



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 24, 2026 – 09:25 PM EDT

PDB ID : 1BS2 / pdb_00001bs2
Title : YEAST ARGINYL-TRNA SYNTHETASE
Authors : Cavarelli, J.; Delagouute, B.; Eriani, G.; Gangloff, J.; Moras, D.
Deposited on : 1998-08-31
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	:	4-5-2 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

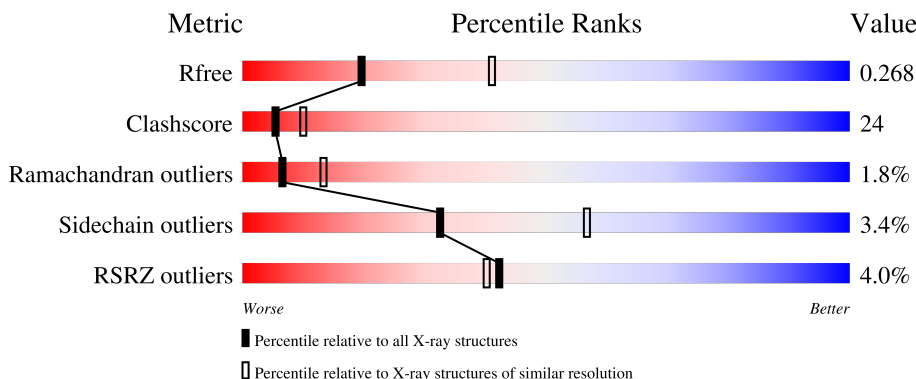
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.75 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}	180053	1009 (2.76-2.76)
Clashscore	190562	1044 (2.76-2.76)
Ramachandran outliers	187476	1024 (2.76-2.76)
Sidechain outliers	187428	1024 (2.76-2.76)
RSRZ outliers	180081	1009 (2.76-2.76)

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 $\leq 5\%$. 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	607	

2 Entry composition [i](#)

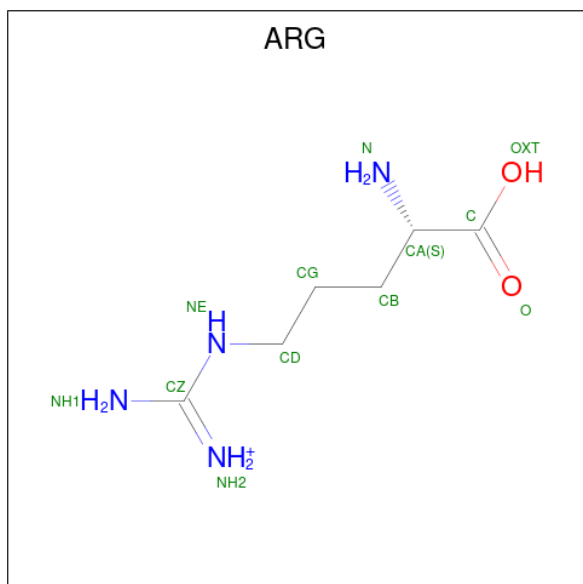
There are 3 unique types of molecules in this entry. The entry contains 5157 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 PROTEIN (ARGINYL-TRNA SYNTHETASE).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	603	Total	C	N	O	S	0	0	0
			4874	3128	825	900	21			

- Molecule 2 is ARGinine (CCD ID: ARG) (formula: $C_6H_{15}N_4O_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			12	6	4	2		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	271	Total	O	0	0
			271	271		

- Molecule 1: PROTEIN (ARGINYL-TRNA SYNTHETASE)



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	100.37Å 100.37Å 204.34Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.75 20.00 – 2.75	Depositor EDS
% Data completeness (in resolution range)	97.3 (20.00-2.75) 96.9 (20.00-2.75)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.04	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.91 (at 2.76Å)	Xtriage
Refinement program	CNS 0.1-0.4	Depositor
R, R_{free}	0.207 , 0.269 0.207 , 0.268	Depositor DCC
R_{free} test set	2038 reflections (7.48%)	wwPDB-VP
Wilson B-factor (Å ²)	48.7	Xtriage
Anisotropy	0.486	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 46.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5157	wwPDB-VP
Average B, all atoms (Å ²)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.61% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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	0.41	0/4978	0.94	15/6711 (0.2%)

There are no bond length outliers.

