



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 22, 2020 – 01:12 AM BST

PDB ID : 6O76
Title : Human cytosolic Histidyl-tRNA synthetase (HisRS) with WHEP domain
Authors : Kuhle, B.; Yang, X.L.
Deposited on : 2019-03-07
Resolution : 2.79 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	:	2.13.1
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)	:	2.13.1

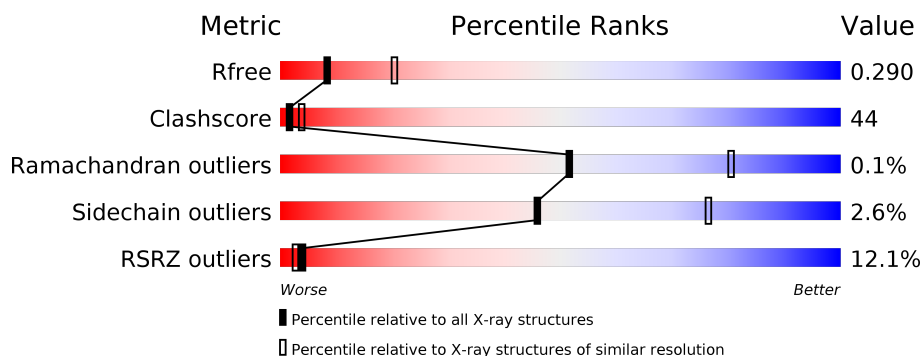
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.79 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	4107 (2.80-2.76)
Clashscore	141614	4575 (2.80-2.76)
Ramachandran outliers	138981	4487 (2.80-2.76)
Sidechain outliers	138945	4489 (2.80-2.76)
RSRZ outliers	127900	4027 (2.80-2.76)

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 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	A	509	<div> <div>5%</div> <div>46%</div> <div>39%</div> <div>14%</div> </div>
1	B	509	<div> <div>17%</div> <div>39%</div> <div>49%</div> <div>11%</div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7015 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 Histidine-tRNA ligase, cytoplasmic.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	438	Total	C	N	O	S	0	1	0
			3469	2209	595	648	17			
1	B	451	Total	C	N	O	S	0	0	0
			3482	2224	599	647	12			

- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Cl	0	0
			2	2		

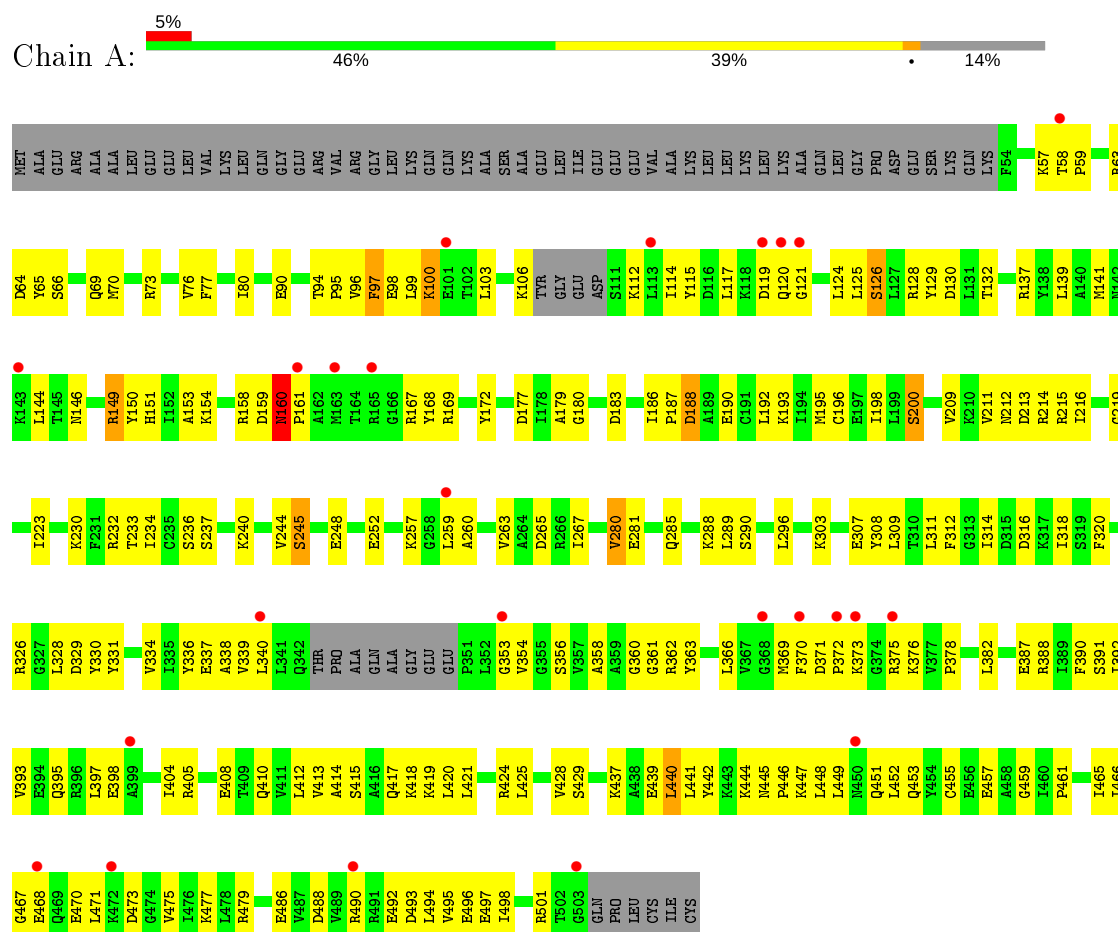
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	35	Total	O	0	0
			35	35		
3	B	27	Total	O	0	0
			27	27		

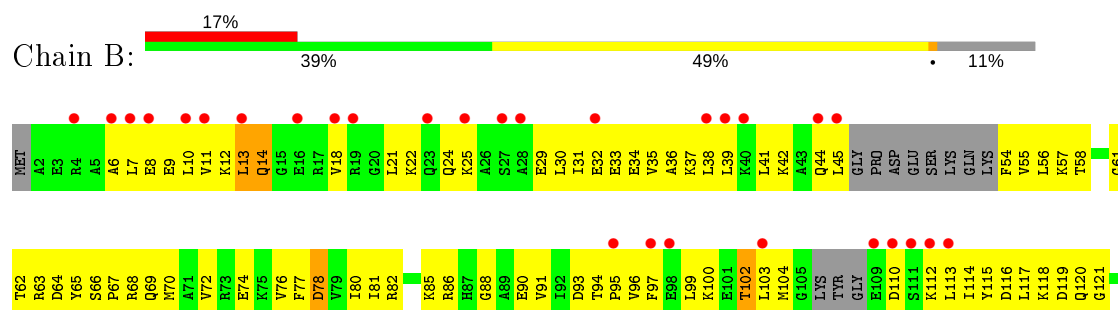
3 Residue-property plots

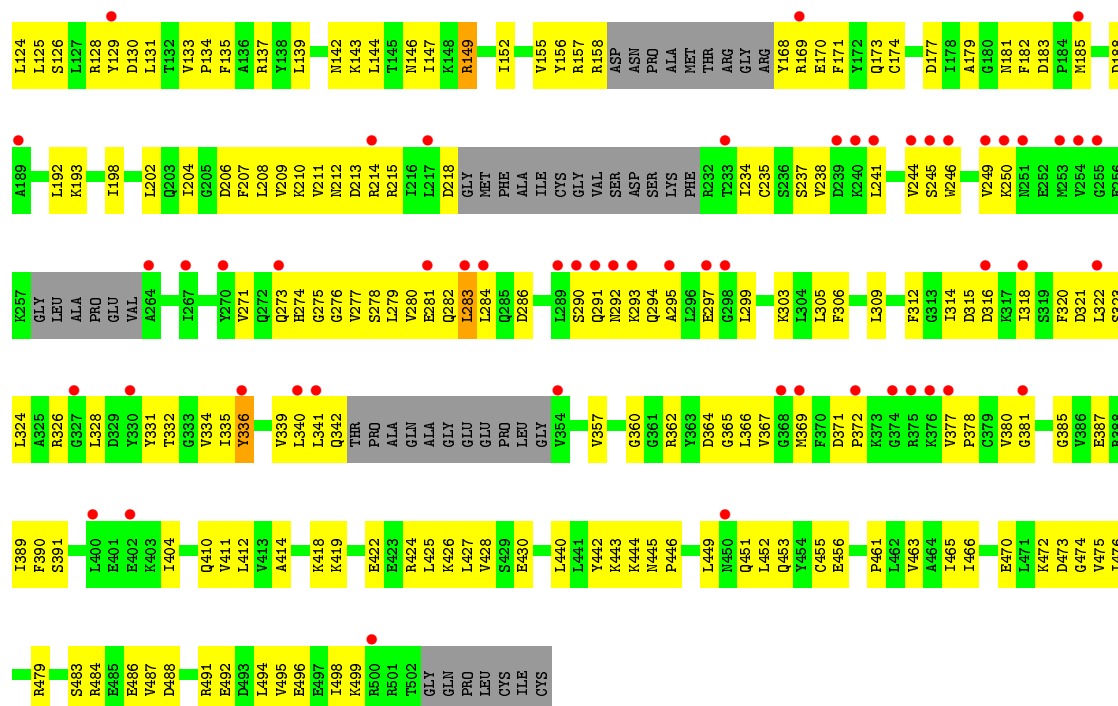
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Histidine–tRNA ligase, cytoplasmic



