



Full wwPDB X-ray Structure Validation Report ⓘ

May 13, 2020 – 01:32 am BST

PDB ID : 2DU4
Title : Crystal structure of Archaeoglobus fulgidus O-phosphoseryl-tRNA synthetase complexed with tRNACys
Authors : Fukunaga, R.
Deposited on : 2006-07-20
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 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 : 2.11
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) : 2.11

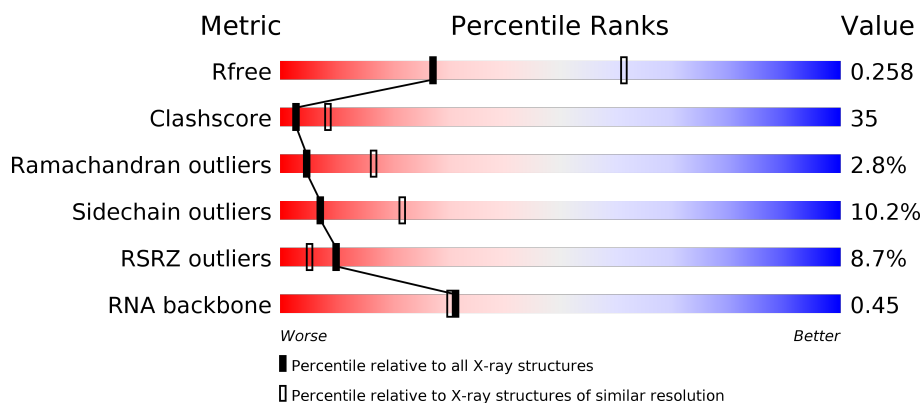
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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)
RNA backbone	3102	1227 (3.10-2.50)

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 on 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	C	71	<div> <div>38%</div> <div>28% 34% 38%</div> </div>
2	A	534	<div> <div>4%</div> <div>42% 40% 5% 13%</div> </div>
2	B	534	<div> <div>7%</div> <div>40% 40% 6% 13%</div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 9117 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 RNA chain called tRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	C	71	Total	C	N	O	P	0	0	0
			1520	675	272	502	71			

- Molecule 2 is a protein called O-phosphoseryl-tRNA synthetase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	466	Total	C	N	O	S	0	0	0
			3777	2440	631	693	13			
2	B	465	Total	C	N	O	S	0	0	0
			3763	2429	630	691	13			

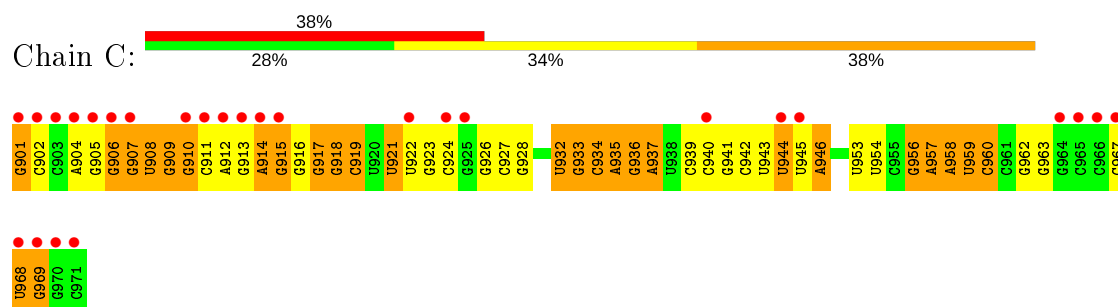
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	26	Total	O	0	0
			26	26		
3	B	31	Total	O	0	0
			31	31		

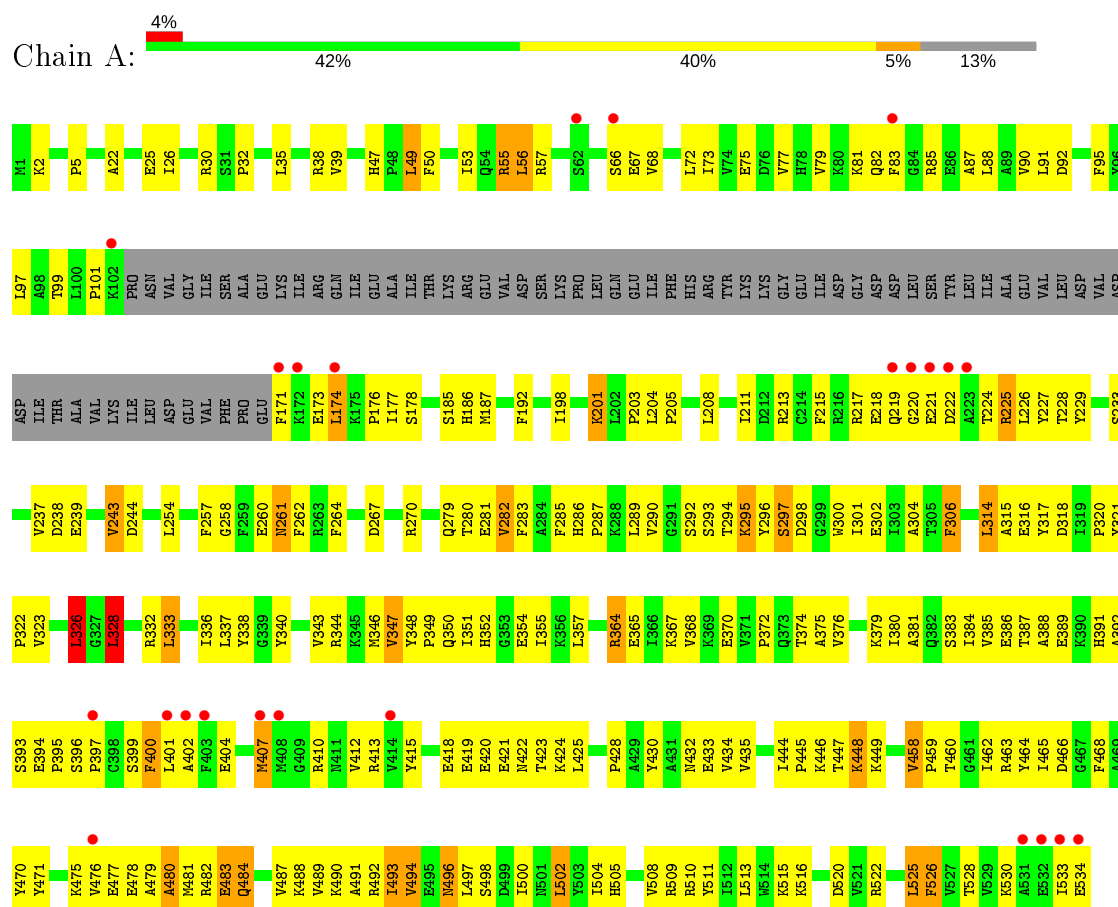
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