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	123	VAL	N-CA-C	8.06	118.16	110.42
1	A	197	GLY	N-CA-C	-7.51	103.78	112.50
1	A	254	ARG	N-CA-C	-7.13	103.61	114.16
1	A	255	MET	N-CA-C	-6.26	104.70	112.90
1	A	72	PRO	N-CA-C	-6.24	100.38	110.74
1	A	183	VAL	N-CA-C	6.13	116.75	108.17
1	A	234	GLU	CB-CA-C	-6.10	108.29	117.07
1	A	269	PHE	N-CA-C	-5.91	104.74	111.07
1	A	416	VAL	N-CA-C	-5.91	100.45	109.78
1	A	242	GLN	N-CA-C	-5.74	106.05	113.16
1	A	180	GLY	N-CA-C	5.64	122.25	114.92
1	A	182	GLU	N-CA-C	-5.35	100.01	108.73
1	A	389	MET	N-CA-C	-5.34	106.73	113.20
1	A	314	LEU	N-CA-C	-5.29	107.47	114.04
1	A	34	LEU	N-CA-C	-5.02	105.70	111.07

There are no chirality outliers.

There are no planarity outliers.

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	4874	0	4889	234	0
2	A	12	0	12	1	0
3	A	271	0	0	12	0
All	All	5157	0	4901	234	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 24.