- Molecule 1: Histidine–tRNA ligase, cytoplasmic





4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	97.67Å 97.67Å 254.41Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.02 – 2.79 29.02 – 2.79	Depositor EDS
% Data completeness (in resolution range)	96.9 (29.02-2.79) 96.9 (29.02-2.79)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.77 (at 2.80Å)	Xtriage
Refinement program	PHENIX (1.10.1 _2155: ???)	Depositor
R, R_{free}	0.236 , 0.295 0.260 , 0.290	Depositor DCC
R_{free} test set	1555 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	66.0	Xtriage
Anisotropy	0.364	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 68.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	7015	wwPDB-VP
Average B, all atoms (Å ²)	90.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.16% 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

Bond lengths and bond angles in the following residue types are not validated in this section: CL

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	0/3519	0.64	5/4734 (0.1%)
1	B	0.41	0/3520	0.60	0/4734
All	All	0.41	0/7039	0.62	5/9468 (0.1%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	387	GLU	O-C-N	-7.75	110.31	122.70
1	A	387	GLU	CA-C-N	6.48	131.46	117.20
1	A	100	LYS	CD-CE-NZ	-5.88	98.17	111.70
1	A	126	SER	CB-CA-C	-5.48	99.69	110.10
1	A	160	ASN	C-N-CD	5.26	139.45	128.40

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	3469	0	3543	264	0
1	B	3482	0	3506	404	0
2	A	2	0	0	0	0
3	A	35	0	0	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	27	0	0	10	0
All	All	7015	0	7049	622	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 44.

All (622) 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:246:TRP:HA	1:B:249:VAL:CG2	1.22	1.68
1:A:336:TYR:CE1	1:A:360:GLY:HA3	1.46	1.50
1:B:246:TRP:CA	1:B:249:VAL:CG2	1.90	1.47
1:B:246:TRP:C	1:B:249:VAL:HG22	1.31	1.46
1:B:331:TYR:CD2	1:B:335:ILE:HD12	1.55	1.41
1:A:414:ALA:CB	1:A:451:GLN:OE1	1.76	1.32
1:B:495:VAL:CG1	3:B:604:HOH:O	1.73	1.32
1:B:246:TRP:CA	1:B:249:VAL:HG22	1.54	1.29
1:B:12:LYS:NZ	1:B:168:TYR:CZ	1.98	1.29
1:B:130:ASP:OD2	1:B:133:VAL:HG23	1.35	1.25
1:A:414:ALA:HB1	1:A:451:GLN:OE1	1.28	1.23
1:B:331:TYR:HD2	1:B:335:ILE:CD1	1.51	1.22
1:B:234:ILE:O	1:B:238:VAL:HG23	1.35	1.22
1:B:246:TRP:CA	1:B:249:VAL:HG21	1.59	1.20
1:B:218:ASP:OD1	1:B:294:GLN:NE2	1.73	1.20
1:B:472:LYS:HE2	1:B:472:LYS:HA	1.24	1.19
1:B:246:TRP:C	1:B:249:VAL:CG2	2.09	1.17
1:B:241:LEU:CD2	1:B:271:VAL:HG11	1.74	1.16
1:B:21:LEU:HD21	1:B:342:GLN:HG2	1.20	1.15
1:A:331:TYR:CE1	1:A:361:GLY:HA3	1.81	1.14
1:B:214:ARG:NH1	1:B:332:THR:HA	1.62	1.14
1:B:246:TRP:O	1:B:249:VAL:CG2	1.97	1.13
1:B:414:ALA:HB1	1:B:451:GLN:OE1	1.49	1.12
1:B:282:GLN:HG3	1:B:283:LEU:HD23	1.23	1.11
1:B:214:ARG:NE	1:B:331:TYR:O	1.84	1.10
1:A:158:ARG:NH1	1:B:120:GLN:HB3	1.64	1.10
1:A:336:TYR:CE1	1:A:360:GLY:CA	2.33	1.09
1:B:324:LEU:HD21	1:B:335:ILE:HG21	1.32	1.08
1:A:160:ASN:O	1:A:167:ARG:NH2	1.88	1.05
1:A:158:ARG:HH11	1:B:120:GLN:HB3	0.89	1.03
1:B:303:LYS:O	3:B:601:HOH:O	1.77	1.02
1:B:214:ARG:HH11	1:B:332:THR:CA	1.72	1.02