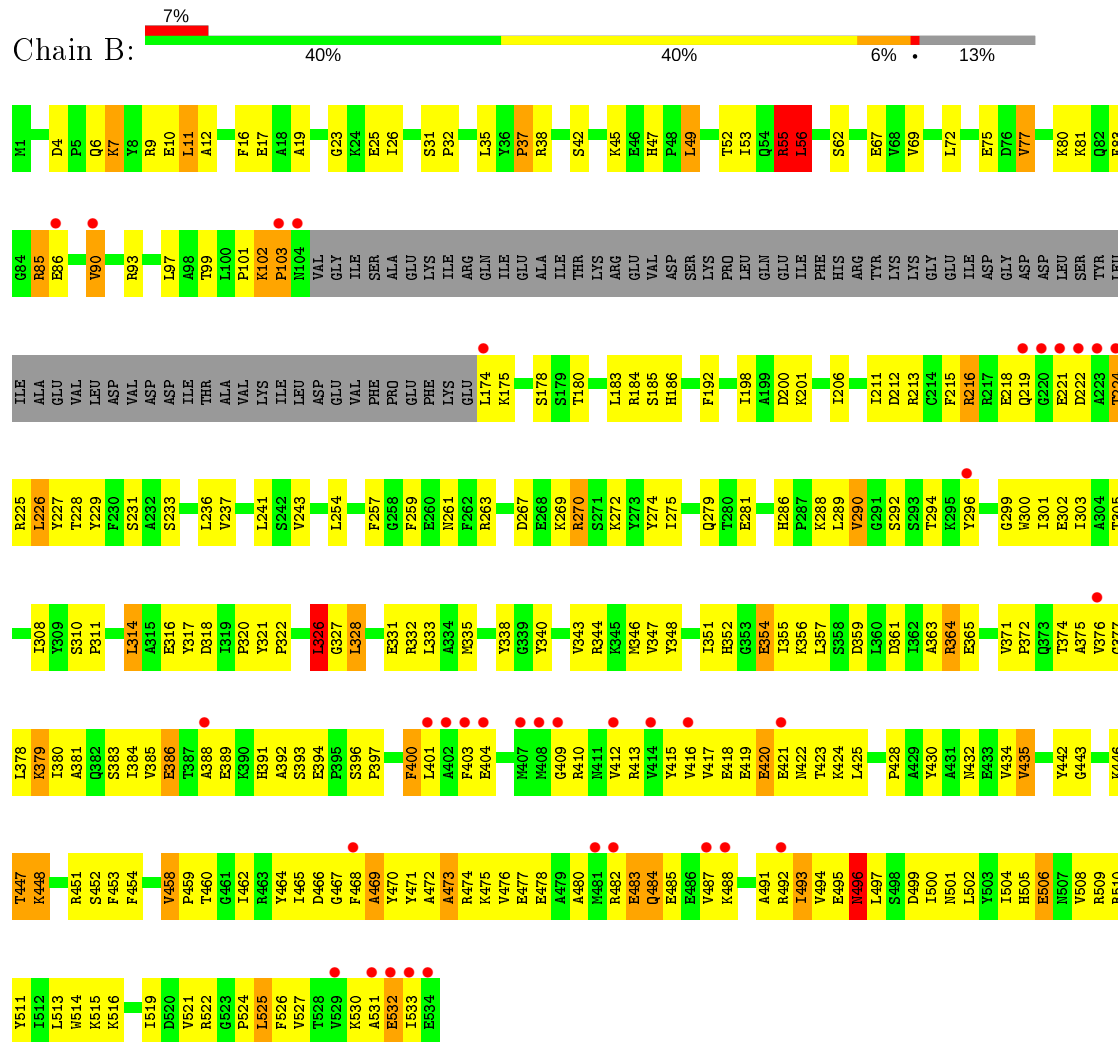
• Molecule 1: tRNA



• Molecule 2: O-phosphoseryl-tRNA synthetase



• Molecule 2: O-phosphoseryl-tRNA synthetase



4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	148.43Å 148.43Å 151.53Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	49.01 – 2.80 49.01 – 2.80	Depositor EDS
% Data completeness (in resolution range)	98.4 (49.01-2.80) 98.6 (49.01-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.39 (at 2.81Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.207 , 0.269 0.205 , 0.258	Depositor DCC
R_{free} test set	2362 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	81.2	Xtriage
Anisotropy	0.149	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 72.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.020 for -h,-k,l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	9117	wwPDB-VP
Average B, all atoms (Å ²)	98.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.52% 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

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	C	0.59	1/1697 (0.1%)	0.81	0/2644
2	A	0.63	0/3865	0.83	2/5218 (0.0%)
2	B	0.64	0/3851	0.85	5/5202 (0.1%)
All	All	0.63	1/9413 (0.0%)	0.84	7/13064 (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	C	0	1
2	A	0	1
2	B	0	2
All	All	0	4

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	901	G	OP3-P	-6.95	1.52	1.61

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	326	LEU	CA-CB-CG	6.70	130.71	115.30
2	B	56	LEU	CA-CB-CG	6.18	129.51	115.30
2	A	326	LEU	CA-CB-CG	5.69	128.38	115.30
2	A	328	LEU	CA-CB-CG	5.65	128.31	115.30
2	B	443	GLY	N-CA-C	-5.48	99.39	113.10
2	B	212	ASP	CB-CG-OD1	5.12	122.91	118.30
2	B	55	ARG	NE-CZ-NH1	-5.07	117.77	120.30

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	A	338	TYR	Sidechain
2	B	274	TYR	Sidechain
2	B	338	TYR	Sidechain
1	C	956	G	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	C	1520	0	769	65	0
2	A	3777	0	3789	278	0
2	B	3763	0	3774	295	0
3	A	26	0	0	4	0
3	B	31	0	0	1	0
All	All	9117	0	8332	613	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 35.

