209	GLY	N-CA-C	-8.68	91.40	113.10

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	287	TYR	Sidechain

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	3568	0	3520	105	0
1	B	3554	0	3510	121	0
2	C	184	0	41	8	0
3	D	78	0	17	4	0
4	A	17	0	0	1	0
4	B	6	0	0	1	0
All	All	7407	0	7088	221	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 15.

All (221) 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:B:413:ILE:HG13	1:B:463:ILE:HD11	1.41	1.00
1:A:74:LEU:HD13	1:A:168:MET:HE1	1.46	0.97
1:B:300:HIS:HE1	1:B:303:LEU:HD12	1.44	0.83
1:A:21:SER:HB3	1:A:31:VAL:HG23	1.60	0.80
1:B:21:SER:HB3	1:B:31:VAL:HG23	1.65	0.79
1:A:408:LYS:HE3	1:A:438:GLY:HA2	1.63	0.78
1:A:300:HIS:HE1	1:A:303:LEU:HD12	1.49	0.77
1:B:300:HIS:CE1	1:B:303:LEU:HD12	2.19	0.77
1:B:467:LYS:H	1:B:467:LYS:HD3	1.51	0.75
1:A:253:HIS:O	1:A:257:VAL:HG23	1.86	0.75
1:A:260:ARG:HD3	1:A:306:GLU:OE2	1.87	0.75
1:A:300:HIS:CE1	1:A:303:LEU:HD12	2.22	0.75
1:A:161:PRO:HB3	2:C:115:UNK:HA	1.71	0.73
1:B:253:HIS:O	1:B:257:VAL:HG23	1.90	0.72
1:B:169:PHE:HD2	1:B:219:PHE:HB3	1.58	0.68
1:B:1:ALA:N	1:B:377:THR:HG22	2.08	0.68
1:B:260:ARG:HD3	1:B:306:GLU:OE2	1.93	0.68
1:B:71:ARG:HH21	1:B:179:ARG:HE	1.42	0.67
1:B:450:VAL:HG23	1:B:452:THR:HG23	1.76	0.67
1:A:467:LYS:H	1:A:467:LYS:HD3	1.60	0.66
1:A:450:VAL:HG23	1:A:452:THR:HG23	1.77	0.66
1:A:169:PHE:CD2	1:A:219:PHE:HB3	2.29	0.66
1:B:253:HIS:HD2	1:B:310:GLN:CB	2.08	0.66
1:B:408:LYS:HE3	1:B:438:GLY:HA2	1.77	0.66
1:A:472:ARG:HB3	1:A:472:ARG:NH1	2.11	0.66
1:B:413:ILE:CG1	1:B:463:ILE:HD11	2.20	0.65
1:B:316:LEU:HD12	1:B:355:PRO:HD2	1.78	0.65
1:A:169:PHE:HD2	1:A:219:PHE:HB3	1.60	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:219:PHE:CE2	1:A:234:GLU:HG3	2.31	0.65
1:A:316:LEU:HD12	1:A:355:PRO:HD2	1.80	0.64
1:A:160:THR:HB	1:A:161:PRO:HD2	1.79	0.64
1:A:217:LYS:HE3	4:B:510:HOH:O	1.97	0.64
1:B:219:PHE:CE2	1:B:234:GLU:HG3	2.33	0.64
1:B:1:ALA:H2	1:B:377:THR:HG22	1.63	0.63
1:A:74:LEU:HD13	1:A:168:MET:CE	2.26	0.63
1:B:169:PHE:CD2	1:B:219:PHE:HB3	2.33	0.63