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:364:ASP:OD1	1:B:378:PRO:HA	1.59	1.01
1:B:277:VAL:HG12	1:B:306:PHE:CD1	1.95	1.01
1:B:110:ASP:HB2	1:B:113:LEU:HD13	1.41	1.00
1:B:419:LYS:H	1:B:445:ASN:ND2	1.58	1.00
1:B:112:LYS:HA	1:B:112:LYS:HE2	1.42	0.99
1:B:214:ARG:HH11	1:B:332:THR:HA	0.85	0.99
1:A:230:LYS:O	1:A:233:THR:HG22	1.63	0.98
1:B:188:ASP:CG	1:B:362:ARG:HH21	1.67	0.98
1:B:321:ASP:CG	1:B:323:SER:HG	1.66	0.98
1:A:415:SER:OG	1:A:424:ARG:NH1	1.97	0.98
1:B:244:VAL:HG13	1:B:249:VAL:HG12	1.46	0.97
1:B:246:TRP:O	1:B:249:VAL:HG22	1.57	0.97
1:B:12:LYS:NZ	1:B:168:TYR:OH	1.96	0.97
1:A:414:ALA:HB2	1:A:451:GLN:OE1	1.61	0.96
1:B:12:LYS:NZ	1:B:168:TYR:CE1	2.31	0.96
1:B:211:VAL:HG12	1:B:336:TYR:HB3	1.46	0.96
1:B:321:ASP:OD2	1:B:323:SER:OG	1.83	0.96
1:B:241:LEU:CD2	1:B:271:VAL:CG1	2.43	0.96
1:B:331:TYR:CD2	1:B:335:ILE:CD1	2.35	0.95
1:B:99:LEU:O	1:B:102:THR:OG1	1.85	0.95
1:A:373:LYS:HD2	1:A:375:ARG:HH21	1.29	0.94
1:A:397:LEU:HD12	1:A:404:ILE:HD11	1.49	0.94
1:B:246:TRP:O	1:B:249:VAL:HG23	1.67	0.94
1:B:21:LEU:CD2	1:B:342:GLN:HG2	1.95	0.94
1:B:238:VAL:HG12	1:B:323:SER:O	1.67	0.94
1:B:96:VAL:O	1:B:128:ARG:HG3	1.68	0.93
1:A:103:LEU:HD23	1:A:129:TYR:CE1	2.04	0.92
1:B:143:LYS:NZ	1:B:371:ASP:OD2	2.02	0.92
1:A:66:SER:H	1:A:69:GLN:HE21	1.11	0.92
1:B:212:ASN:OD1	1:B:213:ASP:N	2.01	0.92
1:A:492:GLU:N	1:A:492:GLU:OE1	2.03	0.91
1:B:367:VAL:HG11	1:B:377:VAL:CG2	1.99	0.91
1:A:446:PRO:HG2	1:A:451:GLN:NE2	1.83	0.91
1:B:367:VAL:HG11	1:B:377:VAL:HG21	1.48	0.91
1:B:321:ASP:OD1	1:B:323:SER:OG	1.88	0.90
1:B:321:ASP:CG	1:B:323:SER:OG	2.09	0.90
1:B:110:ASP:HB2	1:B:113:LEU:CD1	2.01	0.90
1:B:419:LYS:H	1:B:445:ASN:HD21	0.91	0.90
1:A:214:ARG:NH1	1:A:328:LEU:O	2.06	0.89
1:A:195:MET:HE1	1:A:338:ALA:HB2	1.50	0.89
1:A:213:ASP:OD1	3:A:701:HOH:O	1.87	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:241:LEU:HD21	1:B:271:VAL:CG1	2.04	0.88
1:B:9:GLU:O	1:B:12:LYS:HG2	1.74	0.87
1:B:7:LEU:HD21	1:B:44:GLN:CB	2.03	0.87
1:A:63:ARG:HD3	3:A:718:HOH:O	1.73	0.87
1:B:476:ILE:HD12	1:B:494:LEU:HD22	1.55	0.87
1:B:38:LEU:HD21	1:B:42:LYS:HE3	1.57	0.87
1:B:100:LYS:HB3	1:B:124:LEU:CD1	2.05	0.87
1:B:495:VAL:HG12	3:B:604:HOH:O	1.53	0.86
1:A:309:LEU:HD23	1:A:314:ILE:HD11	1.55	0.86
1:A:158:ARG:HH11	1:B:120:GLN:CB	1.84	0.86
1:B:158:ARG:HA	1:B:169:ARG:HD2	1.58	0.86
1:B:100:LYS:HB3	1:B:124:LEU:HD11	1.58	0.85
1:A:331:TYR:CD1	1:A:361:GLY:HA3	2.13	0.84
1:A:424:ARG:HG2	1:A:466:ILE:HD12	1.59	0.83
1:B:492:GLU:OE1	1:B:492:GLU:N	2.10	0.83
1:A:66:SER:H	1:A:69:GLN:NE2	1.77	0.83
1:B:234:ILE:O	1:B:237:SER:OG	1.97	0.83
1:B:305:LEU:HD12	1:B:305:LEU:O	1.79	0.83
1:B:340:LEU:HD23	1:B:341:LEU:N	1.92	0.83
1:B:124:LEU:HD12	1:B:124:LEU:O	1.78	0.83
1:A:114:ILE:HG23	3:A:711:HOH:O	1.79	0.83
1:A:397:LEU:HD12	1:A:404:ILE:CD1	2.07	0.83
1:A:373:LYS:HD2	1:A:375:ARG:NH2	1.93	0.83
1:B:367:VAL:CG1	1:B:377:VAL:CG2	2.57	0.83
1:B:8:GLU:O	1:B:11:VAL:HG22	1.79	0.82
1:B:286:ASP:O	1:B:290:SER:OG	1.95	0.82
1:B:14:GLN:NE2	1:B:34:GLU:OE1	2.12	0.82
1:B:115:TYR:CE2	1:B:158:ARG:HB3	2.14	0.81
1:A:373:LYS:CD	1:A:375:ARG:HH21	1.94	0.81
1:B:118:LYS:O	1:B:120:GLN:NE2	2.12	0.81
1:A:429:SER:OG	1:B:312:PHE:HD1	1.64	0.81
1:B:156:TYR:CE2	1:B:170:GLU:HG3	2.16	0.81
1:B:218:ASP:OD1	1:B:294:GLN:CD	2.18	0.81
1:B:100:LYS:CB	1:B:124:LEU:HD13	2.10	0.81
1:B:100:LYS:HB2	1:B:124:LEU:HD13	1.60	0.81
1:B:340:LEU:HD23	1:B:341:LEU:H	1.44	0.80
1:B:130:ASP:CG	1:B:133:VAL:HG23	2.00	0.80
1:B:9:GLU:CG	1:B:168:TYR:OH	2.29	0.80
1:B:282:GLN:CG	1:B:283:LEU:HD23	2.10	0.80
1:B:495:VAL:HG13	3:B:604:HOH:O	1.55	0.80
1:A:180:GLY:O	1:A:378:PRO:HG2	1.82	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:94:THR:HG23	1:B:95:PRO:HD2	1.64	0.80
1:B:238:VAL:O	1:B:241:LEU:HB3	1.82	0.80
1:B:24:GLN:O	1:B:25:LYS:HG3	1.82	0.80
1:B:100:LYS:CB	1:B:124:LEU:CD1	2.61	0.79
1:B:32:GLU:O	1:B:35:VAL:HG22	1.82	0.79
1:A:326:ARG:CZ	1:A:337:GLU:OE1	2.31	0.79
1:B:188:ASP:OD1	1:B:362:ARG:NH2	2.15	0.79
1:B:246:TRP:O	1:B:250:LYS:N	2.15	0.78
1:B:7:LEU:HD21	1:B:44:GLN:HB3	1.65	0.78
1:B:282:GLN:HG3	1:B:283:LEU:CD2	2.11	0.78
1:B:367:VAL:CG1	1:B:377:VAL:HG21	2.13	0.78
1:B:9:GLU:CG	1:B:12:LYS:HE2	2.12	0.78
1:B:328:LEU:HD12	1:B:328:LEU:O	1.82	0.78
1:B:277:VAL:CG1	1:B:306:PHE:CD1	2.66	0.78
1:B:31:ILE:O	1:B:35:VAL:HG13	1.84	0.78
1:A:388[A]:ARG:NH2	3:A:702:HOH:O	2.02	0.78
1:B:177:ASP:OD1	1:B:381:GLY:HA3	1.84	0.78
1:A:237:SER:OG	1:A:257:LYS:NZ	2.16	0.77
1:A:159:ASP:OD1	1:A:160:ASN:N	2.17	0.77
1:A:420:LEU:N	3:A:703:HOH:O	2.05	0.77
1:B:367:VAL:HG11	1:B:377:VAL:CB	2.15	0.77
1:B:68:ARG:NH1	1:B:404:ILE:HD12	1.99	0.77
1:A:479:ARG:NH2	1:A:486:GLU:OE2	2.18	0.77
1:B:66:SER:OG	1:B:69:GLN:NE2	2.16	0.77
1:B:218:ASP:CG	1:B:294:GLN:HE22	1.88	0.77
1:B:419:LYS:N	1:B:445:ASN:HD21	1.77	0.76
1:B:11:VAL:HG12	1:B:41:LEU:HB3	1.67	0.76
1:B:479:ARG:NH2	1:B:486:GLU:OE2	2.17	0.76
1:A:158:ARG:NH1	1:B:120:GLN:CB	2.46	0.76
1:B:38:LEU:HD23	1:B:38:LEU:O	1.86	0.76
1:B:324:LEU:HD21	1:B:335:ILE:CG2	2.14	0.75
1:B:66:SER:H	1:B:69:GLN:NE2	1.83	0.75
1:B:21:LEU:HD21	1:B:342:GLN:CG	2.11	0.75
1:A:188:ASP:OD1	1:A:362:ARG:NH2	2.19	0.75
1:A:371:ASP:OD1	1:A:372:PRO:HD2	1.86	0.75
1:B:66:SER:CB	1:B:69:GLN:HE21	2.00	0.74