All (613) 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)
2:A:55:ARG:HG2	2:A:55:ARG:HH21	1.10	1.07
2:B:55:ARG:HH21	2:B:55:ARG:HG2	1.18	1.01
2:B:47:HIS:HD2	2:B:49:LEU:H	1.12	0.97
2:B:85:ARG:H	2:B:85:ARG:HD2	1.33	0.94
1:C:942:C:H2'	1:C:943:U:H5'	1.48	0.93
2:B:292:SER:OG	2:B:294:THR:HG22	1.70	0.91
2:A:224:THR:O	2:A:225:ARG:HG3	1.71	0.91
2:B:488:LYS:HG2	2:B:530:LYS:HG2	1.53	0.90
2:A:397:PRO:HD3	2:A:421:GLU:HG2	1.54	0.89
2:A:55:ARG:HG2	2:A:55:ARG:NH2	1.86	0.89
1:C:967:C:H2'	1:C:968:U:O4'	1.73	0.88
2:A:494:VAL:HG21	2:A:500:ILE:HD13	1.55	0.87
2:A:101:PRO:HB3	2:A:177:ILE:HD11	1.58	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:393:SER:O	2:B:424:LYS:HD3	1.75	0.85
2:B:47:HIS:CD2	2:B:49:LEU:H	1.93	0.85
2:A:22:ALA:O	2:A:25:GLU:HG2	1.77	0.85
2:B:391:HIS:O	2:B:425:LEU:HD23	1.77	0.84
2:A:488:LYS:HD3	2:A:530:LYS:HE2	1.59	0.84
2:A:85:ARG:HG3	2:A:85:ARG:HH21	1.43	0.83
2:B:85:ARG:N	2:B:85:ARG:HD2	1.93	0.83
2:B:267:ASP:HB3	2:B:279:GLN:HG2	1.60	0.83
2:B:448:LYS:HD3	2:B:448:LYS:H	1.42	0.82
2:B:55:ARG:NH2	2:B:55:ARG:HG2	1.88	0.81
2:B:286:HIS:HD2	2:B:288:LYS:H	1.26	0.81
2:B:175:LYS:N	2:B:175:LYS:HD2	1.95	0.81
2:A:490:LYS:HB3	2:A:528:THR:HG23	1.61	0.81
2:A:448:LYS:H	2:A:448:LYS:HD3	1.45	0.80
2:B:289:LEU:O	2:B:292:SER:HB2	1.81	0.79
2:A:267:ASP:HB3	2:A:279:GLN:HG2	1.63	0.79
2:B:294:THR:HG23	2:B:296:TYR:H	1.47	0.79
2:A:374:THR:HG22	2:A:376:VAL:H	1.46	0.79
2:B:488:LYS:HE3	2:B:530:LYS:HE3	1.66	0.78
2:A:287:PRO:O	2:A:290:VAL:HG22	1.83	0.78
2:A:504:ILE:HB	2:A:508:VAL:HG21	1.65	0.78
2:A:47:HIS:CD2	2:A:49:LEU:H	2.01	0.78
2:B:394:GLU:HG3	2:B:400:PHE:HZ	1.49	0.78
2:A:430:TYR:HA	2:A:525:LEU:CD2	2.14	0.77
2:B:412:VAL:HG21	2:B:533:ILE:HG22	1.64	0.77
2:A:301:ILE:HD11	2:A:332:ARG:HD3	1.66	0.77
2:A:430:TYR:HA	2:A:525:LEU:HD23	1.67	0.77
2:B:401:LEU:HD21	2:B:404:GLU:OE2	1.85	0.77
1:C:909:G:H5'	1:C:910:G:OP2	1.85	0.77
2:A:434:VAL:O	2:A:460:THR:HG22	1.85	0.77
2:B:460:THR:HG23	2:B:462:ILE:H	1.49	0.76
2:B:448:LYS:CD	2:B:448:LYS:H	1.97	0.75
2:B:385:VAL:HG23	2:B:469:ALA:HB2	1.67	0.75
2:B:504:ILE:HB	2:B:508:VAL:HG21	1.68	0.75
2:B:7:LYS:HE2	2:B:7:LYS:N	2.01	0.75
1:C:907:G:H5'	1:C:908:U:OP2	1.86	0.75
2:B:7:LYS:O	2:B:11:LEU:HB2	1.87	0.74
2:A:430:TYR:HD2	2:A:465:ILE:HG21	1.52	0.74
2:A:391:HIS:HB3	2:A:394:GLU:HG3	1.68	0.74
2:B:464:TYR:HA	2:B:500:ILE:HD11	1.70	0.73
2:B:32:PRO:HA	2:B:35:LEU:HD12	1.69	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:417:VAL:HG21	2:B:530:LYS:NZ	2.03	0.73
2:A:434:VAL:HB	2:A:460:THR:HG21	1.70	0.73
2:A:99:THR:O	2:A:176:PRO:HA	1.89	0.73
2:A:479:ALA:HB2	2:A:487:VAL:HG11	1.70	0.73
2:B:401:LEU:HD13	2:B:415:TYR:CE1	2.24	0.72
2:A:75:GLU:HB3	2:A:77:VAL:HG12	1.71	0.72
2:A:85:ARG:NH2	2:A:85:ARG:HG3	2.03	0.72
2:B:385:VAL:HG23	2:B:469:ALA:CB	2.20	0.72
2:A:56:LEU:HD13	2:A:257:PHE:CZ	2.24	0.72
2:B:504:ILE:HD12	2:B:508:VAL:HG23	1.70	0.72
2:B:101:PRO:O	2:B:103:PRO:HD3	1.89	0.71
1:C:959:U:H5'	1:C:960:C:OP2	1.90	0.71
1:C:927:C:H2'	1:C:928:G:H8	1.55	0.71
2:B:464:TYR:CA	2:B:500:ILE:HD11	2.21	0.71
2:A:478:GLU:HB3	2:A:482:ARG:HH12	1.56	0.71
2:B:496:ASN:HD22	2:B:496:ASN:C	1.94	0.71
2:B:83:PHE:CD2	2:B:90:VAL:HG21	2.25	0.70
2:A:448:LYS:N	2:A:448:LYS:HD3	2.06	0.70
2:A:326:LEU:HD12	2:A:326:LEU:C	2.12	0.70
2:B:448:LYS:N	2:B:448:LYS:HD3	2.07	0.69
2:B:55:ARG:HH21	2:B:55:ARG:CG	2.03	0.69
2:B:374:THR:HG22	2:B:376:VAL:H	1.55	0.69
2:A:412:VAL:HG13	2:A:533:ILE:HG22	1.72	0.69
2:A:430:TYR:O	2:A:465:ILE:HG12	1.92	0.69
2:B:93:ARG:HD2	2:B:216:ARG:HD2	1.75	0.69
1:C:917:G:H2'	1:C:956:G:N2	2.07	0.69
2:B:23:GLY:O	2:B:26:ILE:HG12	1.93	0.69
2:A:401:LEU:HD13	2:A:415:TYR:CE1	2.28	0.69
2:A:219:GLN:HB2	2:A:221:GLU:OE2	1.92	0.69
1:C:933:G:H22	2:A:492:ARG:HD3	1.58	0.69
2:B:326:LEU:HD13	2:B:327:GLY:N	2.09	0.68
2:B:380:ILE:HG22	2:B:381:ALA:N	2.09	0.68
2:A:301:ILE:HD13	2:A:336:ILE:HD11	1.76	0.68
2:A:505:HIS:O	2:A:508:VAL:HG22	1.93	0.68
2:B:451:ARG:HH21	2:B:451:ARG:HG3	1.58	0.68
2:A:47:HIS:HD2	2:A:49:LEU:H	1.40	0.68
2:B:394:GLU:HG3	2:B:400:PHE:CZ	2.28	0.67
2:B:412:VAL:HG13	2:B:532:GLU:O	1.93	0.67
2:A:101:PRO:HD3	2:A:177:ILE:HG13	1.77	0.67
2:B:75:GLU:OE2	2:B:180:THR:HG23	1.94	0.67
2:B:4:ASP:HB3	2:B:7:LYS:HD2	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:467:GLY:O	2:B:501:ASN:HB3	1.95	0.67
1:C:941:G:H2'	1:C:942:C:H5'	1.76	0.67
2:A:101:PRO:HB3	2:A:177:ILE:CD1	2.24	0.67
2:A:88:LEU:H	2:A:88:LEU:HD12	1.58	0.66
2:B:506:GLU:HB2	2:B:510:ARG:HH12	1.61	0.66
1:C:957:A:H4'	1:C:958:A:OP1	1.96	0.66
2:B:417:VAL:HG21	2:B:530:LYS:HZ2	1.60	0.66
2:B:420:GLU:HG3	2:B:421:GLU:H	1.61	0.66
2:A:101:PRO:CB	2:A:177:ILE:HD11	2.24	0.66
1:C:935:A:OP2	2:A:428:PRO:HG3	1.95	0.66
2:A:385:VAL:HG13	2:A:465:ILE:HD12	1.78	0.65
2:B:241:LEU:HD12	2:B:322:PRO:HB2	1.77	0.65
1:C:942:C:C2'	1:C:943:U:H5'	2.23	0.65
2:B:47:HIS:HD2	2:B:49:LEU:N	1.91	0.65
2:B:488:LYS:HE3	2:B:530:LYS:CE	2.27	0.65
2:B:290:VAL:HG12	2:B:299:GLY:HA3	1.78	0.65
2:A:368:VAL:HA	2:A:502:LEU:HD12	1.79	0.65
2:B:412:VAL:HG12	2:B:413:ARG:N	2.12	0.65
2:B:372:PRO:HB2	2:B:378:LEU:HD23	1.77	0.65
2:A:376:VAL:HG11	2:A:407:MET:HB3	1.78	0.65
2:A:447:THR:HG22	2:A:449:LYS:H	1.60	0.65
1:C:936:G:N2	2:A:522:ARG:H	1.95	0.64
2:A:368:VAL:HG22	2:A:502:LEU:HD11	1.78	0.64
2:A:475:LYS:HE2	2:A:475:LYS:HA	1.78	0.64
2:B:86:GLU:OE2	2:B:272:LYS:HG2	1.98	0.64
2:A:391:HIS:O	2:A:425:LEU:HD23	1.98	0.64