1:B:475:ASP:O	1:B:492:VAL:HG23	1.99	0.63
1:B:323:GLN:NE2	1:B:335:ASN:H	1.95	0.63
1:B:492:VAL:O	1:B:495:LEU:HB3	1.99	0.63
1:B:399:ILE:HB	1:B:452:THR:CG2	2.29	0.62
1:A:21:SER:CB	1:A:31:VAL:HG23	2.26	0.62
1:A:189:THR:HG21	1:A:214:GLN:HG2	1.81	0.62
1:B:189:THR:HG23	1:B:214:GLN:OE1	1.99	0.62
1:A:253:HIS:HD2	1:A:310:GLN:CB	2.13	0.61
1:B:253:HIS:HD2	1:B:310:GLN:HB2	1.65	0.61
2:C:97:UNK:C	2:C:99:UNK:N	2.60	0.61
1:A:35:GLY:O	1:A:39:VAL:HG23	2.01	0.61
1:B:399:ILE:HB	1:B:452:THR:HG21	1.83	0.60
1:A:226:ARG:H	1:A:231:ARG:HB2	1.67	0.59
1:A:253:HIS:HD2	1:A:310:GLN:HB2	1.67	0.59
1:B:189:THR:HG21	1:B:214:GLN:HG2	1.84	0.59
1:A:87:MET:HG2	1:A:88:VAL:N	2.18	0.58
1:A:413:ILE:HG13	1:A:463:ILE:HD11	1.84	0.58
1:B:480:ARG:HG2	1:B:480:ARG:HH11	1.67	0.58
1:A:249:ASP:HB2	1:A:310:GLN:HE22	1.67	0.58
1:B:21:SER:CB	1:B:31:VAL:HG23	2.32	0.58
1:B:71:ARG:NH2	1:B:179:ARG:HE	2.02	0.58
1:B:161:PRO:HB3	3:D:106:UNK:N	2.19	0.57
1:B:459:ASP:OD2	1:B:489:ARG:NH2	2.37	0.57
1:A:36:PRO:CG	1:B:61:GLU:HG3	2.35	0.57
1:B:2:ALA:HB2	1:B:376:PHE:HB3	1.87	0.57
1:B:169:PHE:HZ	1:B:233:ARG:HD3	1.70	0.57
1:A:323:GLN:NE2	1:A:335:ASN:H	2.02	0.56
1:A:413:ILE:CG1	1:A:463:ILE:HD11	2.34	0.56
1:A:88:VAL:HG12	1:A:162:PRO:HA	1.86	0.56
1:B:286:HIS:CE1	1:B:331:ARG:HG3	2.41	0.56
1:B:168:MET:HE3	1:B:187:PRO:HG3	1.86	0.56
1:A:189:THR:HG23	1:A:214:GLN:OE1	2.05	0.56
1:B:170:GLN:HB3	1:B:184:TYR:CD1	2.41	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:189:THR:HB	1:A:239:GLU:OE1	2.05	0.55
1:B:37:LEU:HD23	1:B:398:PRO:HB2	1.89	0.55
1:A:234:GLU:OE1	1:B:66:SER:HB2	2.07	0.54
1:B:189:THR:HB	1:B:239:GLU:OE1	2.07	0.54
1:B:35:GLY:O	1:B:39:VAL:HG23	2.07	0.54
1:B:70:HIS:HD2	1:B:71:ARG:N	2.06	0.54
1:A:475:ASP:O	1:A:492:VAL:HG23	2.06	0.54
1:A:399:ILE:HB	1:A:452:THR:CG2	2.36	0.54
1:B:167:MET:CE	1:B:220:ARG:HD3	2.37	0.54
1:A:226:ARG:HB2	1:A:231:ARG:HG3	1.91	0.53
1:A:399:ILE:HB	1:A:452:THR:HG21	1.89	0.53
1:B:300:HIS:HE1	1:B:303:LEU:CD1	2.19	0.53
1:A:492:VAL:O	1:A:495:LEU:HB3	2.08	0.53
1:A:70:HIS:HD2	1:A:71:ARG:N	2.07	0.53