1:A:232:ARG:HH12	1:A:329:ASP:HB3	1.53	0.74
1:A:467:GLY:HA3	1:A:470:GLU:OE1	1.86	0.74
1:B:158:ARG:HA	1:B:169:ARG:CD	2.17	0.74
1:B:188:ASP:CG	1:B:362:ARG:NH2	2.41	0.74
1:A:195:MET:CE	1:A:338:ALA:HB2	2.18	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:10:LEU:HD23	1:B:391:SER:HB2	1.71	0.73
1:A:412:LEU:HD12	1:A:413:VAL:N	2.04	0.73
1:A:429:SER:OG	1:B:312:PHE:CD1	2.41	0.72
1:B:449:LEU:O	1:B:453:GLN:HG3	1.88	0.72
1:A:285:GLN:NE2	1:A:285:GLN:HA	2.03	0.72
1:B:331:TYR:HD2	1:B:335:ILE:HD13	1.53	0.72
1:A:412:LEU:HD12	1:A:413:VAL:H	1.52	0.72
1:B:110:ASP:CB	1:B:113:LEU:HD13	2.18	0.72
1:A:223:ILE:HD11	1:A:288:LYS:HB3	1.71	0.71
1:B:39:LEU:H	1:B:39:LEU:HD12	1.54	0.71
1:B:241:LEU:HD23	1:B:271:VAL:HG11	1.69	0.71
1:A:103:LEU:HD23	1:A:129:TYR:CD1	2.25	0.71
1:B:279:LEU:O	1:B:282:GLN:HG2	1.90	0.71
1:B:13:LEU:HD23	1:B:391:SER:OG	1.91	0.71
1:A:331:TYR:CE1	1:A:361:GLY:CA	2.69	0.70
1:A:497:GLU:O	1:A:501:ARG:HG2	1.91	0.70
1:B:241:LEU:HD21	1:B:271:VAL:HG11	1.62	0.70
1:B:61:GLY:O	1:B:168:TYR:HB3	1.91	0.70
1:A:449:LEU:O	1:A:453:GLN:HG3	1.91	0.70
1:A:373:LYS:HD2	1:A:375:ARG:HE	1.56	0.70
1:B:299:LEU:O	1:B:303:LYS:CG	2.40	0.70
1:B:410:GLN:O	1:B:461:PRO:HG2	1.91	0.70
1:A:103:LEU:HD23	1:A:129:TYR:HE1	1.49	0.70
1:A:397:LEU:CD1	1:A:404:ILE:HD11	2.21	0.70
1:B:135:PHE:HB2	1:B:149:ARG:NH1	2.07	0.70
1:B:472:LYS:HA	1:B:472:LYS:CE	2.07	0.70
1:A:336:TYR:HE1	1:A:360:GLY:HA3	0.95	0.70
1:A:190:GLU:OE2	1:B:442:TYR:OH	2.06	0.69
1:A:425:LEU:HD23	1:A:440:LEU:HD21	1.73	0.69
1:B:112:LYS:O	1:B:112:LYS:HD3	1.91	0.69
1:B:112:LYS:HA	1:B:112:LYS:CE	2.20	0.69
1:B:97:PHE:CD1	1:B:125:LEU:HD22	2.28	0.69
1:B:283:LEU:N	1:B:283:LEU:HD23	2.07	0.69
1:B:277:VAL:HG12	1:B:306:PHE:CG	2.27	0.69
1:B:9:GLU:CG	1:B:168:TYR:HH	2.05	0.69
1:A:371:ASP:OD1	1:A:372:PRO:CD	2.41	0.69
1:B:362:ARG:NH2	3:B:602:HOH:O	2.26	0.69
1:A:369:MET:HE3	1:A:370:PHE:HE2	1.58	0.68
1:A:149:ARG:HD2	1:A:149:ARG:C	2.14	0.68
1:A:448:LEU:HD23	1:A:448:LEU:C	2.14	0.68
3:A:723:HOH:O	1:B:102:THR:HG21	1.94	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:367:VAL:CB	1:B:377:VAL:HB	2.24	0.68
1:B:7:LEU:O	1:B:11:VAL:HG13	1.92	0.68
1:B:414:ALA:O	1:B:465:ILE:HA	1.93	0.68
1:B:54:PHE:O	1:B:55:VAL:HG12	1.93	0.68
1:B:241:LEU:HD21	1:B:271:VAL:HG12	1.74	0.68
1:B:206:ASP:O	1:B:340:LEU:HD23	1.94	0.68
1:B:215:ARG:HA	1:B:218:ASP:OD2	1.95	0.67
1:B:241:LEU:HD23	1:B:271:VAL:CG1	2.23	0.67
1:B:24:GLN:OE1	1:B:342:GLN:NE2	2.27	0.67
1:B:472:LYS:HE2	1:B:472:LYS:CA	2.14	0.67
1:A:212:ASN:OD1	1:A:213:ASP:N	2.27	0.67
1:B:142:ASN:HB2	1:B:144:LEU:CD1	2.24	0.67
1:B:324:LEU:HD23	1:B:324:LEU:C	2.14	0.67
1:A:196:CYS:O	1:A:200:SER:OG	2.06	0.67
1:A:146:ASN:HA	1:A:179:ALA:O	1.94	0.67
1:B:419:LYS:N	1:B:445:ASN:ND2	2.39	0.67
1:A:497:GLU:OE2	1:A:501:ARG:NH1	2.24	0.67
1:B:68:ARG:CZ	1:B:404:ILE:HD12	2.25	0.67
1:B:77:PHE:O	1:B:81:ILE:HG12	1.94	0.67
1:A:492:GLU:H	1:A:492:GLU:CD	1.95	0.66
1:B:275:GLY:O	1:B:320:PHE:N	2.27	0.66
1:A:307:GLU:OE2	1:B:422:GLU:OE2	2.13	0.66
1:A:336:TYR:CD1	1:A:360:GLY:HA3	2.26	0.66
1:B:470:GLU:OE1	1:B:470:GLU:N	2.26	0.66
1:A:439:GLU:HG3	3:A:719:HOH:O	1.93	0.66
1:B:113:LEU:O	1:B:158:ARG:HG2	1.95	0.66
1:B:367:VAL:HG11	1:B:377:VAL:HB	1.78	0.66
1:B:492:GLU:H	1:B:492:GLU:CD	1.96	0.66
1:A:369:MET:HE3	1:A:370:PHE:CE2	2.30	0.65
1:A:448:LEU:HD23	1:A:448:LEU:O	1.97	0.65
1:A:66:SER:N	1:A:69:GLN:HE21	1.89	0.65
1:A:80:ILE:HG23	1:A:198:ILE:HD13	1.78	0.65
1:B:103:LEU:HD22	1:B:129:TYR:CE2	2.31	0.65
1:B:188:ASP:OD1	1:B:380:VAL:HG21	1.96	0.65
1:B:276:GLY:O	1:B:280:VAL:HG23	1.96	0.65
1:B:142:ASN:CB	1:B:144:LEU:HD11	2.26	0.65
1:B:142:ASN:HB2	1:B:144:LEU:HD11	1.78	0.65
1:B:155:VAL:HG11	1:B:173:GLN:OE1	1.96	0.65
1:A:281:GLU:HG3	1:A:303:LYS:NZ	2.11	0.65
1:A:160:ASN:HD22	1:A:160:ASN:N	1.95	0.65
1:A:340:LEU:O	1:A:353:GLY:HA2	1.96	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:146:ASN:HA	1:B:179:ALA:O	1.97	0.64
1:A:115:TYR:OH	1:A:169:ARG:HD3	1.97	0.64
1:B:88:GLY:HA2	3:B:614:HOH:O	1.96	0.64
1:A:244:VAL:HG22	1:A:245:SER:H	1.60	0.64
1:A:338:ALA:HB3	1:A:358:ALA:HB3	1.80	0.64
1:A:440:LEU:C	1:A:440:LEU:HD12	2.18	0.63
1:A:370:PHE:CE1	1:B:56:LEU:HD21	2.33	0.63
1:A:370:PHE:CD1	1:B:56:LEU:HD21	2.33	0.63
1:B:241:LEU:HD22	1:B:271:VAL:HG11	1.75	0.63
1:B:39:LEU:N	1:B:39:LEU:HD12	2.13	0.63
1:B:476:ILE:HD12	1:B:494:LEU:CD2	2.28	0.63
1:B:192:LEU:HD21	1:B:336:TYR:CD1	2.34	0.63
1:B:425:LEU:HD23	1:B:440:LEU:HD11	1.80	0.63
1:A:370:PHE:HD1	1:B:56:LEU:HD11	1.63	0.63
1:B:13:LEU:HD12	1:B:13:LEU:O	1.99	0.63
1:B:367:VAL:CG1	1:B:377:VAL:HB	2.28	0.63
1:B:367:VAL:HB	1:B:377:VAL:HB	1.79	0.63
1:A:376:LYS:O	1:A:376:LYS:HG3	1.98	0.62
1:A:366:LEU:HD23	1:A:366:LEU:O	1.98	0.62
1:A:369:MET:HE2	1:A:370:PHE:CD2	2.34	0.62
1:A:373:LYS:HD2	1:A:375:ARG:NE	2.13	0.62
1:A:120:GLN:HB3	1:B:158:ARG:NH1	2.14	0.62
1:A:429:SER:HG	1:B:312:PHE:HD1	1.48	0.62
1:B:246:TRP:HA	1:B:249:VAL:HG21	0.63	0.62
1:A:117:LEU:CD2	1:B:115:TYR:HD1	2.13	0.62
1:B:7:LEU:HD21	1:B:44:GLN:HB2	1.81	0.62
1:B:135:PHE:HB2	1:B:149:ARG:HH11	1.65	0.62
1:A:405:ARG:HD3	1:A:459:GLY:HA3	1.82	0.62
1:B:495:VAL:O	1:B:499:LYS:HG3	2.00	0.61
1:A:370:PHE:CD1	1:B:56:LEU:HD11	2.35	0.61
1:B:284:LEU:O	1:B:290:SER:OG	2.18	0.61
1:B:483:SER:O	1:B:484:ARG:HB2	2.00	0.61