All (234) 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:468:ILE:H	1:A:468:ILE:HD12	1.17	1.10
1:A:442:GLN:HA	3:A:1132:HOH:O	1.58	1.03
1:A:417:PHE:HD1	1:A:418:LEU:H	1.25	0.85
1:A:468:ILE:H	1:A:468:ILE:CD1	1.91	0.82
1:A:226:ARG:HG2	1:A:229:LYS:NZ	1.97	0.79
1:A:464:GLN:O	1:A:548:THR:HG23	1.83	0.78
1:A:330:ASN:HD22	1:A:333:LEU:HG	1.49	0.77
1:A:260:GLU:C	1:A:262:ALA:H	1.93	0.76
1:A:304:LYS:HE3	1:A:308:LEU:HD21	1.67	0.76
1:A:290:VAL:HG21	1:A:362:TYR:OH	1.85	0.76
1:A:315:THR:HG23	1:A:322:VAL:HG13	1.69	0.74
1:A:468:ILE:HD12	1:A:468:ILE:N	1.98	0.73
1:A:297:VAL:HG11	1:A:302:MET:HE2	1.70	0.73
1:A:422:LEU:O	1:A:426:LYS:HD3	1.89	0.73
1:A:35:MET:HG2	1:A:114:PHE:CE1	2.24	0.72
1:A:226:ARG:O	1:A:229:LYS:HG3	1.91	0.70
1:A:422:LEU:HB3	1:A:426:LYS:NZ	2.08	0.69
1:A:337:ILE:HG22	1:A:346:LEU:HD11	1.76	0.68
1:A:408:MET:O	1:A:410:THR:N	2.27	0.68
1:A:422:LEU:HB3	1:A:426:LYS:HZ3	1.60	0.67
1:A:84:LYS:HE2	3:A:1067:HOH:O	1.95	0.66
1:A:203:PHE:CD1	1:A:207:GLY:HA3	2.30	0.66
1:A:496:LEU:HD13	1:A:589:ARG:HA	1.78	0.66
1:A:389:MET:HE2	1:A:391:PHE:HE2	1.61	0.65
1:A:413:GLY:O	1:A:414:THR:HG23	1.95	0.65
1:A:299:LYS:HD2	1:A:300:GLU:H	1.62	0.65
1:A:36:ARG:HH22	1:A:536:ASP:CG	2.05	0.64
1:A:330:ASN:HD21	1:A:332:LYS:HB2	1.62	0.64
1:A:307:ASP:O	1:A:310:LYS:HG2	1.96	0.64
1:A:411:ARG:HD3	1:A:414:THR:OG1	1.99	0.63
1:A:131:LYS:HE2	1:A:508:GLN:HE22	1.65	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:460:ILE:O	1:A:464:GLN:HG3	1.98	0.62
1:A:132:GLU:HB2	3:A:1169:HOH:O	1.99	0.62
1:A:140:VAL:HG13	1:A:143:LYS:HB2	1.82	0.62
1:A:497:ARG:HG3	1:A:497:ARG:HH11	1.64	0.61
1:A:213:VAL:HG12	1:A:272:PHE:CE2	2.36	0.61
1:A:164:ARG:HG3	1:A:164:ARG:HH11	1.66	0.61
1:A:302:MET:HE1	1:A:350:ARG:HA	1.82	0.61
1:A:325:ASP:OD1	1:A:327:THR:HB	2.01	0.61
1:A:524:ALA:HB2	1:A:568:LEU:HD11	1.83	0.61
1:A:268:ARG:HA	1:A:271:GLU:HG2	1.82	0.61
1:A:23:LYS:O	1:A:24:ASP:HB2	2.00	0.60
1:A:264:LYS:O	1:A:268:ARG:HG3	2.02	0.60
1:A:384:GLU:OE2	1:A:387:LYS:HD3	2.02	0.60
1:A:458:VAL:HG22	1:A:478:MET:HE1	1.83	0.60
1:A:81:ALA:HB1	1:A:86:LEU:HD11	1.83	0.59
1:A:576:GLU:H	1:A:576:GLU:CD	2.11	0.59
1:A:341:SER:C	1:A:343:GLY:H	2.10	0.59
1:A:35:MET:HG2	1:A:114:PHE:CD1	2.37	0.59
1:A:330:ASN:ND2	1:A:332:LYS:HB2	2.17	0.59
1:A:418:LEU:HD23	3:A:970:HOH:O	2.01	0.58
1:A:539:ARG:HH22	1:A:543:LYS:HZ3	1.52	0.58
1:A:226:ARG:HG2	1:A:229:LYS:HZ1	1.68	0.58
1:A:173:ALA:O	1:A:177:GLU:HG3	2.03	0.58
1:A:405:VAL:HG22	1:A:471:TYR:CE2	2.39	0.58
1:A:458:VAL:CG2	1:A:478:MET:HE1	2.34	0.58
1:A:429:MET:O	1:A:433:MET:HB2	2.05	0.57
1:A:514:ALA:HB2	1:A:579:THR:HG22	1.86	0.57