1:B:163:ARG:HG3	1:B:163:ARG:HH11	1.73	0.53
1:A:480:ARG:HH11	1:A:480:ARG:HG2	1.74	0.53
1:B:467:LYS:HD3	1:B:467:LYS:N	2.21	0.52
1:A:1:ALA:N	1:A:377:THR:HG22	2.23	0.52
1:A:15:ARG:NH1	1:A:446:ARG:HA	2.25	0.52
1:A:159:TRP:HD1	2:C:121:UNK:HA	1.74	0.52
1:B:163:ARG:HB2	1:B:165:PHE:CE1	2.44	0.52
1:B:457:THR:HG23	1:B:478:THR:OG1	2.09	0.52
1:A:445:ARG:NH1	1:A:448:ASP:HB2	2.26	0.51
1:A:189:THR:CG2	1:A:214:GLN:HG2	2.40	0.51
1:A:185:LEU:HD21	1:B:185:LEU:HD11	1.91	0.51
1:A:459:ASP:OD2	1:A:489:ARG:NH2	2.44	0.51
2:C:97:UNK:O	2:C:98:UNK:C	2.58	0.51
1:A:61:GLU:HG3	1:B:36:PRO:CG	2.41	0.50
1:B:347:PRO:HG2	1:B:349:THR:OG1	2.11	0.50
1:B:207:LYS:HD2	1:B:207:LYS:N	2.26	0.50
1:B:83:PHE:HB3	1:B:166:ASN:HA	1.94	0.50
1:A:300:HIS:HE1	1:A:303:LEU:CD1	2.21	0.50
1:B:226:ARG:H	1:B:231:ARG:HB2	1.76	0.50
1:A:207:LYS:N	1:A:207:LYS:HD2	2.27	0.49
1:B:324:GLU:H	1:B:324:GLU:CD	2.15	0.49
1:B:260:ARG:NH2	1:B:263:TRP:CE3	2.81	0.49
1:B:167:MET:HE1	1:B:220:ARG:HD3	1.95	0.49
1:A:36:PRO:HG3	1:B:61:GLU:HG3	1.95	0.49
1:A:442:LYS:O	1:A:442:LYS:HD3	2.12	0.49
1:B:69:THR:OG1	1:B:186:ARG:HB3	2.12	0.49
1:B:172:LEU:HD22	1:B:177:GLY:HA2	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:445:ARG:NH1	1:B:448:ASP:HB2	2.28	0.49
1:A:29:GLN:HB3	1:B:173:ARG:HH22	1.78	0.49
1:A:64:ASP:HB2	1:B:39:VAL:HG13	1.94	0.49
1:B:15:ARG:NH1	1:B:446:ARG:HA	2.27	0.49
1:A:71:ARG:HG2	1:A:71:ARG:HH11	1.78	0.48
1:A:431:ARG:HD3	1:B:55:TYR:CD1	2.48	0.48
1:B:71:ARG:HH11	1:B:71:ARG:HG2	1.77	0.48
1:B:189:THR:CG2	1:B:214:GLN:HG2	2.43	0.48
1:A:88:VAL:CG1	1:A:162:PRO:HA	2.43	0.48
1:B:253:HIS:CD2	1:B:310:GLN:HB3	2.48	0.48
1:A:472:ARG:HB3	1:A:472:ARG:HH11	1.76	0.48
1:A:84:ALA:HB2	1:A:166:ASN:HA	1.96	0.48
1:B:225:PRO:HG2	1:B:233:ARG:NH1	2.29	0.47
1:B:442:LYS:O	1:B:442:LYS:HD3	2.14	0.47
1:A:89:ASP:O	1:A:159:TRP:HA	2.15	0.47
1:B:459:ASP:CG	1:B:489:ARG:HH22	2.17	0.47
1:A:89:ASP:O	1:A:159:TRP:HE3	1.97	0.47
1:B:323:GLN:HE22	1:B:335:ASN:H	1.63	0.47
1:A:21:SER:HA	1:A:33:ASP:OD2	2.14	0.47
1:B:347:PRO:HD2	1:B:351:LYS:H	1.80	0.47
1:B:347:PRO:C	1:B:349:THR:H	2.18	0.47