1:B:494:LEU:O	1:B:498:ILE:HG13	2.00	0.61
1:B:38:LEU:CD2	1:B:42:LYS:HE3	2.28	0.61
1:A:259:LEU:HD12	1:A:260:ALA:H	1.66	0.61
1:A:223:ILE:CD1	1:A:288:LYS:HB3	2.29	0.61
1:B:157:ARG:NH1	1:B:171:PHE:HZ	1.99	0.61
1:B:274:HIS:HB2	1:B:320:PHE:O	2.00	0.61
1:B:81:ILE:HD11	1:B:152:ILE:HD12	1.82	0.61
1:B:322:LEU:HD12	1:B:322:LEU:N	2.16	0.61
1:B:414:ALA:CB	1:B:451:GLN:OE1	2.38	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:214:ARG:HE	1:B:331:TYR:C	2.03	0.61
1:A:421:LEU:O	1:A:421:LEU:HD12	2.01	0.60
1:B:55:VAL:HG13	1:B:55:VAL:O	2.01	0.60
1:A:441:LEU:O	3:A:704:HOH:O	2.15	0.60
1:A:414:ALA:O	1:A:465:ILE:HA	2.00	0.60
1:A:369:MET:CE	1:A:370:PHE:CE2	2.85	0.60
1:B:244:VAL:HG22	1:B:245:SER:N	2.17	0.60
1:B:30:LEU:N	1:B:30:LEU:HD12	2.16	0.60
1:A:65:TYR:HB2	1:B:93:ASP:HB3	1.83	0.60
1:A:309:LEU:HD23	1:A:314:ILE:CD1	2.32	0.59
1:B:57:LYS:HE2	1:B:58:THR:O	2.02	0.59
1:A:425:LEU:O	1:A:428:VAL:HG12	2.02	0.59
1:A:336:TYR:CD1	1:A:360:GLY:CA	2.85	0.59
1:A:490:ARG:HG2	1:A:492:GLU:CD	2.22	0.59
1:B:124:LEU:C	1:B:124:LEU:HD12	2.22	0.59
1:B:473:ASP:HB2	1:B:475:VAL:HG22	1.85	0.59
1:A:215:ARG:NH2	3:A:701:HOH:O	2.35	0.59
1:A:120:GLN:CB	1:B:158:ARG:NH1	2.65	0.59
1:B:24:GLN:C	1:B:25:LYS:HG3	2.22	0.59
1:B:291:GLN:O	1:B:291:GLN:HG3	2.02	0.59
1:B:238:VAL:CG1	1:B:323:SER:O	2.47	0.59
1:B:452:LEU:O	1:B:456:GLU:HG3	2.02	0.59
1:B:476:ILE:CD1	1:B:494:LEU:HD22	2.32	0.59
1:A:232:ARG:NH1	1:A:329:ASP:HB3	2.16	0.59
1:A:281:GLU:HG3	1:A:303:LYS:HZ3	1.65	0.59
1:A:76:VAL:CG2	1:A:390:PHE:HE1	2.16	0.59
1:B:316:ASP:N	1:B:316:ASP:OD1	2.35	0.59
1:A:373:LYS:CE	1:A:375:ARG:HH21	2.14	0.59
1:A:373:LYS:HD2	1:A:375:ARG:CZ	2.32	0.58
1:A:124:LEU:HD12	1:A:124:LEU:N	2.18	0.58
1:B:479:ARG:HB2	1:B:486:GLU:HG2	1.84	0.58
1:B:54:PHE:CG	1:B:55:VAL:N	2.72	0.58
1:B:72:VAL:O	1:B:76:VAL:HG23	2.04	0.58
1:A:440:LEU:O	1:A:440:LEU:HD12	2.04	0.58
1:A:446:PRO:HG2	1:A:451:GLN:HE21	1.65	0.58
1:B:100:LYS:HE3	1:B:124:LEU:HD13	1.86	0.58
1:B:214:ARG:CD	1:B:328:LEU:CD1	2.81	0.58
1:A:211:VAL:HG12	1:A:336:TYR:HB3	1.85	0.57
1:A:177:ASP:OD2	1:A:363:TYR:OH	2.22	0.57
1:A:388[B]:ARG:O	1:A:392:ILE:HG13	2.04	0.57
1:B:38:LEU:HD23	1:B:38:LEU:C	2.24	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:437:LYS:HG2	1:B:86:ARG:HA	1.85	0.57
1:B:157:ARG:O	1:B:169:ARG:HB3	2.05	0.57
1:A:397:LEU:CD1	1:A:404:ILE:CD1	2.78	0.57
1:A:417:GLN:OE1	1:A:468:GLU:HG3	2.05	0.57
1:B:63:ARG:NH2	1:B:65:TYR:CZ	2.73	0.57
1:B:103:LEU:HB3	1:B:129:TYR:HE2	1.68	0.57
1:B:241:LEU:HD12	1:B:249:VAL:HG11	1.87	0.57
1:A:128:ARG:HH12	1:A:153:ALA:CB	2.16	0.57
1:A:388[A]:ARG:O	1:A:392:ILE:HG13	2.04	0.57
1:B:68:ARG:NH2	1:B:404:ILE:HB	2.19	0.57
1:B:214:ARG:CZ	1:B:332:THR:HA	2.33	0.56
1:A:442:TYR:HB2	1:B:182:PHE:HB3	1.87	0.56
1:B:97:PHE:HD1	1:B:125:LEU:HD22	1.69	0.56
1:B:29:GLU:O	1:B:33:GLU:HG3	2.05	0.56
1:B:94:THR:CG2	1:B:95:PRO:HD2	2.35	0.56
1:A:285:GLN:HE21	1:A:285:GLN:HA	1.69	0.56
1:A:192:LEU:HD11	1:A:336:TYR:CD2	2.40	0.56
1:B:234:ILE:O	1:B:238:VAL:CG2	2.30	0.56
1:B:367:VAL:CG1	1:B:377:VAL:CB	2.84	0.56
1:B:411:VAL:HG22	1:B:412:LEU:N	2.21	0.56
1:B:424:ARG:NE	3:B:605:HOH:O	2.35	0.56
1:A:209:VAL:HB	1:A:318:ILE:HD13	1.87	0.56
1:B:334:VAL:HG12	1:B:335:ILE:N	2.19	0.55
1:A:369:MET:HE2	1:A:370:PHE:HD2	1.71	0.55
1:A:132:THR:HG21	1:A:330:TYR:OH	2.06	0.55
1:A:183:ASP:OD2	1:B:444:LYS:N	2.39	0.55
1:A:421:LEU:HD22	1:A:444:LYS:HA	1.88	0.55
1:A:490:ARG:HG2	1:A:492:GLU:OE2	2.06	0.55
1:A:395:GLN:HA	1:A:398:GLU:HB3	1.88	0.55
1:B:18:VAL:HG22	1:B:34:GLU:HB3	1.89	0.55
1:B:158:ARG:CA	1:B:169:ARG:HD2	2.35	0.55
1:A:444:LYS:N	1:B:183:ASP:OD2	2.39	0.55
1:B:214:ARG:CD	1:B:328:LEU:HD12	2.37	0.54
1:B:425:LEU:O	1:B:428:VAL:HG12	2.08	0.54
1:B:115:TYR:OH	1:B:169:ARG:NE	2.41	0.54
1:B:116:ASP:OD1	1:B:126:SER:HB3	2.07	0.54
1:A:453:GLN:O	1:A:457:GLU:HG3	2.07	0.54
1:B:249:VAL:HG23	1:B:250:LYS:N	2.21	0.54
1:B:234:ILE:C	1:B:238:VAL:HG23	2.23	0.54
1:B:39:LEU:H	1:B:39:LEU:CD1	2.21	0.54
1:A:330:TYR:CE2	1:A:366:LEU:HD13	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:271:VAL:HG13	1:B:323:SER:HA	1.89	0.54
1:B:326:ARG:HD2	1:B:326:ARG:N	2.22	0.54
1:A:418:LYS:O	1:A:419:LYS:HB3	2.07	0.54
1:A:180:GLY:C	1:A:378:PRO:HG2	2.28	0.54
1:B:275:GLY:N	1:B:320:PHE:O	2.38	0.54
1:A:493:ASP:O	1:A:496:GLU:HG3	2.08	0.53
1:A:106:LYS:CB	1:A:129:TYR:OH	2.55	0.53
1:A:421:LEU:HB3	3:A:727:HOH:O	2.09	0.53
1:A:309:LEU:CD2	1:A:314:ILE:HD11	2.31	0.53
1:B:8:GLU:N	1:B:45:LEU:HD21	2.23	0.53
1:A:370:PHE:CE1	1:B:56:LEU:CD2	2.91	0.53
1:A:308:TYR:HA	1:A:311:LEU:HD12	1.89	0.53
1:A:354:VAL:O	1:A:354:VAL:HG12	2.09	0.53
1:B:367:VAL:HG12	1:B:377:VAL:CG2	2.37	0.53
1:A:119:ASP:OD1	1:A:121:GLY:N	2.42	0.53
1:A:281:GLU:CG	1:A:303:LYS:NZ	2.72	0.53
1:B:364:ASP:OD1	1:B:378:PRO:CA	2.44	0.53
1:A:158:ARG:HH12	1:B:120:GLN:C	2.12	0.52
1:B:214:ARG:HD2	1:B:328:LEU:CD1	2.40	0.52
1:A:439:GLU:CG	3:A:719:HOH:O	2.54	0.52
1:A:479:ARG:HB2	1:A:486:GLU:HG2	1.91	0.52
1:A:130:ASP:OD2	1:A:132:THR:OG1	2.27	0.52
1:A:95:PRO:HD3	1:B:64:ASP:OD1	2.09	0.52
1:B:30:LEU:CD1	1:B:30:LEU:N	2.73	0.52
1:B:112:LYS:HE2	1:B:112:LYS:CA	2.17	0.52
1:B:339:VAL:HG23	1:B:339:VAL:O	2.08	0.52
1:B:446:PRO:HG2	1:B:451:GLN:NE2	2.24	0.52
1:A:188:ASP:N	1:A:188:ASP:OD1	2.41	0.52