1:A:426:LYS:HD2	1:A:475:TRP:HH2	1.70	0.57
1:A:252:PHE:O	1:A:254:ARG:HG2	2.04	0.57
1:A:422:LEU:HD22	1:A:426:LYS:NZ	2.20	0.57
1:A:36:ARG:HD3	3:A:1166:HOH:O	2.04	0.57
1:A:40:SER:HB3	1:A:51:SER:HB2	1.87	0.56
1:A:64:MET:HE1	1:A:530:LEU:HD22	1.87	0.56
1:A:260:GLU:C	1:A:262:ALA:N	2.63	0.56
1:A:322:VAL:C	1:A:323:LEU:HD12	2.31	0.56
1:A:337:ILE:CG2	1:A:346:LEU:HD11	2.35	0.56
1:A:430:HIS:ND1	1:A:479:LEU:HD22	2.22	0.55
1:A:405:VAL:HG22	1:A:471:TYR:CZ	2.41	0.55
1:A:149:PHE:HA	3:A:978:HOH:O	2.06	0.55
1:A:226:ARG:HG2	1:A:229:LYS:HZ2	1.70	0.55
1:A:410:THR:O	1:A:412:LYS:HD3	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:348:LEU:CD1	1:A:382:PHE:HB3	2.37	0.55
1:A:187:ASN:HB2	1:A:288:TYR:CD2	2.41	0.55
1:A:316:HIS:CG	1:A:316:HIS:O	2.60	0.54
1:A:415:VAL:HG22	1:A:416:VAL:N	2.21	0.54
1:A:377:LEU:O	1:A:381:GLN:HG3	2.07	0.54
1:A:115:ASN:HB3	1:A:118:PHE:HB3	1.88	0.54
1:A:126:ASP:OD1	1:A:130:ARG:HD3	2.07	0.54
1:A:417:PHE:CD1	1:A:418:LEU:N	2.75	0.54
1:A:10:GLN:HG2	1:A:122:LEU:HD23	1.89	0.54
1:A:324:ILE:CD1	1:A:338:VAL:HG11	2.38	0.54
1:A:187:ASN:HB2	1:A:288:TYR:CE2	2.43	0.54
1:A:304:LYS:O	1:A:304:LYS:HD3	2.08	0.53
1:A:159:HIS:HD2	1:A:161:GLY:N	2.06	0.53
1:A:251:TYR:HD1	1:A:251:TYR:O	1.90	0.53
1:A:415:VAL:HG22	1:A:416:VAL:O	2.08	0.53
1:A:253:LYS:HA	1:A:256:GLU:OE2	2.08	0.53
1:A:173:ALA:HB3	1:A:185:ARG:NH1	2.23	0.53
1:A:191:ASP:HA	1:A:196:PHE:CZ	2.44	0.53
1:A:258:GLY:O	1:A:260:GLU:HG3	2.08	0.53
1:A:58:LEU:HD23	1:A:71:ILE:HG13	1.91	0.53
1:A:410:THR:HG21	3:A:938:HOH:O	2.07	0.52
1:A:206:TYR:CD2	1:A:226:ARG:HD2	2.45	0.52
1:A:41:GLN:O	1:A:45:LYS:HG3	2.09	0.52
1:A:356:MET:HE3	1:A:391:PHE:HZ	1.74	0.52
1:A:497:ARG:HG3	1:A:497:ARG:NH1	2.24	0.52
1:A:502:ASN:C	1:A:502:ASN:HD22	2.17	0.52
1:A:124:ILE:HB	1:A:125:PRO:HD3	1.92	0.52
1:A:251:TYR:HE1	1:A:262:ALA:HA	1.74	0.52
1:A:284:LEU:HD21	1:A:423:GLU:OE2	2.09	0.52
1:A:149:PHE:HE2	1:A:286:ILE:HD13	1.75	0.52
1:A:304:LYS:O	1:A:308:LEU:HG	2.09	0.51
1:A:58:LEU:HD23	1:A:71:ILE:CG1	2.40	0.51
1:A:218:HIS:HE1	1:A:421:ILE:HD11	1.75	0.51
1:A:342:ASP:OD1	1:A:344:THR:HG22	2.11	0.51
1:A:318:ASP:OD1	1:A:319:LYS:HG3	2.11	0.51
1:A:163:LEU:CD2	1:A:408:MET:HE1	2.40	0.51
1:A:367:MET:HE2	1:A:397:LEU:CD2	2.40	0.51
1:A:367:MET:HE3	1:A:369:TYR:CE1	2.45	0.51
1:A:443:ILE:HD13	1:A:443:ILE:N	2.26	0.51
1:A:412:LYS:HE2	3:A:1120:HOH:O	2.09	0.51
1:A:476:GLU:HG2	1:A:477:ARG:H	1.74	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:413:GLY:O	1:A:414:THR:CG2	2.59	0.51
1:A:252:PHE:O	1:A:254:ARG:N	2.44	0.50
1:A:416:VAL:HB	1:A:422:LEU:HD21	1.94	0.50