2:B:286:HIS:CD2	2:B:288:LYS:H	2.12	0.64
2:B:286:HIS:NE2	2:B:288:LYS:HG3	2.13	0.64
1:C:936:G:HO2'	1:C:937:A:P	2.21	0.64
2:B:381:ALA:HB2	2:B:473:ALA:CB	2.28	0.64
2:A:47:HIS:CD2	2:A:49:LEU:HB2	2.33	0.63
1:C:943:U:H2'	1:C:943:U:O2	1.96	0.63
1:C:936:G:H21	2:A:522:ARG:H	1.47	0.63
2:B:412:VAL:HG13	2:B:533:ILE:HA	1.81	0.63
2:A:88:LEU:N	2:A:88:LEU:HD12	2.13	0.63
2:B:224:THR:O	2:B:225:ARG:HG3	1.99	0.63
2:A:101:PRO:O	2:A:174:LEU:HD22	1.99	0.62
2:A:500:ILE:CG2	2:A:502:LEU:HD22	2.29	0.62
2:B:12:ALA:HB2	2:B:19:ALA:CB	2.28	0.62
2:A:447:THR:C	2:A:449:LYS:H	2.03	0.62
2:A:494:VAL:O	2:A:522:ARG:HA	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:902:C:O2	1:C:902:C:H2'	1.99	0.62
2:A:460:THR:HG23	2:A:462:ILE:H	1.64	0.62
2:A:500:ILE:HG22	2:A:502:LEU:HB2	1.80	0.62
2:B:412:VAL:HG12	2:B:413:ARG:H	1.65	0.62
2:B:90:VAL:O	2:B:93:ARG:HG2	1.99	0.62
2:A:413:ARG:HD2	2:A:415:TYR:OH	1.99	0.61
2:A:491:ALA:O	2:A:526:PHE:HA	2.00	0.61
2:B:351:ILE:HG22	2:B:351:ILE:O	1.99	0.61
2:A:500:ILE:HG23	2:A:502:LEU:HD22	1.81	0.61
2:A:295:LYS:C	2:A:297:SER:H	2.04	0.61
2:B:396:SER:HB2	2:B:418:GLU:HG3	1.83	0.61
2:A:320:PRO:HG2	2:A:321:TYR:CD1	2.35	0.61
2:A:32:PRO:O	2:A:38:ARG:NH1	2.34	0.61
2:A:380:ILE:O	2:A:384:ILE:HG13	2.01	0.61
1:C:933:G:H22	2:A:492:ARG:CD	2.14	0.61
1:C:942:C:H2'	1:C:942:C:O2	2.00	0.61
2:A:504:ILE:HB	2:A:508:VAL:CG2	2.30	0.61
2:A:407:MET:O	2:A:407:MET:HG3	2.01	0.60
2:B:185:SER:O	2:B:229:TYR:OH	2.19	0.60
2:B:496:ASN:ND2	2:B:499:ASP:H	1.99	0.60
2:A:220:GLY:HA2	2:A:227:TYR:OH	2.01	0.60
2:A:237:VAL:HG22	2:A:323:VAL:HG22	1.83	0.60
2:A:410:ARG:CD	2:A:533:ILE:HD12	2.30	0.60
1:C:905:G:C2	1:C:906:G:H1'	2.36	0.60
2:A:432:ASN:O	2:A:463:ARG:HA	2.02	0.60
2:B:505:HIS:O	2:B:508:VAL:HG22	2.01	0.60
2:A:47:HIS:HD2	2:A:49:LEU:N	2.00	0.60
2:B:183:LEU:HD13	2:B:215:PHE:CG	2.36	0.60
2:B:504:ILE:HB	2:B:508:VAL:CG2	2.31	0.60
2:B:495:GLU:O	2:B:496:ASN:HB3	2.01	0.60
2:B:77:VAL:O	2:B:81:LYS:HG3	2.02	0.59
2:B:474:ARG:O	2:B:478:GLU:HG3	2.02	0.59
2:B:410:ARG:HH11	2:B:533:ILE:HD12	1.67	0.59
2:A:509:ARG:HD2	3:A:547:HOH:O	2.00	0.59
2:B:292:SER:C	2:B:294:THR:H	2.06	0.59
2:B:7:LYS:HE2	2:B:7:LYS:H	1.67	0.59
2:A:396:SER:HB2	2:A:420:GLU:O	2.03	0.59
2:A:484:GLN:O	2:A:533:ILE:HD11	2.03	0.59
2:B:7:LYS:O	2:B:11:LEU:CB	2.51	0.59
2:B:434:VAL:HB	2:B:460:THR:HG21	1.84	0.59
1:C:934:C:H4'	1:C:935:A:OP2	2.01	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:480:ALA:HA	2:B:533:ILE:HD12	1.85	0.59
2:A:343:VAL:HG13	2:A:344:ARG:N	2.17	0.59
1:C:917:G:H2'	1:C:956:G:H22	1.67	0.59
2:A:326:LEU:C	2:A:326:LEU:CD1	2.70	0.58
1:C:962:G:H2'	1:C:963:G:O4'	2.03	0.58
2:B:263:ARG:HG2	2:B:300:TRP:CZ3	2.39	0.58
2:B:328:LEU:HD12	2:B:328:LEU:C	2.23	0.58
2:A:448:LYS:CD	2:A:448:LYS:H	2.05	0.58
2:A:66:SER:OG	2:B:45:LYS:HE3	2.03	0.58
2:B:510:ARG:NH1	2:B:510:ARG:HB2	2.18	0.58
2:A:185:SER:HA	2:A:215:PHE:O	2.02	0.58
2:A:423:THR:HG23	2:A:424:LYS:N	2.19	0.58
2:B:286:HIS:HD2	2:B:288:LYS:N	1.99	0.58
2:B:465:ILE:HG13	2:B:466:ASP:N	2.19	0.58
2:A:494:VAL:HG12	2:A:522:ARG:HA	1.85	0.57
2:B:340:TYR:CD1	2:B:346:MET:HG3	2.39	0.57
2:A:482:ARG:HB2	2:A:484:GLN:HE21	1.69	0.57
2:B:493:ILE:HD12	2:B:493:ILE:O	2.04	0.57
2:B:85:ARG:CA	2:B:85:ARG:HH21	2.18	0.57
2:A:351:ILE:HG22	2:A:352:HIS:ND1	2.20	0.57
2:A:511:TYR:HB2	2:B:201:LYS:O	2.04	0.57
2:A:222:ASP:O	2:A:344:ARG:HD3	2.04	0.57
2:A:509:ARG:O	2:A:513:LEU:HD13	2.03	0.57
2:B:221:GLU:HB2	2:B:224:THR:HB	1.85	0.57
2:B:335:MET:SD	2:B:343:VAL:HG22	2.44	0.57
1:C:932:U:OP1	1:C:932:U:H6	1.87	0.57
2:B:289:LEU:O	2:B:292:SER:CB	2.51	0.57
2:B:192:PHE:HE2	2:B:314:LEU:HD13	1.70	0.57
2:B:380:ILE:HG12	2:B:403:PHE:CD1	2.39	0.57
2:A:364:ARG:O	2:A:364:ARG:HG3	2.05	0.57
2:A:480:ALA:HA	2:A:533:ILE:HD13	1.87	0.57
2:A:101:PRO:CG	2:A:177:ILE:HD11	2.35	0.57
2:B:303:ILE:O	2:B:303:ILE:HG13	2.05	0.56
2:B:47:HIS:CD2	2:B:49:LEU:HB2	2.41	0.56
2:A:301:ILE:CD1	2:A:332:ARG:HD3	2.35	0.56
2:B:468:PHE:O	2:B:471:TYR:N	2.38	0.56
2:B:506:GLU:O	2:B:510:ARG:NH1	2.39	0.56
2:A:395:PRO:HA	2:A:423:THR:O	2.05	0.56
2:B:468:PHE:CE2	2:B:491:ALA:HB2	2.40	0.56
2:A:218:GLU:HA	2:A:218:GLU:OE2	2.06	0.56
2:B:420:GLU:HG3	2:B:421:GLU:N	2.19	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:482:ARG:C	2:B:484:GLN:H	2.09	0.56
2:B:412:VAL:CG2	2:B:533:ILE:HG22	2.33	0.56
2:B:101:PRO:O	2:B:103:PRO:CD	2.54	0.56
2:B:343:VAL:HG23	3:B:549:HOH:O	2.06	0.56
2:A:261:ASN:HD22	2:A:262:PHE:H	1.55	0.55
2:A:292:SER:OG	2:A:294:THR:HG22	2.06	0.55
2:B:460:THR:CG2	2:B:462:ILE:H	2.16	0.55
1:C:926:G:H2'	1:C:927:C:C6	2.41	0.55
2:A:447:THR:HG22	2:A:449:LYS:N	2.21	0.55
1:C:936:G:O2'	2:A:522:ARG:NH1	2.39	0.55
2:B:404:GLU:HG2	2:B:413:ARG:HG2	1.89	0.55
2:B:381:ALA:HB2	2:B:473:ALA:HB3	1.89	0.55
2:B:397:PRO:HB3	2:B:419:GLU:HA	1.88	0.55
2:A:430:TYR:HD2	2:A:465:ILE:CG2	2.17	0.55
1:C:957:A:O2'	1:C:958:A:O5'	2.24	0.55
2:B:10:GLU:O	2:B:12:ALA:N	2.39	0.55
2:B:75:GLU:HB3	2:B:77:VAL:HG12	1.89	0.55
2:A:407:MET:HE1	2:A:476:VAL:HG23	1.89	0.54
2:B:301:ILE:HD11	2:B:332:ARG:HD3	1.88	0.54
2:A:292:SER:C	2:A:294:THR:H	2.11	0.54
2:A:497:LEU:HB3	2:A:502:LEU:O	2.07	0.54
2:B:484:GLN:O	2:B:533:ILE:HD11	2.07	0.54
2:A:394:GLU:HG3	2:A:400:PHE:CZ	2.43	0.54
2:B:519:ILE:HG22	2:B:521:VAL:HG23	1.89	0.54
2:B:428:PRO:HD2	2:B:524:PRO:HB2	1.90	0.54
2:A:264:PHE:HB3	2:A:280:THR:CG2	2.38	0.54
2:A:376:VAL:HG11	2:A:407:MET:CB	2.37	0.54