1:A:240:ILE:HB	1:A:360:PRO:HD2	1.97	0.47
1:B:86:PRO:HA	1:B:163:ARG:O	2.15	0.46
1:B:249:ASP:HB2	1:B:310:GLN:HE22	1.79	0.46
1:A:324:GLU:CD	1:A:324:GLU:H	2.18	0.46
1:A:68:LEU:HA	1:A:68:LEU:HD23	1.63	0.46
1:B:168:MET:CE	1:B:187:PRO:HG3	2.45	0.46
1:B:253:HIS:CD2	1:B:310:GLN:CB	2.95	0.46
1:B:182:LEU:HD12	1:B:183:ALA:N	2.31	0.46
1:B:369:LEU:HA	1:B:369:LEU:HD23	1.65	0.46
1:B:395:GLN:HB3	1:B:505:TRP:CE2	2.51	0.45
1:B:390:LEU:HD23	1:B:390:LEU:HA	1.72	0.45
1:A:66:SER:HB2	1:B:234:GLU:OE1	2.17	0.45
1:A:74:LEU:CD1	1:A:168:MET:HE1	2.32	0.45
2:C:125:UNK:C	2:C:127:UNK:N	2.75	0.45
1:A:222:GLU:CD	1:A:231:ARG:HH12	2.19	0.45
1:A:61:GLU:HG3	1:B:36:PRO:HG3	1.99	0.45
1:A:345:ARG:O	1:A:346:ASP:HB3	2.17	0.45
1:A:174:GLY:HA3	1:A:175:PRO:HD3	1.80	0.45
1:B:161:PRO:HG3	3:D:106:UNK:HA	1.99	0.45
1:A:2:ALA:HB2	1:A:376:PHE:HB3	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:399:ILE:O	1:B:452:THR:HB	2.17	0.45
1:A:60:MET:CE	1:A:213:ALA:HB2	2.47	0.45
2:C:97:UNK:O	2:C:99:UNK:N	2.50	0.45
1:A:1:ALA:H2	1:A:377:THR:HG22	1.82	0.44
1:B:208:LEU:HD23	1:B:208:LEU:HA	1.84	0.44
1:A:170:GLN:HB2	1:A:182:LEU:HD11	2.00	0.44
1:A:260:ARG:NH1	1:A:306:GLU:OE1	2.51	0.44
1:A:457:THR:HG23	1:A:478:THR:OG1	2.18	0.44
1:B:291:THR:HB	1:B:309:ALA:HA	2.00	0.44
1:B:308:ILE:N	1:B:308:ILE:HD12	2.33	0.44
1:B:347:PRO:O	1:B:348:GLU:HB3	2.17	0.44
1:A:390:LEU:HD23	1:A:390:LEU:HA	1.77	0.44
1:B:87:MET:HB2	1:B:165:PHE:CD1	2.52	0.44
1:A:70:HIS:CD2	1:A:72:LEU:H	2.36	0.44
2:C:117:UNK:C	2:C:119:UNK:N	2.81	0.44
1:A:444:TYR:OH	1:A:457:THR:HG21	2.18	0.44
1:B:68:LEU:HD23	1:B:68:LEU:HA	1.65	0.44
1:B:395:GLN:HB3	1:B:505:TRP:CZ2	2.53	0.44
1:A:376:PHE:CD1	1:A:376:PHE:C	2.91	0.43
1:B:52:ARG:NH1	1:B:259:GLU:OE2	2.51	0.43
1:B:345:ARG:O	1:B:346:ASP:HB3	2.18	0.43
1:B:21:SER:HA	1:B:33:ASP:OD2	2.18	0.43
1:A:431:ARG:HD2	4:A:515:HOH:O	2.18	0.43
1:A:253:HIS:HD2	1:A:310:GLN:HB3	1.84	0.43
1:A:305:LEU:HD23	1:A:305:LEU:HA	1.88	0.43
1:B:172:LEU:HD22	1:B:177:GLY:C	2.39	0.43
1:A:290:ALA:C	1:A:291:THR:HG22	2.38	0.43