1:A:32:VAL:HG12	1:A:36:ARG:NH2	2.26	0.50
1:A:89:GLN:O	1:A:92:GLU:HB3	2.11	0.50
1:A:55:PHE:HB3	1:A:56:PRO:CD	2.42	0.50
1:A:163:LEU:HD22	1:A:408:MET:HE1	1.93	0.49
1:A:258:GLY:O	1:A:259:ASP:C	2.54	0.49
1:A:55:PHE:HB3	1:A:56:PRO:HD3	1.94	0.49
1:A:422:LEU:O	1:A:425:THR:HG22	2.11	0.49
1:A:541:ALA:O	1:A:545:HIS:N	2.43	0.49
1:A:196:PHE:HB3	1:A:254:ARG:HH22	1.77	0.49
1:A:294:GLU:HB3	1:A:350:ARG:HD2	1.94	0.49
1:A:315:THR:CG2	1:A:322:VAL:HG13	2.40	0.49
1:A:296:GLN:HA	1:A:296:GLN:NE2	2.27	0.49
1:A:410:THR:O	1:A:411:ARG:C	2.55	0.49
1:A:297:VAL:CG1	1:A:302:MET:HE2	2.41	0.49
1:A:534:TYR:HB3	1:A:535:PRO:HD3	1.95	0.49
1:A:441:ALA:HB1	1:A:443:ILE:HD12	1.95	0.49
1:A:70:LEU:C	1:A:70:LEU:HD12	2.38	0.48
1:A:131:LYS:HE2	1:A:508:GLN:NE2	2.27	0.48
1:A:140:VAL:CG1	1:A:143:LYS:HB2	2.43	0.48
1:A:260:GLU:O	1:A:261:GLU:HB2	2.13	0.48
1:A:47:SER:HB3	1:A:90:TRP:CZ2	2.48	0.48
1:A:145:VAL:HA	1:A:366:LYS:O	2.14	0.48
1:A:356:MET:HE3	1:A:391:PHE:CZ	2.48	0.48
1:A:97:GLY:O	1:A:98:ASP:HB2	2.13	0.48
1:A:444:GLU:C	1:A:446:PRO:HD3	2.39	0.48
1:A:496:LEU:HD13	1:A:589:ARG:CA	2.42	0.48
1:A:297:VAL:HG11	1:A:302:MET:CE	2.40	0.48
1:A:159:HIS:HD2	1:A:161:GLY:H	1.62	0.47
1:A:173:ALA:CB	1:A:185:ARG:NH1	2.77	0.47
1:A:348:LEU:HA	1:A:378:HIS:HE1	1.79	0.47
1:A:417:PHE:HD1	1:A:418:LEU:N	2.02	0.47
1:A:341:SER:O	1:A:343:GLY:N	2.48	0.47
1:A:476:GLU:H	1:A:476:GLU:CD	2.22	0.47
1:A:159:HIS:CD2	1:A:161:GLY:H	2.33	0.47
1:A:82:ASN:HD22	1:A:82:ASN:C	2.21	0.47
1:A:557:LEU:O	1:A:561:VAL:HG23	2.15	0.47
1:A:502:ASN:C	1:A:502:ASN:ND2	2.73	0.46
1:A:265:ILE:HG23	1:A:266:TRP:N	2.29	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:315:THR:CG2	1:A:316:HIS:N	2.78	0.46
1:A:148:GLU:HA	1:A:186:MET:O	2.14	0.46
1:A:179:LEU:HD12	1:A:542:ILE:HD12	1.98	0.46
1:A:437:GLU:HB3	3:A:1042:HOH:O	2.15	0.46
1:A:426:LYS:HG2	1:A:458:VAL:HG21	1.97	0.46
1:A:151:SER:HA	1:A:187:ASN:OD1	2.16	0.46
1:A:72:PRO:HB2	1:A:75:ARG:HG2	1.98	0.46
1:A:425:THR:HG23	1:A:426:LYS:HD2	1.97	0.46
1:A:348:LEU:HA	1:A:378:HIS:CE1	2.50	0.46
1:A:340:LYS:HG3	1:A:344:THR:HG22	1.98	0.46
1:A:164:ARG:HD2	1:A:405:VAL:HG23	1.97	0.46
1:A:200:ALA:O	1:A:204:GLU:HG2	2.16	0.46
1:A:314:LEU:HB3	1:A:324:ILE:HG23	1.99	0.45
1:A:531:LEU:HD21	1:A:588:ALA:HA	1.98	0.45
1:A:238:ILE:O	1:A:238:ILE:HG23	2.15	0.45
1:A:587:ALA:O	1:A:591:VAL:HG23	2.16	0.45
1:A:250:GLU:OE2	1:A:253:LYS:HD3	2.16	0.45
1:A:257:ASP:HB2	1:A:260:GLU:OE2	2.16	0.45
1:A:401:ASN:O	1:A:467:ARG:NH1	2.50	0.45
1:A:413:GLY:C	1:A:414:THR:HG23	2.41	0.45
1:A:10:GLN:HG2	1:A:122:LEU:CD2	2.47	0.45
1:A:114:PHE:O	1:A:116:PRO:HD3	2.17	0.45