2:A:368:VAL:HG22	2:A:502:LEU:CD1	2.38	0.54
2:B:430:TYR:HD2	2:B:465:ILE:HG21	1.73	0.54
2:B:493:ILE:O	2:B:493:ILE:CD1	2.56	0.54
2:A:365:GLU:HG2	3:A:551:HOH:O	2.08	0.54
2:B:81:LYS:HB3	2:B:316:GLU:HG2	1.89	0.54
2:B:32:PRO:O	2:B:38:ARG:NH1	2.41	0.54
2:A:400:PHE:CD2	2:A:400:PHE:N	2.77	0.53
2:B:471:TYR:CZ	2:B:475:LYS:HE3	2.42	0.53
2:B:388:ALA:O	2:B:392:ALA:HB2	2.09	0.53
2:A:496:ASN:ND2	2:A:498:SER:HB3	2.23	0.53
2:B:494:VAL:O	2:B:522:ARG:HA	2.09	0.53
2:B:419:GLU:O	2:B:420:GLU:O	2.25	0.53
2:B:328:LEU:HD12	2:B:328:LEU:O	2.08	0.53
2:B:222:ASP:OD1	2:B:344:ARG:HD2	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:491:ALA:HB3	2:B:527:VAL:O	2.08	0.53
2:A:264:PHE:HB3	2:A:280:THR:HG21	1.91	0.53
2:B:410:ARG:O	2:B:412:VAL:HG23	2.09	0.53
1:C:968:U:H2'	1:C:969:G:C8	2.43	0.53
2:A:213:ARG:HG2	2:A:213:ARG:HH21	1.74	0.53
2:A:478:GLU:HB3	2:A:482:ARG:NH1	2.23	0.53
2:A:50:PHE:CE1	2:B:69:VAL:HG22	2.44	0.53
1:C:941:G:C2'	1:C:942:C:H5'	2.38	0.53
2:A:221:GLU:OE2	2:A:224:THR:HB	2.08	0.52
2:A:475:LYS:CA	2:A:475:LYS:HE2	2.39	0.52
2:B:10:GLU:C	2:B:12:ALA:H	2.11	0.52
1:C:918:G:O2'	1:C:919:C:OP1	2.22	0.52
2:A:347:VAL:CG2	2:A:348:TYR:CD2	2.91	0.52
2:B:37:PRO:O	2:B:364:ARG:HD3	2.09	0.52
2:B:388:ALA:HB2	2:B:416:VAL:HG11	1.90	0.52
2:B:432:ASN:HB2	2:B:464:TYR:CD1	2.44	0.52
2:B:492:ARG:HB3	2:B:526:PHE:CE2	2.45	0.52
2:A:343:VAL:CG1	2:A:344:ARG:N	2.72	0.52
2:A:381:ALA:O	2:A:385:VAL:HG23	2.08	0.52
2:B:218:GLU:HG3	2:B:225:ARG:HD2	1.91	0.52
2:B:428:PRO:HD2	2:B:524:PRO:CG	2.39	0.52
2:B:415:TYR:N	2:B:530:LYS:O	2.32	0.52
2:B:386:GLU:O	2:B:389:GLU:HB2	2.10	0.52
2:A:83:PHE:CE2	2:A:90:VAL:HG21	2.45	0.52
1:C:913:G:H21	1:C:921:U:H5	1.58	0.52
2:A:387:THR:HG21	2:A:402:ALA:HA	1.91	0.52
1:C:959:U:H5"	1:C:960:C:H5	1.75	0.52
2:B:32:PRO:HA	2:B:35:LEU:CD1	2.38	0.52
2:B:85:ARG:HA	2:B:85:ARG:HH21	1.74	0.52
2:A:404:GLU:HA	2:A:412:VAL:O	2.10	0.51
2:B:286:HIS:CD2	2:B:288:LYS:HG3	2.46	0.51
2:B:347:VAL:HG12	2:B:348:TYR:CD2	2.45	0.51
1:C:936:G:HO2'	2:A:522:ARG:NH1	2.08	0.51
2:A:494:VAL:CG2	2:A:500:ILE:HD13	2.35	0.51
2:B:185:SER:HB2	2:B:216:ARG:HD3	1.92	0.51
2:B:506:GLU:CB	2:B:510:ARG:HH12	2.23	0.51
2:B:222:ASP:CG	2:B:344:ARG:HD2	2.31	0.51
2:A:213:ARG:HH21	2:A:228:THR:CG2	2.23	0.51
2:A:282:VAL:HG13	2:A:304:ALA:HB3	1.93	0.51
2:B:359:ASP:HB3	2:B:458:VAL:HG13	1.92	0.51
1:C:909:G:C5'	1:C:910:G:OP2	2.56	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:488:LYS:HD3	2:A:530:LYS:CE	2.37	0.51
2:A:53:ILE:O	2:A:57:ARG:HG3	2.10	0.51
2:B:442:TYR:CE2	2:B:453:PHE:HE2	2.28	0.51
1:C:957:A:O2'	1:C:958:A:H3'	2.10	0.51
2:A:511:TYR:CE1	2:A:515:LYS:HG3	2.46	0.51
2:B:224:THR:HG22	2:B:225:ARG:N	2.25	0.51
2:A:479:ALA:C	2:A:481:MET:H	2.14	0.50
2:B:259:PHE:CE2	2:B:286:HIS:HB2	2.45	0.50
2:A:410:ARG:HD3	2:A:533:ILE:HD12	1.93	0.50
2:B:465:ILE:HG13	2:B:466:ASP:H	1.75	0.50
2:B:491:ALA:O	2:B:526:PHE:HA	2.12	0.50
2:A:187:MET:HG2	2:A:233:SER:HB3	1.93	0.50
2:A:370:GLU:HA	3:A:554:HOH:O	2.11	0.50
2:B:56:LEU:HB3	2:B:211:ILE:CD1	2.41	0.50
2:B:510:ARG:HB2	2:B:510:ARG:HH11	1.75	0.50
2:A:326:LEU:HD12	2:A:326:LEU:O	2.11	0.50
2:A:85:ARG:HH21	2:A:85:ARG:CG	2.19	0.50
2:B:412:VAL:HG13	2:B:532:GLU:C	2.30	0.50
2:B:263:ARG:HG2	2:B:300:TRP:CH2	2.46	0.50
2:A:434:VAL:HB	2:A:460:THR:CG2	2.39	0.50
2:A:494:VAL:HG21	2:A:500:ILE:CD1	2.36	0.50
2:B:447:THR:HG22	2:B:448:LYS:HE2	1.94	0.50
1:C:908:U:H5''	1:C:909:G:OP1	2.12	0.50
2:A:260:GLU:OE2	2:A:287:PRO:HG2	2.12	0.50
2:A:289:LEU:HD22	2:A:296:TYR:HB2	1.94	0.50
2:A:315:ALA:O	2:A:317:TYR:N	2.45	0.50
2:A:418:GLU:HB2	2:A:425:LEU:HA	1.94	0.50
2:B:294:THR:HG23	2:B:296:TYR:N	2.23	0.50
2:B:396:SER:HB3	2:B:418:GLU:HG2	1.92	0.50
2:B:482:ARG:O	2:B:484:GLN:N	2.44	0.50
2:B:496:ASN:ND2	2:B:496:ASN:C	2.64	0.50
2:A:511:TYR:CZ	2:A:515:LYS:HG3	2.46	0.49
2:B:497:LEU:O	2:B:500:ILE:HG22	2.11	0.49
2:A:460:THR:HG23	2:A:462:ILE:N	2.26	0.49
2:A:496:ASN:HD21	2:A:498:SER:HB3	1.77	0.49
2:A:173:GLU:O	2:A:174:LEU:O	2.30	0.49
2:B:497:LEU:HG	2:B:521:VAL:HG21	1.94	0.49
2:A:376:VAL:O	2:A:380:ILE:HG13	2.13	0.49
2:B:464:TYR:O	2:B:500:ILE:HD11	2.13	0.49
1:C:917:G:O2'	1:C:918:G:O5'	2.30	0.49
2:B:381:ALA:HB2	2:B:473:ALA:HB2	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:914:A:H2'	1:C:915:G:O4'	2.12	0.49
2:B:377:GLY:HA3	2:B:477:GLU:OE1	2.12	0.49
2:B:496:ASN:HD21	2:B:499:ASP:H	1.60	0.49
2:A:201:LYS:HD3	2:B:514:TRP:CG	2.48	0.49
2:B:77:VAL:HA	2:B:80:LYS:HD2	1.94	0.49
2:B:378:LEU:O	2:B:380:ILE:N	2.46	0.49
2:A:464:TYR:N	2:A:464:TYR:CD1	2.79	0.48
2:B:504:ILE:HD11	2:B:509:ARG:HB2	1.95	0.48
2:B:383:SER:O	2:B:386:GLU:N	2.46	0.48
2:A:75:GLU:OE2	2:A:75:GLU:HA	2.13	0.48
2:A:203:PRO:CG	2:B:357:LEU:HD11	2.43	0.48
2:A:258:GLY:HA3	2:A:286:HIS:HE1	1.79	0.48
1:C:934:C:H5''	1:C:935:A:O5'	2.14	0.48
2:B:409:GLY:O	2:B:410:ARG:HG2	2.12	0.48
1:C:944:U:O2	1:C:946:A:H5'	2.14	0.48
2:A:394:GLU:HG3	2:A:400:PHE:HZ	1.76	0.48
2:A:477:GLU:O	2:A:481:MET:HE2	2.13	0.48
2:B:464:TYR:HA	2:B:500:ILE:CD1	2.41	0.48
1:C:916:G:H2'	1:C:959:U:O2'	2.14	0.48
2:B:383:SER:O	2:B:384:ILE:C	2.52	0.48
2:B:391:HIS:HB3	2:B:400:PHE:CZ	2.49	0.48
2:B:488:LYS:HG2	2:B:530:LYS:CG	2.34	0.48
2:B:446:LYS:HG3	2:B:454:PHE:CE2	2.49	0.47
2:A:347:VAL:HG22	2:A:348:TYR:CD2	2.49	0.47
2:A:346:MET:CE	2:A:347:VAL:HG12	2.43	0.47
2:A:464:TYR:HB3	2:A:500:ILE:HD11	1.96	0.47
2:B:340:TYR:CG	2:B:346:MET:HG3	2.49	0.47
2:B:31:SER:HB2	2:B:32:PRO:HD2	1.95	0.47