1:B:249:ASP:OD2	1:B:310:GLN:NE2	2.51	0.43
1:A:312:THR:O	1:A:356:TYR:HA	2.19	0.43
1:B:480:ARG:HG2	1:B:480:ARG:NH1	2.33	0.43
1:A:260:ARG:NH2	1:A:263:TRP:CE3	2.87	0.43
1:B:70:HIS:CD2	1:B:71:ARG:N	2.85	0.43
1:B:410:ARG:O	1:B:414:THR:HG23	2.19	0.42
1:B:484:THR:O	1:B:485:MET:HB2	2.20	0.42
1:A:15:ARG:NH1	1:A:449:GLU:OE1	2.51	0.42
1:B:167:MET:HE3	1:B:220:ARG:HD3	2.01	0.42
1:A:37:LEU:HD23	1:A:398:PRO:HB2	2.02	0.42
1:B:379:GLU:O	1:B:386:GLU:HA	2.20	0.42
1:A:313:ASP:HB2	1:A:354:VAL:CG1	2.49	0.42
1:B:189:THR:CG2	1:B:214:GLN:OE1	2.67	0.42
1:A:37:LEU:HD13	1:A:450:VAL:HG11	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:182:LEU:HD12	1:B:183:ALA:H	1.85	0.41
1:B:196:ASN:O	1:B:200:VAL:HG23	2.20	0.41
1:A:459:ASP:CG	1:A:489:ARG:HH22	2.22	0.41
1:A:55:TYR:CD1	1:B:431:ARG:HD3	2.54	0.41
1:B:310:GLN:HG3	1:B:310:GLN:O	2.20	0.41
1:B:472:ARG:CZ	1:B:472:ARG:HB3	2.50	0.41
1:A:70:HIS:CD2	1:A:71:ARG:N	2.86	0.41
1:B:61:GLU:O	1:B:212:ILE:HA	2.21	0.41
1:B:162:PRO:HD2	3:D:105:UNK:CB	2.51	0.41
1:A:445:ARG:HH12	1:A:448:ASP:HB2	1.84	0.41
1:B:2:ALA:HB2	1:B:376:PHE:CG	2.55	0.41
1:A:29:GLN:HB3	1:B:173:ARG:NH2	2.35	0.41
1:B:452:THR:HA	1:B:453:PRO:HD2	1.87	0.41
1:B:70:HIS:CD2	1:B:72:LEU:H	2.37	0.41
1:B:376:PHE:C	1:B:376:PHE:CD1	2.94	0.41
1:A:445:ARG:CZ	1:A:445:ARG:HA	2.50	0.41
1:A:484:THR:O	1:A:485:MET:HB2	2.21	0.41
1:B:60:MET:HE2	1:B:240:ILE:HD13	2.02	0.41
1:A:354:VAL:HA	1:A:355:PRO:HD3	1.93	0.41
1:B:445:ARG:HH12	1:B:448:ASP:HB2	1.86	0.41
2:C:124:UNK:O	2:C:125:UNK:C	2.69	0.41
1:A:408:LYS:CE	1:A:438:GLY:HA2	2.42	0.40
1:A:410:ARG:HA	1:A:411:PRO:HD2	1.96	0.40
3:D:102:UNK:C	3:D:104:UNK:H	2.34	0.40
1:A:404:ILE:O	1:A:457:THR:HA	2.21	0.40
1:B:2:ALA:HB2	1:B:376:PHE:CB	2.50	0.40
1:A:447:HIS:HA	1:A:450:VAL:HG22	2.03	0.40
1:A:231:ARG:HB3	1:A:231:ARG:HH11	1.86	0.40
1:B:271:ARG:O	1:B:271:ARG:NH1	2.53	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	433/505 (86%)	403 (93%)	25 (6%)	5 (1%)	13 23
1	B	432/505 (86%)	401 (93%)	23 (5%)	8 (2%)	8 14
All	All	865/1010 (86%)	804 (93%)	48 (6%)	13 (2%)	10 18