1:A:443:ILE:H	1:A:443:ILE:CD1	2.30	0.45
1:A:251:TYR:OH	1:A:265:ILE:HG21	2.17	0.44
1:A:427:GLU:OE1	1:A:451:ASP:HB2	2.18	0.44
1:A:348:LEU:HD11	1:A:382:PHE:HB3	1.98	0.44
1:A:208:ASN:HD22	1:A:211:ALA:HB2	1.83	0.44
1:A:423:GLU:HA	1:A:423:GLU:OE1	2.16	0.44
1:A:341:SER:C	1:A:343:GLY:N	2.74	0.44
1:A:63:THR:HB	3:A:1086:HOH:O	2.17	0.44
1:A:476:GLU:HG2	1:A:477:ARG:N	2.33	0.43
1:A:195:GLN:HG3	1:A:196:PHE:CD1	2.53	0.43
1:A:337:ILE:HG22	1:A:346:LEU:CD1	2.45	0.43
1:A:506:ILE:O	1:A:509:GLU:HB3	2.18	0.43
1:A:44:SER:O	1:A:47:SER:O	2.36	0.43
1:A:576:GLU:CD	1:A:576:GLU:N	2.77	0.43
1:A:149:PHE:N	1:A:149:PHE:CD1	2.86	0.43
1:A:527:LEU:HD23	1:A:584:LEU:HG	2.00	0.43
1:A:238:ILE:O	1:A:239:PRO:C	2.61	0.42
1:A:296:GLN:HA	1:A:296:GLN:HE21	1.83	0.42
1:A:348:LEU:HD12	1:A:382:PHE:HB3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:322:VAL:HB	1:A:339:GLN:HB3	2.01	0.42
1:A:177:GLU:CD	1:A:185:ARG:HH21	2.27	0.42
1:A:218:HIS:CE1	1:A:418:LEU:HD13	2.53	0.42
1:A:260:GLU:O	1:A:262:ALA:N	2.49	0.42
1:A:138:LYS:C	1:A:140:VAL:H	2.28	0.42
1:A:175:LEU:HA	1:A:598:LEU:HD11	2.02	0.42
1:A:274:ILE:O	1:A:278:ILE:HG13	2.19	0.42
1:A:55:PHE:N	1:A:56:PRO:HD2	2.35	0.42
1:A:68:ASP:O	1:A:69:LEU:HD12	2.20	0.42
1:A:164:ARG:HH11	1:A:164:ARG:CG	2.32	0.42
1:A:256:GLU:H	1:A:256:GLU:CD	2.28	0.42
1:A:359:TYR:O	1:A:363:HIS:N	2.44	0.42
1:A:347:TYR:OH	2:A:900:ARG:HG2	2.20	0.41
1:A:415:VAL:CG2	1:A:416:VAL:N	2.82	0.41
1:A:218:HIS:CD2	1:A:418:LEU:HD13	2.56	0.41
1:A:153:ASN:HB2	1:A:156:LYS:HB2	2.02	0.41
1:A:198:LEU:CD1	1:A:231:ILE:HD11	2.51	0.41
1:A:299:LYS:HD2	1:A:299:LYS:N	2.34	0.41
1:A:390:GLY:O	1:A:391:PHE:C	2.63	0.41
1:A:530:LEU:HD12	1:A:530:LEU:HA	1.90	0.41
1:A:557:LEU:HD23	1:A:557:LEU:C	2.46	0.41
1:A:449:VAL:O	1:A:453:VAL:HG23	2.19	0.41
1:A:96:CYS:O	1:A:97:GLY:C	2.64	0.41
1:A:179:LEU:HD12	1:A:542:ILE:CD1	2.51	0.41
1:A:198:LEU:HD13	1:A:231:ILE:HD11	2.02	0.41
1:A:540:ASN:O	1:A:543:LYS:HB3	2.20	0.41
1:A:259:ASP:C	1:A:261:GLU:N	2.77	0.41
1:A:426:LYS:HG2	1:A:458:VAL:CG2	2.51	0.41
1:A:445:HIS:HB3	1:A:448:GLU:OE1	2.20	0.41
1:A:472:GLU:HG2	3:A:935:HOH:O	2.20	0.41
1:A:474:LYS:NZ	3:A:930:HOH:O	2.52	0.41
1:A:36:ARG:NH2	1:A:536:ASP:OD1	2.47	0.41
1:A:507:THR:C	1:A:509:GLU:N	2.79	0.41
1:A:267:LYS:O	1:A:271:GLU:HG2	2.21	0.40
1:A:172:LEU:HA	1:A:172:LEU:HD23	1.80	0.40
1:A:226:ARG:CG	1:A:229:LYS:HZ1	2.33	0.40
1:A:43:LEU:HD11	1:A:90:TRP:CE3	2.55	0.40
1:A:417:PHE:CD1	1:A:417:PHE:N	2.79	0.40
1:A:443:ILE:HD13	1:A:443:ILE:H	1.86	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	601/607 (99%)	545 (91%)	45 (8%)	11 (2%)	6	13