1:A:336:TYR:CE1	1:A:360:GLY:C	2.83	0.52
1:B:142:ASN:CB	1:B:144:LEU:CD1	2.85	0.52
1:B:245:SER:O	1:B:249:VAL:N	2.43	0.52
1:B:214:ARG:HD3	1:B:328:LEU:HD12	1.91	0.52
1:A:334:VAL:HG22	3:A:712:HOH:O	2.10	0.51
1:B:446:PRO:CG	1:B:451:GLN:NE2	2.73	0.51
1:A:97:PHE:HE1	1:B:62:THR:HG21	1.74	0.51
1:A:213:ASP:HB3	1:A:216:ILE:HG13	1.92	0.51
1:A:59:PRO:HB3	1:B:125:LEU:HD21	1.92	0.51
1:B:331:TYR:OH	1:B:360:GLY:HA2	2.09	0.51
1:B:212:ASN:O	1:B:335:ILE:N	2.30	0.51
1:A:76:VAL:CG2	1:A:390:PHE:CE1	2.93	0.51
1:A:444:LYS:HG2	1:B:183:ASP:OD2	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:119:ASP:O	1:B:121:GLY:N	2.35	0.51
1:B:114:ILE:HG23	3:B:616:HOH:O	2.10	0.50
1:B:193:LYS:HA	1:B:314:ILE:HD13	1.92	0.50
1:A:96:VAL:O	1:A:128:ARG:HG2	2.11	0.50
1:B:18:VAL:O	1:B:22:LYS:HG3	2.11	0.50
1:B:305:LEU:C	1:B:305:LEU:HD12	2.31	0.50
1:A:446:PRO:CG	1:A:451:GLN:NE2	2.67	0.50
1:B:110:ASP:HB2	1:B:113:LEU:HD11	1.93	0.50
1:A:425:LEU:HD23	1:A:440:LEU:CD2	2.42	0.50
1:B:244:VAL:CG2	1:B:245:SER:N	2.74	0.50
1:A:447:LYS:O	1:A:451:GLN:HG3	2.11	0.50
1:A:473:ASP:HB3	1:A:475:VAL:HG22	1.94	0.50
1:B:142:ASN:HB3	1:B:144:LEU:HD11	1.93	0.50
1:B:244:VAL:O	1:B:249:VAL:HG11	2.12	0.49
1:B:9:GLU:CB	1:B:168:TYR:OH	2.59	0.49
1:A:408:GLU:OE1	1:B:85:LYS:HD3	2.12	0.49
1:A:240:LYS:O	1:A:244:VAL:HG12	2.12	0.49
1:A:309:LEU:HD22	1:A:314:ILE:HG13	1.94	0.49
1:A:103:LEU:CD2	1:A:129:TYR:CD1	2.94	0.49
1:A:316:ASP:N	1:A:316:ASP:OD1	2.45	0.49
1:A:59:PRO:HB3	1:B:125:LEU:CD2	2.43	0.49
1:B:113:LEU:CD1	1:B:113:LEU:N	2.75	0.49
1:B:292:ASN:OD1	1:B:295:ALA:N	2.33	0.49
1:A:371:ASP:OD1	1:A:372:PRO:N	2.46	0.49
1:B:7:LEU:CD2	1:B:44:GLN:HB3	2.39	0.49
1:A:245:SER:HB3	1:A:248:GLU:OE1	2.13	0.49
1:B:331:TYR:OH	1:B:360:GLY:CA	2.61	0.49
1:A:366:LEU:HD23	1:A:366:LEU:C	2.33	0.49
1:A:219:GLY:O	1:A:223:ILE:HG22	2.13	0.49
1:B:321:ASP:OD2	1:B:323:SER:N	2.37	0.49
1:B:10:LEU:CD2	1:B:391:SER:HB2	2.42	0.48
1:B:445:ASN:ND2	3:B:609:HOH:O	2.43	0.48
1:B:8:GLU:CG	1:B:45:LEU:HD22	2.43	0.48
1:B:66:SER:CB	1:B:69:GLN:NE2	2.73	0.48
1:A:329:ASP:N	1:A:329:ASP:OD2	2.45	0.48
1:B:9:GLU:HB2	1:B:168:TYR:OH	2.12	0.48
1:B:293:LYS:O	1:B:297:GLU:CG	2.61	0.48
1:A:120:GLN:HB2	1:B:158:ARG:HH12	1.77	0.48
1:A:193:LYS:HA	1:A:314:ILE:HD13	1.95	0.48
1:A:326:ARG:NH1	1:A:337:GLU:OE1	2.47	0.48
1:A:120:GLN:CB	1:B:158:ARG:HH12	2.27	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:282:GLN:HG3	1:B:283:LEU:N	2.28	0.48
1:A:183:ASP:OD2	1:B:444:LYS:HG2	2.12	0.48
1:A:259:LEU:HD12	1:A:260:ALA:N	2.27	0.48
1:B:237:SER:O	1:B:241:LEU:N	2.46	0.48
1:A:96:VAL:HA	1:A:128:ARG:HE	1.79	0.48
1:A:57:LYS:HE2	1:A:58:THR:O	2.14	0.48
1:A:97:PHE:HA	1:A:126:SER:O	2.13	0.48
1:A:76:VAL:HG21	1:A:390:PHE:CE1	2.48	0.48
1:A:149:ARG:HD2	1:A:150:TYR:N	2.29	0.48
1:B:131:LEU:C	1:B:134:PRO:HD2	2.33	0.48
1:B:202:LEU:HD13	1:B:389:ILE:HG21	1.96	0.48
1:B:331:TYR:N	1:B:331:TYR:CD1	2.81	0.48
1:B:177:ASP:OD1	1:B:381:GLY:CA	2.59	0.47
1:B:280:VAL:HG22	1:B:320:PHE:CD2	2.49	0.47
1:A:494:LEU:HD12	1:A:494:LEU:O	2.14	0.47
1:A:117:LEU:HD23	1:B:115:TYR:HD1	1.79	0.47
1:B:14:GLN:HE21	1:B:14:GLN:CA	2.27	0.47
1:B:7:LEU:HD21	1:B:44:GLN:C	2.35	0.47
1:A:493:ASP:O	1:A:496:GLU:CG	2.62	0.47
1:A:233:THR:HG23	1:A:234:ILE:N	2.30	0.47
1:A:419:LYS:O	1:A:419:LYS:HG2	2.15	0.47
1:A:441:LEU:HD12	1:A:451:GLN:HG2	1.97	0.47
1:A:137:ARG:O	1:A:141:MET:HB2	2.14	0.47
1:A:160:ASN:HD22	1:A:160:ASN:H	1.62	0.47
1:B:94:THR:HG21	1:B:134:PRO:HB3	1.96	0.47
1:B:426:LYS:O	1:B:430:GLU:HG3	2.14	0.47
1:B:8:GLU:CG	1:B:45:LEU:CD2	2.93	0.47
1:B:113:LEU:HD12	1:B:113:LEU:N	2.30	0.47
1:B:213:ASP:HA	1:B:334:VAL:HA	1.96	0.47
1:B:340:LEU:CD2	1:B:341:LEU:N	2.73	0.47
1:B:322:LEU:HD12	1:B:322:LEU:H	1.80	0.47
1:A:192:LEU:HD13	3:A:731:HOH:O	2.13	0.47
1:B:207:PHE:O	1:B:208:LEU:HD23	2.15	0.47
1:A:193:LYS:HD3	1:A:312:PHE:HB3	1.96	0.47
1:B:103:LEU:HD12	1:B:126:SER:OG	2.15	0.47
1:B:331:TYR:N	1:B:331:TYR:HD1	2.13	0.47
1:B:63:ARG:NH2	1:B:65:TYR:OH	2.48	0.47
1:B:74:GLU:O	1:B:78:ASP:HB2	2.14	0.47
1:A:195:MET:HG3	1:A:382:LEU:HD22	1.97	0.46
1:B:130:ASP:OD2	1:B:133:VAL:CG2	2.30	0.46
1:A:96:VAL:HB	1:B:156:TYR:OH	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:244:VAL:O	1:B:249:VAL:CG1	2.63	0.46
1:A:289:LEU:HA	1:A:289:LEU:HD23	1.77	0.46
1:A:160:ASN:HB2	1:A:167:ARG:HH22	1.81	0.46
1:A:309:LEU:CD2	1:A:314:ILE:CD1	2.93	0.46
1:B:273:GLN:O	1:B:322:LEU:HD13	2.16	0.46
1:B:8:GLU:CA	1:B:45:LEU:HD21	2.46	0.46
1:A:479:ARG:NE	1:A:486:GLU:OE2	2.49	0.46
1:A:154:LYS:HE2	1:A:172:TYR:CE2	2.51	0.45
1:A:290:SER:O	1:A:296:LEU:HD21	2.16	0.45
1:B:209:VAL:HB	1:B:318:ILE:HD13	1.98	0.45
1:B:66:SER:N	1:B:69:GLN:NE2	2.60	0.45
1:B:97:PHE:CE1	1:B:125:LEU:HD22	2.51	0.45
1:B:185:MET:HE3	1:B:305:LEU:HB2	1.98	0.45
1:B:282:GLN:CG	1:B:283:LEU:CD2	2.86	0.45
1:A:90:GLU:HB3	1:B:67:PRO:HB3	1.99	0.45
1:A:369:MET:HG3	1:A:370:PHE:N	2.31	0.45
1:B:455:CYS:SG	1:B:463:VAL:HG22	2.56	0.45
1:B:185:MET:CE	1:B:305:LEU:HB2	2.47	0.45
1:A:470:GLU:OE2	1:A:477:LYS:HE3	2.17	0.45
1:A:495:VAL:HG13	1:A:496:GLU:N	2.31	0.45
1:B:80:ILE:HG12	1:B:198:ILE:HG21	1.97	0.45
1:B:24:GLN:C	1:B:25:LYS:CG	2.85	0.45
1:A:124:LEU:N	1:A:124:LEU:CD1	2.80	0.45
1:A:214:ARG:NH1	1:A:328:LEU:C	2.70	0.45