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	227	ASN
1	A	227	ASN
1	A	29	GLN
1	A	346	ASP
1	B	29	GLN
1	B	346	ASP
1	A	175	PRO
1	B	281	PRO
1	B	175	PRO
1	B	86	PRO
1	A	327	GLY
1	B	246	PRO
1	B	327	GLY

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	372/427 (87%)	337 (91%)	35 (9%)	8 15
1	B	371/427 (87%)	335 (90%)	36 (10%)	8 14
All	All	743/854 (87%)	672 (90%)	71 (10%)	8 14

All (71) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	SER
1	A	5	LEU
1	A	39	VAL

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Mol	Chain	Res	Type
1	A	85	ASP
1	A	163	ARG
1	A	173	ARG
1	A	210	PHE
1	A	217	LYS
1	A	228	PHE
1	A	231	ARG
1	A	246	PRO
1	A	254	ARG
1	A	262	LYS
1	A	291	THR
1	A	297	ARG
1	A	303	LEU
1	A	310	GLN
1	A	324	GLU
1	A	331	ARG
1	A	345	ARG
1	A	352	TRP
1	A	365	ASP
1	A	369	LEU
1	A	407	VAL
1	A	408	LYS
1	A	415	GLU
1	A	431	ARG
1	A	433	LEU
1	A	442	LYS
1	A	457	THR
1	A	467	LYS
1	A	477	VAL
1	A	479	VAL
1	A	490	LEU
1	A	502	ARG
1	B	4	SER
1	B	5	LEU
1	B	39	VAL
1	B	88	VAL
1	B	89	ASP
1	B	170	GLN
1	B	173	ARG
1	B	176	ARG
1	B	210	PHE
1	B	217	LYS

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Mol	Chain	Res	Type
1	B	228	PHE
1	B	246	PRO
1	B	254	ARG
1	B	262	LYS
1	B	291	THR
1	B	297	ARG
1	B	303	LEU
1	B	310	GLN
1	B	324	GLU
1	B	331	ARG
1	B	345	ARG
1	B	352	TRP
1	B	365	ASP
1	B	369	LEU
1	B	407	VAL
1	B	408	LYS
1	B	431	ARG
1	B	433	LEU
1	B	442	LYS
1	B	457	THR
1	B	467	LYS
1	B	477	VAL
1	B	479	VAL
1	B	484	THR
1	B	490	LEU
1	B	502	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	43	ASN
1	A	44	ASN
1	A	70	HIS
1	A	170	GLN
1	A	253	HIS
1	A	300	HIS
1	A	323	GLN
1	B	43	ASN
1	B	44	ASN
1	B	70	HIS
1	B	170	GLN
1	B	253	HIS

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Mol	Chain	Res	Type
1	B	300	HIS
1	B	323	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 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

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	C	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	99:UNK	C	103:UNK	N	9.82

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	437/505 (86%)	-0.31	7 (1%) 72 79	37, 63, 114, 148	0
1	B	436/505 (86%)	-0.27	11 (2%) 57 66	38, 66, 115, 145	0
2	C	0/37	-	-	-	-
3	D	0/16	-	-	-	-
All	All	873/1063 (82%)	-0.29	18 (2%) 63 72	37, 65, 115, 148	0

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	347	PRO	5.2
1	A	176	ARG	4.1
1	A	348	GLU	3.8
1	A	347	PRO	3.3
1	B	351	LYS	3.1
1	B	85	ASP	2.8
1	B	282	GLU	2.7
1	B	159	TRP	2.7
1	B	176	ARG	2.6
1	A	334	ARG	2.6
1	B	331	ARG	2.4
1	A	351	LYS	2.4
1	A	410	ARG	2.3
1	B	467	LYS	2.2
1	B	348	GLU	2.2
1	B	409	ASN	2.1
1	A	226	ARG	2.1
1	B	173	ARG	2.1

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.