2:B:267:ASP:HB2	2:B:281:GLU:HG3	1.97	0.47
2:A:95:PHE:HD2	2:B:97:LEU:HB3	1.80	0.47
1:C:922:U:H2'	1:C:923:G:C8	2.49	0.47
2:A:30:ARG:HB2	2:A:35:LEU:CD1	2.44	0.47
2:A:447:THR:C	2:A:449:LYS:N	2.67	0.47
2:B:213:ARG:HD3	2:B:228:THR:HG21	1.96	0.47
2:B:448:LYS:HA	2:B:451:ARG:HG2	1.96	0.47
2:A:198:ILE:HG22	2:B:355:ILE:HG21	1.96	0.47
2:B:311:PRO:HA	2:B:314:LEU:HB2	1.96	0.47
2:A:204:LEU:HD23	2:A:239:GLU:HG3	1.97	0.47
2:A:430:TYR:HB2	2:A:465:ILE:HG23	1.96	0.47
2:A:482:ARG:C	2:A:484:GLN:H	2.17	0.47
2:A:483:GLU:O	2:A:484:GLN:O	2.33	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:496:ASN:C	2:A:496:ASN:HD22	2.19	0.47
2:A:192:PHE:HE2	2:A:314:LEU:CD1	2.28	0.47
2:A:72:LEU:HD21	2:A:215:PHE:HE1	1.80	0.47
2:A:494:VAL:O	2:A:494:VAL:HG12	2.14	0.47
2:A:83:PHE:CD2	2:A:90:VAL:HG21	2.50	0.47
1:C:911:C:C4	1:C:912:A:N7	2.83	0.46
2:A:224:THR:O	2:A:225:ARG:CG	2.55	0.46
2:A:388:ALA:O	2:A:392:ALA:HB2	2.15	0.46
2:B:10:GLU:C	2:B:12:ALA:N	2.68	0.46
2:B:397:PRO:HB3	2:B:419:GLU:O	2.15	0.46
2:B:478:GLU:O	2:B:482:ARG:NH2	2.48	0.46
2:B:412:VAL:HG22	2:B:533:ILE:HA	1.97	0.46
2:A:267:ASP:HB2	2:A:281:GLU:HG3	1.97	0.46
2:A:238:ASP:O	2:A:322:PRO:HD2	2.15	0.46
2:A:493:ILE:H	2:A:493:ILE:HD12	1.80	0.46
2:B:451:ARG:HH21	2:B:451:ARG:CG	2.28	0.46
2:B:6:GLN:HG2	2:B:9:ARG:HH11	1.79	0.46
2:B:332:ARG:HB2	2:B:332:ARG:HE	1.43	0.46
2:B:290:VAL:HG12	2:B:299:GLY:CA	2.46	0.46
2:B:363:ALA:HB2	2:B:458:VAL:HG22	1.97	0.46
2:A:458:VAL:HA	2:A:459:PRO:HD3	1.71	0.46
2:B:213:ARG:HH21	2:B:228:THR:CG2	2.29	0.46
2:B:434:VAL:O	2:B:460:THR:HG22	2.15	0.46
2:A:82:GLN:CD	2:A:192:PHE:CD1	2.89	0.46
2:A:221:GLU:OE2	2:A:224:THR:CB	2.63	0.46
2:A:295:LYS:C	2:A:297:SER:N	2.68	0.46
2:A:88:LEU:CD1	2:A:88:LEU:H	2.25	0.46
2:B:183:LEU:HD13	2:B:215:PHE:CD1	2.50	0.46
2:B:378:LEU:C	2:B:380:ILE:N	2.69	0.46
1:C:904:A:H2'	1:C:905:G:C8	2.51	0.46
2:A:39:VAL:O	2:A:364:ARG:NH2	2.49	0.46
2:A:82:GLN:CD	2:A:192:PHE:HD1	2.19	0.46
2:B:351:ILE:O	2:B:351:ILE:CG2	2.62	0.46
1:C:916:G:O5'	1:C:916:G:H8	1.98	0.46
2:B:417:VAL:HG21	2:B:530:LYS:HZ3	1.77	0.45
2:A:349:PRO:HG2	2:A:350:GLN:OE1	2.16	0.45
2:A:407:MET:CE	2:A:476:VAL:HG23	2.46	0.45
2:A:468:PHE:O	2:A:471:TYR:N	2.49	0.45
2:A:47:HIS:H	2:B:67:GLU:HB3	1.82	0.45
2:B:174:LEU:HB3	2:B:175:LYS:H	1.55	0.45
2:B:376:VAL:HA	2:B:379:LYS:HE3	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:468:PHE:O	2:B:470:TYR:N	2.49	0.45
1:C:907:G:C5'	1:C:908:U:OP2	2.59	0.45
2:A:68:VAL:HG21	2:A:208:LEU:HD13	1.98	0.45
2:A:243:VAL:HG22	2:A:306:PHE:HE1	1.81	0.45
2:A:468:PHE:CD2	2:A:491:ALA:HB2	2.52	0.45
2:B:16:PHE:O	2:B:19:ALA:N	2.50	0.45
2:A:47:HIS:CE1	2:A:347:VAL:HA	2.51	0.45
1:C:902:C:O2	1:C:902:C:C2'	2.65	0.45
1:C:922:U:H2'	1:C:923:G:H8	1.80	0.45
2:A:298:ASP:OD2	2:A:298:ASP:N	2.49	0.45
2:A:404:GLU:HG3	2:A:413:ARG:CG	2.46	0.45
2:A:466:ASP:O	2:A:470:TYR:CD2	2.69	0.45
2:B:174:LEU:HD23	2:B:175:LYS:NZ	2.32	0.45
2:B:259:PHE:CD2	2:B:286:HIS:HB2	2.52	0.45
2:B:301:ILE:HG12	2:B:302:GLU:N	2.31	0.45
2:B:460:THR:HG23	2:B:462:ILE:N	2.26	0.45
1:C:904:A:H2'	1:C:905:G:H8	1.81	0.45
2:A:333:LEU:HD22	2:A:337:LEU:HG	1.99	0.45
2:B:483:GLU:O	2:B:484:GLN:O	2.33	0.45
2:B:72:LEU:HA	2:B:184:ARG:HG2	1.98	0.45
2:A:283:PHE:CE1	2:A:302:GLU:HB2	2.52	0.45
2:A:217:ARG:HH22	2:B:102:LYS:HZ2	1.64	0.45
2:B:404:GLU:HA	2:B:412:VAL:O	2.17	0.45
2:B:292:SER:C	2:B:294:THR:N	2.71	0.45
2:B:434:VAL:HB	2:B:460:THR:CG2	2.47	0.45
2:B:85:ARG:CD	2:B:85:ARG:N	2.73	0.45
2:A:448:LYS:CD	2:A:448:LYS:N	2.75	0.44
2:A:500:ILE:HG23	2:A:500:ILE:O	2.16	0.44
2:A:515:LYS:O	2:A:516:LYS:HB2	2.17	0.44
2:A:79:VAL:HG21	2:A:91:LEU:HD21	1.99	0.44
2:B:225:ARG:HH21	2:B:225:ARG:HG3	1.82	0.44
2:B:396:SER:CB	2:B:418:GLU:HG3	2.47	0.44
2:A:328:LEU:HD12	2:A:328:LEU:C	2.37	0.44
2:A:383:SER:O	2:A:387:THR:HG23	2.17	0.44
2:A:488:LYS:HD3	2:A:530:LYS:HG2	1.99	0.44
2:A:286:HIS:HB3	2:A:289:LEU:HD12	1.99	0.44
2:B:218:GLU:OE2	2:B:218:GLU:HA	2.17	0.44
2:A:410:ARG:HB2	2:A:534:GLU:OXT	2.17	0.44
2:B:7:LYS:HE2	2:B:7:LYS:CA	2.47	0.44
1:C:936:G:H21	2:A:522:ARG:N	2.12	0.44
2:A:239:GLU:HG2	2:A:321:TYR:CE2	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:384:ILE:O	2:A:388:ALA:HB2	2.18	0.44
2:A:433:GLU:N	2:A:444:ILE:O	2.44	0.44
2:B:435:VAL:HB	2:B:459:PRO:HA	1.99	0.44
2:B:492:ARG:HB3	2:B:526:PHE:HE2	1.83	0.44
2:B:501:ASN:O	2:B:502:LEU:HD12	2.17	0.44
2:A:282:VAL:HG13	2:A:304:ALA:C	2.38	0.44
2:B:432:ASN:HB3	2:B:464:TYR:CE1	2.52	0.44
2:A:171:PHE:O	2:A:174:LEU:HG	2.18	0.44
2:B:275:ILE:HG13	2:B:310:SER:HA	1.99	0.44
2:B:85:ARG:HH21	2:B:85:ARG:N	2.16	0.44
1:C:908:U:OP2	1:C:908:U:H6	2.01	0.44
1:C:957:A:H1'	1:C:959:U:C5	2.53	0.44
2:A:306:PHE:CD1	2:A:306:PHE:C	2.90	0.44
2:A:55:ARG:NH2	2:A:55:ARG:CG	2.66	0.44
2:B:174:LEU:C	2:B:175:LYS:HD2	2.36	0.44
2:A:101:PRO:HD3	2:A:177:ILE:CG1	2.48	0.43
2:A:315:ALA:C	2:A:317:TYR:H	2.21	0.43
2:A:203:PRO:HG3	2:B:357:LEU:HD11	1.99	0.43
2:A:347:VAL:CG2	2:A:348:TYR:CE2	3.01	0.43
2:B:391:HIS:CG	2:B:400:PHE:CE1	3.06	0.43
1:C:912:A:H1'	1:C:923:G:N2	2.33	0.43
2:A:228:THR:HG22	2:A:229:TYR:N	2.33	0.43
2:A:430:TYR:HA	2:A:525:LEU:HD21	1.95	0.43
2:A:213:ARG:HH21	2:A:228:THR:HG21	1.83	0.43
2:A:410:ARG:NE	2:A:533:ILE:HD12	2.33	0.43
2:A:399:SER:C	2:A:400:PHE:CD2	2.92	0.43
2:B:294:THR:HG21	2:B:296:TYR:CD1	2.54	0.43
2:B:303:ILE:HD12	2:B:332:ARG:HG2	2.00	0.43
2:B:331:GLU:O	2:B:335:MET:HG3	2.18	0.43