1:A:336:TYR:HE2	3:A:731:HOH:O	2.00	0.45
1:A:440:LEU:CD1	1:A:440:LEU:C	2.85	0.45
1:A:370:PHE:CD1	1:B:56:LEU:CD2	3.00	0.45
1:A:369:MET:CE	1:A:370:PHE:HE2	2.24	0.45
1:A:373:LYS:CD	1:A:375:ARG:HE	2.27	0.45
1:A:448:LEU:CD2	1:A:452:LEU:HD12	2.46	0.45
1:B:411:VAL:CG2	1:B:412:LEU:N	2.80	0.45
1:A:233:THR:O	1:A:236:SER:OG	2.25	0.45
1:A:397:LEU:HD12	1:A:404:ILE:HD13	1.96	0.45
1:B:418:LYS:HA	1:B:445:ASN:ND2	2.31	0.45
1:A:280:VAL:HG12	1:A:320:PHE:CD2	2.52	0.44
1:A:393:VAL:O	1:A:397:LEU:HG	2.17	0.44
1:B:12:LYS:CE	1:B:168:TYR:OH	2.64	0.44
1:B:366:LEU:HA	1:B:369:MET:CG	2.46	0.44
1:B:387:GLU:O	1:B:390:PHE:HB2	2.17	0.44
1:A:467:GLY:CA	1:A:470:GLU:OE1	2.59	0.44
1:B:249:VAL:CG2	1:B:250:LYS:N	2.81	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:335:ILE:HG23	3:B:612:HOH:O	2.18	0.44
1:A:494:LEU:O	1:A:498:ILE:HG13	2.17	0.44
1:B:38:LEU:CD2	1:B:38:LEU:C	2.86	0.44
1:A:73:ARG:HA	1:A:390:PHE:CE1	2.53	0.44
1:B:11:VAL:HG12	1:B:41:LEU:CB	2.44	0.44
1:B:214:ARG:HH11	1:B:332:THR:CB	2.30	0.44
1:A:370:PHE:CD1	1:B:56:LEU:CD1	3.01	0.44
1:A:124:LEU:CD1	1:A:124:LEU:H	2.31	0.44
1:A:369:MET:CE	1:A:370:PHE:CD2	3.01	0.44
1:B:103:LEU:HD22	1:B:129:TYR:HE2	1.82	0.44
1:B:336:TYR:CE2	1:B:360:GLY:C	2.91	0.44
1:B:366:LEU:HD12	1:B:366:LEU:O	2.18	0.44
1:B:7:LEU:HD23	1:B:45:LEU:HA	2.00	0.44
1:B:315:ASP:OD2	1:B:315:ASP:N	2.49	0.44
1:B:68:ARG:NH1	1:B:404:ILE:CD1	2.78	0.44
1:B:70:MET:O	1:B:74:GLU:HG3	2.17	0.44
1:A:448:LEU:HD21	1:A:452:LEU:HD12	2.00	0.43
1:B:14:GLN:HA	1:B:14:GLN:NE2	2.33	0.43
1:A:98:GLU:HB2	1:A:103:LEU:HD11	2.00	0.43
1:B:277:VAL:CG1	1:B:306:PHE:HD1	2.27	0.43
1:A:370:PHE:HD1	1:B:56:LEU:HD21	1.83	0.43
1:B:427:LEU:HD22	1:B:466:ILE:HD11	2.00	0.43
1:A:99:LEU:HD11	1:B:57:LYS:HG3	2.01	0.43
1:B:334:VAL:CG1	1:B:335:ILE:N	2.81	0.43
1:B:90:GLU:O	1:B:149:ARG:HA	2.18	0.43
1:B:371:ASP:OD1	1:B:372:PRO:HD2	2.19	0.43
1:B:479:ARG:NE	1:B:486:GLU:OE2	2.51	0.43
1:A:160:ASN:N	1:A:160:ASN:ND2	2.66	0.43
1:B:130:ASP:OD1	1:B:133:VAL:CG2	2.67	0.43
1:A:420:LEU:CA	3:A:703:HOH:O	2.57	0.43
1:B:213:ASP:OD2	1:B:215:ARG:N	2.48	0.43
1:A:97:PHE:CE1	1:B:62:THR:HG21	2.54	0.43
1:B:357:VAL:O	1:B:385:GLY:N	2.39	0.42
1:A:467:GLY:O	1:A:471:LEU:HB2	2.19	0.42
1:B:282:GLN:HE21	1:B:283:LEU:CD2	2.31	0.42
1:A:408:GLU:CD	1:B:85:LYS:HD3	2.39	0.42
1:B:324:LEU:CD2	1:B:324:LEU:C	2.85	0.42
1:B:235:CYS:O	1:B:238:VAL:HB	2.20	0.42
1:A:339:VAL:HG12	1:A:356:SER:HA	2.01	0.42
1:B:66:SER:H	1:B:69:GLN:HE21	1.59	0.42
1:A:98:GLU:HB2	1:A:103:LEU:CD1	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:192:LEU:HD12	1:B:309:LEU:HD21	2.00	0.42
1:A:139:LEU:HD22	1:A:144:LEU:HB2	2.01	0.42
1:A:412:LEU:HD23	1:A:455:CYS:SG	2.59	0.42
1:B:78:ASP:O	1:B:82:ARG:HG3	2.20	0.42
1:A:99:LEU:HD23	1:A:125:LEU:CD2	2.49	0.42
1:B:367:VAL:HG12	1:B:377:VAL:HG23	2.01	0.42
1:B:37:LYS:O	1:B:41:LEU:HG	2.19	0.42
1:B:36:ALA:HA	1:B:39:LEU:HD13	2.00	0.42
1:A:370:PHE:HE1	1:B:56:LEU:HD21	1.83	0.42
1:A:263:VAL:O	1:A:267:ILE:HG13	2.20	0.41
1:B:143:LYS:HA	1:B:143:LYS:HD2	1.90	0.41
1:B:214:ARG:HD2	1:B:328:LEU:HD11	2.01	0.41
1:B:36:ALA:CA	1:B:39:LEU:HD13	2.50	0.41
1:A:76:VAL:HG22	1:A:390:PHE:HE1	1.83	0.41
1:B:210:LYS:HE2	1:B:321:ASP:HB2	2.02	0.41
1:B:204:ILE:O	1:B:340:LEU:HD11	2.20	0.41
1:B:495:VAL:HG13	1:B:496:GLU:N	2.35	0.41
1:B:130:ASP:CG	1:B:133:VAL:CG2	2.80	0.41
1:B:487:VAL:HG12	1:B:488:ASP:N	2.36	0.41
1:A:296:LEU:HD22	1:A:296:LEU:N	2.36	0.41
1:B:103:LEU:O	1:B:104:MET:HG2	2.20	0.41
1:B:208:LEU:CD1	1:B:341:LEU:HD21	2.51	0.41
1:B:365:GLY:O	1:B:369:MET:SD	2.79	0.41
1:A:94:THR:HG23	1:A:151:HIS:CE1	2.56	0.41
1:A:391:SER:O	1:A:395:GLN:HG3	2.21	0.41
1:A:117:LEU:HA	1:B:117:LEU:HA	2.02	0.41
1:A:64:ASP:CG	1:B:137:ARG:HH22	2.24	0.41
1:B:281:GLU:HA	1:B:281:GLU:OE1	2.21	0.41
1:B:39:LEU:CD1	1:B:39:LEU:N	2.82	0.41
1:A:186:ILE:CG2	1:B:442:TYR:HD1	2.34	0.41
1:A:373:LYS:NZ	1:A:375:ARG:HH21	2.19	0.41
1:A:448:LEU:HD21	1:A:452:LEU:CD1	2.50	0.41
1:A:65:TYR:HA	1:A:69:GLN:NE2	2.35	0.41
1:B:6:ALA:HB2	1:B:69:GLN:OE1	2.21	0.41
1:B:94:THR:CG2	1:B:95:PRO:CD	2.98	0.41
1:A:100:LYS:HE3	1:A:112:LYS:NZ	2.35	0.41
1:A:187:PRO:HG2	1:A:188:ASP:OD1	2.21	0.41
1:A:330:TYR:CE2	1:A:366:LEU:CD1	3.03	0.41
1:A:410:GLN:O	1:A:461:PRO:HG2	2.21	0.41
1:B:442:TYR:O	1:B:443:LYS:HD3	2.20	0.41
1:B:103:LEU:O	1:B:104:MET:SD	2.79	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:139:LEU:HD21	1:B:147:ILE:HG21	2.03	0.41
1:B:306:PHE:HA	1:B:309:LEU:HD12	2.02	0.41
1:A:63:ARG:HD2	1:A:168:TYR:CE1	2.56	0.41
1:B:99:LEU:HD23	1:B:125:LEU:HD23	2.02	0.41
1:B:292:ASN:OD1	1:B:295:ALA:CB	2.69	0.40
1:B:80:ILE:HG21	1:B:174:CYS:SG	2.61	0.40
1:B:94:THR:HG22	1:B:95:PRO:N	2.35	0.40
1:A:77:PHE:HA	1:A:77:PHE:HD1	1.76	0.40
1:A:418:LYS:HG2	1:A:445:ASN:HB3	2.02	0.40
1:B:474:GLY:O	1:B:491:ARG:HG2	2.21	0.40
1:A:223:ILE:HD11	1:A:288:LYS:CB	2.45	0.40
1:A:330:TYR:CD2	1:A:366:LEU:CD1	3.05	0.40
1:B:181:ASN:OD1	1:B:378:PRO:HG2	2.22	0.40
1:A:363:TYR:N	1:A:363:TYR:CD1	2.90	0.40
1:A:70:MET:CB	1:B:91:VAL:HG13	2.52	0.40
1:B:115:TYR:HE2	1:B:157:ARG:C	2.25	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	433/509 (85%)	417 (96%)	15 (4%)	1 (0%)	47	76
1	B	437/509 (86%)	428 (98%)	9 (2%)	0	100	100
All	All	870/1018 (86%)	845 (97%)	24 (3%)	1 (0%)	51	80