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	259	ASP
1	A	409	SER
1	A	97	GLY
1	A	236	ASP
1	A	240	LEU
1	A	342	ASP
1	A	253	LYS
1	A	502	ASN
1	A	239	PRO
1	A	414	THR
1	A	483	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	523/526 (99%)	505 (97%)	18 (3%)	32	57

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	36	ARG
1	A	53	LEU
1	A	69	LEU
1	A	98	ASP
1	A	140	VAL
1	A	214	LYS
1	A	229	LYS
1	A	299	LYS
1	A	374	GLN
1	A	388	GLN
1	A	417	PHE
1	A	418	LEU
1	A	431	GLU
1	A	433	MET
1	A	443	ILE
1	A	468	ILE
1	A	529	ARG
1	A	530	LEU

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	26	HIS
1	A	62	ASN
1	A	82	ASN
1	A	111	GLN
1	A	142	ASN
1	A	159	HIS
1	A	208	ASN
1	A	242	GLN
1	A	245	ASN
1	A	285	ASN
1	A	330	ASN
1	A	381	GLN
1	A	502	ASN
1	A	508	GLN

5.3.3 RNA ⓘ

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](#)

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	ARG	A	900	-	10,11,11	0.67	0	9,13,13	0.22	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	ARG	A	900	-	-	0/11/11/11	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	900	ARG	1	0

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, 95th 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	603/607 (99%)	-0.18	24 (3%) 42 40	26, 48, 99, 131	0

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	410	THR	4.9
1	A	411	ARG	3.9
1	A	414	THR	3.9
1	A	261	GLU	3.8
1	A	5	ALA	3.7
1	A	409	SER	3.6
1	A	417	PHE	3.5
1	A	503	ALA	3.2
1	A	426	LYS	2.8
1	A	235	GLY	2.8
1	A	433	MET	2.5
1	A	257	ASP	2.5
1	A	432	VAL	2.5
1	A	97	GLY	2.4
1	A	306	ILE	2.4
1	A	260	GLU	2.3
1	A	249	ARG	2.3
1	A	240	LEU	2.3
1	A	345	THR	2.3
1	A	241	GLU	2.3
1	A	482	GLU	2.2
1	A	258	GLY	2.2
1	A	607	MET	2.2
1	A	237	SER	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	ARG	A	900	12/12	0.97	0.05	31,42,48,51	0

6.5 Other polymers [i](#)

There are no such residues in this entry.