2:B:347:VAL:CG1	2:B:348:TYR:CE2	3.02	0.43
2:B:428:PRO:HD2	2:B:524:PRO:CB	2.48	0.43
2:B:487:VAL:O	2:B:488:LYS:HG3	2.19	0.43
2:B:52:THR:O	2:B:53:ILE:C	2.56	0.43
2:B:4:ASP:CB	2:B:7:LYS:HD2	2.45	0.43
2:A:509:ARG:NH1	3:A:535:HOH:O	2.50	0.43
2:B:56:LEU:HD13	2:B:257:PHE:CZ	2.54	0.43
1:C:939:C:H2'	1:C:940:C:C6	2.54	0.43
2:A:285:PHE:HB2	2:A:300:TRP:CZ2	2.53	0.43
2:A:481:MET:C	2:A:483:GLU:H	2.21	0.43
2:B:211:ILE:HA	2:B:231:SER:O	2.19	0.43
2:B:374:THR:HG22	2:B:376:VAL:N	2.29	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:380:ILE:HG22	2:B:473:ALA:HB2	2.01	0.43
1:C:953:U:C4	1:C:954:U:C4	3.07	0.43
2:A:510:ARG:HE	2:B:200:ASP:HB2	1.84	0.43
2:B:413:ARG:O	2:B:531:ALA:HA	2.19	0.43
1:C:906:G:H2'	1:C:906:G:N3	2.34	0.43
2:A:385:VAL:O	2:A:389:GLU:HG3	2.19	0.42
2:A:404:GLU:HG3	2:A:413:ARG:HG3	2.01	0.42
2:A:464:TYR:N	2:A:464:TYR:HD1	2.16	0.42
2:B:383:SER:HA	2:B:386:GLU:HB3	2.01	0.42
2:B:412:VAL:CG1	2:B:413:ARG:N	2.81	0.42
2:B:451:ARG:NH2	2:B:451:ARG:HG3	2.31	0.42
2:B:475:LYS:HA	2:B:475:LYS:HD3	1.89	0.42
2:B:55:ARG:HB3	2:B:257:PHE:HE1	1.83	0.42
2:A:2:LYS:HB2	2:A:2:LYS:HE3	1.70	0.42
2:A:290:VAL:O	2:A:290:VAL:HG23	2.20	0.42
2:A:468:PHE:CE2	2:A:491:ALA:HB2	2.55	0.42
2:A:479:ALA:CB	2:A:487:VAL:HG11	2.45	0.42
2:B:447:THR:CG2	2:B:448:LYS:HE2	2.49	0.42
2:A:383:SER:HA	2:A:386:GLU:HB3	2.01	0.42
2:B:31:SER:CB	2:B:32:PRO:HD2	2.48	0.42
2:B:347:VAL:HG11	2:B:348:TYR:CE2	2.54	0.42
2:A:218:GLU:HG3	2:A:225:ARG:CB	2.50	0.42
2:A:340:TYR:CG	2:A:346:MET:HG3	2.55	0.42
2:A:364:ARG:O	2:A:367:LYS:HE2	2.19	0.42
2:A:397:PRO:HD3	2:A:421:GLU:CG	2.38	0.42
2:B:511:TYR:CZ	2:B:515:LYS:HG3	2.55	0.42
2:B:56:LEU:HD13	2:B:257:PHE:CE2	2.54	0.42
2:A:346:MET:HE1	2:A:347:VAL:HG12	2.00	0.42
2:B:269:LYS:O	2:B:270:ARG:C	2.58	0.42
2:A:315:ALA:C	2:A:317:TYR:N	2.73	0.42
2:A:500:ILE:HA	2:A:500:ILE:HD12	1.85	0.42
2:A:497:LEU:HD22	2:A:502:LEU:HB3	2.02	0.42
2:B:513:LEU:O	2:B:516:LYS:N	2.49	0.42
2:A:445:PRO:O	2:A:447:THR:N	2.53	0.42
2:B:12:ALA:HB2	2:B:19:ALA:HB1	2.01	0.42
2:B:206:ILE:HB	2:B:237:VAL:HB	2.01	0.42
2:B:281:GLU:HA	2:B:305:THR:HG22	2.01	0.42
2:B:361:ASP:O	2:B:365:GLU:HG2	2.19	0.42
2:B:364:ARG:HG3	2:B:364:ARG:O	2.18	0.42
2:B:380:ILE:O	2:B:383:SER:N	2.51	0.42
1:C:923:G:O2'	1:C:924:C:H5'	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:419:GLU:OE2	2:A:530:LYS:NZ	2.53	0.42
2:A:88:LEU:CD1	2:A:88:LEU:N	2.82	0.42
2:A:92:ASP:O	2:A:217:ARG:HD3	2.20	0.42
2:A:292:SER:O	2:A:294:THR:N	2.52	0.42
2:A:494:VAL:HG12	2:A:522:ARG:CA	2.49	0.42
2:B:400:PHE:N	2:B:400:PHE:CD2	2.87	0.42
2:B:458:VAL:HA	2:B:459:PRO:HD3	1.77	0.42
2:A:396:SER:HB3	2:A:418:GLU:HG2	2.02	0.41
2:A:500:ILE:CG2	2:A:502:LEU:HB2	2.48	0.41
2:A:53:ILE:HG23	2:A:211:ILE:HG21	2.02	0.41
2:B:218:GLU:C	2:B:219:GLN:HG2	2.41	0.41
2:B:56:LEU:HB3	2:B:211:ILE:HD11	2.01	0.41
1:C:944:U:H2'	1:C:946:A:OP1	2.20	0.41
2:A:67:GLU:HB3	2:B:47:HIS:HB2	2.01	0.41
2:A:95:PHE:CD2	2:B:97:LEU:HB3	2.55	0.41
2:B:394:GLU:OE2	2:B:394:GLU:HA	2.20	0.41
2:B:403:PHE:CG	2:B:404:GLU:N	2.87	0.41
1:C:909:G:C4'	1:C:910:G:OP2	2.68	0.41
2:A:401:LEU:CD1	2:A:415:TYR:CE1	3.00	0.41
2:A:464:TYR:HA	2:A:500:ILE:HG13	2.02	0.41
2:A:520:ASP:OD1	2:A:522:ARG:NH2	2.52	0.41
2:B:401:LEU:HA	2:B:415:TYR:CD1	2.55	0.41
2:A:201:LYS:O	2:B:511:TYR:HB2	2.20	0.41
2:B:378:LEU:C	2:B:380:ILE:H	2.23	0.41
2:B:525:LEU:HD22	2:B:527:VAL:CG1	2.51	0.41
2:A:292:SER:C	2:A:294:THR:N	2.73	0.41
2:A:375:ALA:O	2:A:379:LYS:HG3	2.20	0.41
2:B:352:HIS:O	2:B:354:GLU:OE1	2.38	0.41
2:B:371:VAL:HA	2:B:372:PRO:HD3	1.89	0.41
1:C:917:G:O2'	1:C:918:G:P	2.79	0.41
2:A:218:GLU:HG3	2:A:225:ARG:HD2	2.01	0.41
2:A:393:SER:HA	2:A:424:LYS:CD	2.50	0.41
2:A:479:ALA:O	2:A:481:MET:N	2.54	0.41
2:A:176:PRO:HB2	2:B:178:SER:CB	2.50	0.41
2:B:317:TYR:O	2:B:318:ASP:HB2	2.20	0.41
2:B:451:ARG:O	2:B:452:SER:C	2.59	0.41
2:B:192:PHE:CE2	2:B:314:LEU:HD13	2.52	0.41
2:B:226:LEU:CD2	2:B:344:ARG:HG2	2.51	0.41
1:C:901:G:N3	1:C:901:G:H2'	2.35	0.41
2:A:85:ARG:C	2:A:87:ALA:N	2.73	0.41
2:B:403:PHE:O	2:B:404:GLU:HG3	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:468:PHE:O	2:B:469:ALA:C	2.59	0.41
2:A:394:GLU:CG	2:A:400:PHE:HZ	2.34	0.41
2:A:432:ASN:O	2:A:463:ARG:CA	2.68	0.41
2:A:77:VAL:O	2:A:81:LYS:HG3	2.20	0.41
2:B:401:LEU:HA	2:B:415:TYR:HD1	1.86	0.41
2:B:432:ASN:O	2:B:464:TYR:HD1	2.04	0.41
1:C:911:C:H2'	1:C:912:A:O4'	2.21	0.41
1:C:933:G:H3'	1:C:933:G:C8	2.55	0.41
2:A:239:GLU:O	2:A:322:PRO:HG3	2.20	0.41
2:B:432:ASN:CB	2:B:464:TYR:CD1	3.04	0.41
1:C:936:G:O2'	1:C:937:A:P	2.75	0.41
2:A:72:LEU:HD21	2:A:215:PHE:CE1	2.56	0.40
2:A:73:ILE:CD1	2:B:227:TYR:HB3	2.51	0.40
2:B:320:PRO:HG2	2:B:321:TYR:CE1	2.56	0.40
2:A:101:PRO:HG3	2:A:177:ILE:HD11	2.02	0.40
2:A:400:PHE:CE2	2:A:425:LEU:HD22	2.56	0.40
2:A:490:LYS:CD	2:A:492:ARG:HH12	2.35	0.40
2:B:396:SER:HA	2:B:397:PRO:HA	1.73	0.40
2:B:472:ALA:O	2:B:475:LYS:N	2.50	0.40
2:A:355:ILE:HG21	2:B:198:ILE:HG22	2.04	0.40
2:A:401:LEU:HA	2:A:415:TYR:CD1	2.56	0.40
2:A:492:ARG:HH11	2:A:492:ARG:CG	2.34	0.40
2:A:55:ARG:HH21	2:A:55:ARG:CG	1.99	0.40
2:B:464:TYR:C	2:B:500:ILE:HD11	2.42	0.40
2:B:374:THR:HG22	2:B:375:ALA:N	2.36	0.40
1:C:957:A:H1'	1:C:959:U:H5	1.87	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	
2	A	462/534 (86%)	403 (87%)	48 (10%)	11 (2%)	6	20
2	B	461/534 (86%)	399 (87%)	47 (10%)	15 (3%)	4	13
All	All	923/1068 (86%)	802 (87%)	95 (10%)	26 (3%)	5	17