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	161	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	
1	A	376/438 (86%)	365 (97%)	11 (3%)	42	73
1	B	356/438 (81%)	348 (98%)	8 (2%)	52	80
All	All	732/876 (84%)	713 (97%)	19 (3%)	46	76

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	97	PHE
1	A	149	ARG
1	A	160	ASN
1	A	188	ASP
1	A	200	SER
1	A	245	SER
1	A	252	GLU
1	A	265	ASP
1	A	280	VAL
1	A	440	LEU
1	A	488	ASP
1	B	13	LEU
1	B	14	GLN
1	B	78	ASP
1	B	102	THR
1	B	149	ARG
1	B	278	SER
1	B	283	LEU
1	B	336	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	69	GLN
1	A	160	ASN
1	A	285	GLN

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Mol	Chain	Res	Type
1	B	23	GLN
1	B	69	GLN
1	B	282	GLN
1	B	294	GLN
1	B	445	ASN
1	B	451	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 ⓘ

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

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.

No monomer is involved in short contacts.

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	A	438/509 (86%)	0.27	24 (5%) 25 19	26, 71, 126, 174	0
1	B	451/509 (88%)	0.85	84 (18%) 1 1	25, 93, 211, 282	0
All	All	889/1018 (87%)	0.56	108 (12%) 4 3	25, 79, 187, 282	0

All (108) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	330	TYR	7.0
1	B	291	GLN	6.8
1	B	297	GLU	6.3
1	B	38	LEU	5.9
1	B	376	LYS	5.5
1	B	233	THR	5.4
1	B	244	VAL	5.1
1	B	19	ARG	5.1
1	B	292	ASN	5.0
1	B	340	LEU	5.0
1	B	289	LEU	4.9
1	B	293	LYS	4.8
1	B	239	ASP	4.8
1	A	372	PRO	4.7
1	B	253	MET	4.6
1	B	217	LEU	4.6
1	B	249	VAL	4.6
1	B	109	GLU	4.5
1	B	369	MET	4.3
1	A	373	LYS	4.2
1	B	110	ASP	4.2
1	B	4	ARG	4.2
1	A	503	GLY	4.1
1	B	298	GLY	3.9

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Mol	Chain	Res	Type	RSRZ
1	A	399	ALA	3.9
1	B	16	GLU	3.9
1	B	270	TYR	3.9
1	B	39	LEU	3.9
1	B	214	ARG	3.9
1	B	254	VAL	3.8
1	B	129	TYR	3.7
1	B	246	TRP	3.7
1	A	490	ARG	3.6
1	A	161	PRO	3.6
1	B	241	LEU	3.6
1	B	7	LEU	3.5
1	B	10	LEU	3.5
1	A	119	ASP	3.5
1	B	375	ARG	3.4
1	B	374	GLY	3.4
1	A	165	ARG	3.3
1	B	13	LEU	3.3
1	B	290	SER	3.2
1	B	23	GLN	3.2
1	B	283	LEU	3.1
1	B	368	GLY	3.0
1	B	400	LEU	3.0
1	B	327	GLY	3.0
1	B	281	GLU	3.0
1	B	8	GLU	3.0
1	B	44	GLN	2.9
1	B	240	LYS	2.9
1	B	18	VAL	2.9
1	B	45	LEU	2.9
1	A	368	GLY	2.8
1	B	500	ARG	2.8
1	B	11	VAL	2.8
1	B	381	GLY	2.8
1	B	25	LYS	2.7
1	B	97	PHE	2.7
1	B	450	ASN	2.7
1	B	318	ILE	2.7
1	B	341	LEU	2.7
1	B	372	PRO	2.7
1	B	267	ILE	2.7
1	B	322	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	32	GLU	2.6
1	B	112	LYS	2.6
1	B	354	VAL	2.6
1	A	113	LEU	2.6
1	B	264	ALA	2.6
1	A	120	GLN	2.5
1	B	27	SER	2.5
1	B	111	SER	2.5
1	B	336	TYR	2.5
1	B	402	GLU	2.5
1	B	245	SER	2.5
1	B	284	LEU	2.4
1	A	375	ARG	2.4
1	A	472	LYS	2.4
1	A	370	PHE	2.4
1	B	6	ALA	2.4
1	A	163	MET	2.4
1	B	185	MET	2.3
1	B	316	ASP	2.3
1	B	250	LYS	2.3
1	B	377	VAL	2.3
1	A	259	LEU	2.3
1	B	103	LEU	2.3
1	B	40	LYS	2.3
1	B	98	GLU	2.2
1	B	251	ASN	2.2
1	A	340	LEU	2.2
1	B	113	LEU	2.2
1	B	273	GLN	2.2
1	B	255	GLY	2.2
1	B	169	ARG	2.1
1	B	95	PRO	2.1
1	A	101	GLU	2.1
1	A	450	ASN	2.1
1	A	468	GLU	2.1
1	A	121	GLY	2.1
1	A	143	LYS	2.0
1	B	295	ALA	2.0
1	A	58	THR	2.0
1	A	353	GLY	2.0
1	B	28	ALA	2.0
1	B	189	ALA	2.0

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](#)

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(\AA^2)	Q<0.9
2	CL	A	601	1/1	0.92	0.17	67,67,67,67	0
2	CL	A	602	1/1	0.98	0.18	63,63,63,63	0

6.5 Other polymers [i](#)

There are no such residues in this entry.