All (26) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	174	LEU
2	A	484	GLN
2	B	102	LYS
2	B	420	GLU
2	B	484	GLN
2	A	178	SER
2	A	316	GLU
2	A	480	ALA
2	B	11	LEU
2	B	17	GLU
2	B	270	ARG
2	B	423	THR
2	B	469	ALA
2	A	293	SER
2	A	483	GLU
2	B	379	LYS
2	B	473	ALA
2	B	483	GLU
2	A	225	ARG
2	B	496	ASN
2	A	270	ARG
2	A	446	LYS
2	A	526	PHE
2	B	386	GLU
2	B	90	VAL
2	B	103	PRO

5.3.2 Protein sidechains ⓘ

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	
2	A	403/464 (87%)	363 (90%)	40 (10%)	8	23
2	B	402/464 (87%)	360 (90%)	42 (10%)	7	21
All	All	805/928 (87%)	723 (90%)	82 (10%)	7	22

All (82) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	5	PRO
2	A	26	ILE
2	A	49	LEU
2	A	55	ARG
2	A	56	LEU
2	A	97	LEU
2	A	186	HIS
2	A	201	LYS
2	A	205	PRO
2	A	226	LEU
2	A	243	VAL
2	A	244	ASP
2	A	254	LEU
2	A	261	ASN
2	A	282	VAL
2	A	295	LYS
2	A	297	SER
2	A	306	PHE
2	A	314	LEU
2	A	318	ASP
2	A	326	LEU
2	A	328	LEU
2	A	333	LEU
2	A	347	VAL
2	A	354	GLU
2	A	357	LEU
2	A	364	ARG
2	A	372	PRO
2	A	400	PHE
2	A	407	MET
2	A	422	ASN
2	A	435	VAL
2	A	448	LYS
2	A	458	VAL
2	A	489	VAL

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Mol	Chain	Res	Type
2	A	493	ILE
2	A	494	VAL
2	A	496	ASN
2	A	502	LEU
2	A	525	LEU
2	B	7	LYS
2	B	25	GLU
2	B	37	PRO
2	B	42	SER
2	B	49	LEU
2	B	55	ARG
2	B	56	LEU
2	B	62	SER
2	B	77	VAL
2	B	85	ARG
2	B	99	THR
2	B	186	HIS
2	B	216	ARG
2	B	224	THR
2	B	226	LEU
2	B	233	SER
2	B	236	LEU
2	B	243	VAL
2	B	254	LEU
2	B	261	ASN
2	B	290	VAL
2	B	308	ILE
2	B	314	LEU
2	B	326	LEU
2	B	328	LEU
2	B	333	LEU
2	B	354	GLU
2	B	356	LYS
2	B	364	ARG
2	B	400	PHE
2	B	422	ASN
2	B	435	VAL
2	B	447	THR
2	B	448	LYS
2	B	458	VAL
2	B	476	VAL
2	B	485	GLU

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Mol	Chain	Res	Type
2	B	493	ILE
2	B	496	ASN
2	B	506	GLU
2	B	525	LEU
2	B	532	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
2	A	47	HIS
2	A	186	HIS
2	A	261	ASN
2	A	286	HIS
2	A	382	GLN
2	A	391	HIS
2	A	422	ASN
2	A	484	GLN
2	A	496	ASN
2	B	47	HIS
2	B	186	HIS
2	B	261	ASN
2	B	286	HIS
2	B	382	GLN
2	B	391	HIS
2	B	422	ASN
2	B	496	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	C	70/71 (98%)	22 (31%)	8 (11%)

All (22) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	C	906	G
1	C	907	G
1	C	908	U
1	C	909	G
1	C	910	G

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Mol	Chain	Res	Type
1	C	914	A
1	C	915	G
1	C	917	G
1	C	918	G
1	C	919	C
1	C	921	U
1	C	932	U
1	C	933	G
1	C	935	A
1	C	937	A
1	C	944	U
1	C	945	U
1	C	946	A
1	C	958	A
1	C	960	C
1	C	968	U
1	C	969	G

All (8) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	C	907	G
1	C	909	G
1	C	917	G
1	C	918	G
1	C	934	C
1	C	936	G
1	C	957	A
1	C	959	U

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 carbohydrates 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, 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	C	71/71 (100%)	2.04	27 (38%) 0 0	107, 182, 200, 200	0
2	A	466/534 (87%)	0.46	24 (5%) 27 18	40, 76, 137, 201	0
2	B	465/534 (87%)	0.50	36 (7%) 13 7	39, 74, 157, 199	0
All	All	1002/1139 (87%)	0.59	87 (8%) 10 5	39, 78, 178, 201	0

All (87) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	222	ASP	10.4
2	B	223	ALA	10.2
2	A	220	GLY	8.5
2	A	223	ALA	8.0
1	C	971	C	6.6
2	A	222	ASP	6.6
2	B	220	GLY	6.5
2	A	171	PHE	6.2
1	C	944	U	6.1
1	C	970	G	5.9
1	C	969	G	5.7
1	C	901	G	5.6
2	B	221	GLU	5.5
2	A	219	GLN	5.4
1	C	902	C	5.4
2	B	407	MET	5.4
1	C	904	A	5.4
1	C	968	U	5.0
1	C	903	C	4.9
2	B	104	ASN	4.7
1	C	945	U	4.7
2	A	533	ILE	4.6
2	B	487	VAL	4.5

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Mol	Chain	Res	Type	RSRZ
1	C	906	G	4.3
2	B	414	VAL	4.2
2	A	221	GLU	4.2
2	A	172	LYS	4.2
2	B	533	ILE	4.0
1	C	905	G	3.9
2	B	529	VAL	3.8
1	C	925	G	3.6
2	B	408	MET	3.6
1	C	966	C	3.5
1	C	907	G	3.5
2	B	403	PHE	3.5
2	B	90	VAL	3.3
1	C	913	G	3.3
2	B	224	THR	3.3
1	C	910	G	3.2
2	A	174	LEU	3.2
2	B	219	GLN	3.1
2	A	402	ALA	3.1
2	B	404	GLU	3.1
2	A	408	MET	3.0
2	A	403	PHE	3.0
2	A	102	LYS	3.0
2	B	174	LEU	2.9
1	C	964	G	2.9
1	C	965	C	2.9
2	B	531	ALA	2.9
2	A	397	PRO	2.9
1	C	914	A	2.9
2	B	412	VAL	2.8
2	B	409	GLY	2.8
2	B	481	MET	2.8
2	B	468	PHE	2.7
2	B	402	ALA	2.7
1	C	967	C	2.6
2	A	531	ALA	2.6
1	C	924	C	2.6
2	A	407	MET	2.6
2	B	296	TYR	2.6
2	A	62	SER	2.5
2	B	86	GLU	2.5
2	A	401	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
2	B	103	PRO	2.4
2	A	476	VAL	2.4
2	A	414	VAL	2.3
1	C	940	C	2.3
1	C	922	U	2.3
2	A	534	GLU	2.3
2	B	421	GLU	2.3
1	C	912	A	2.3
2	B	532	GLU	2.3
2	B	488	LYS	2.3
2	B	534	GLU	2.3
2	B	376	VAL	2.2
2	A	83	PHE	2.2
1	C	911	C	2.2
1	C	915	G	2.2
2	B	416	VAL	2.2
2	B	388	ALA	2.1
2	B	482	ARG	2.1
2	A	66	SER	2.1
2	A	532	GLU	2.1
2	B	492	ARG	2.1
2	B	401	LEU	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 carbohydrates 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.